

Fri Jun 21 08:38:25 2002

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OM nucleic - nucleic search, using sw model

Run on: June 20, 2002, 22:13:00 ; Search time 12428.6 Seconds
(without alignments)
2161.914 Million cell updates/sec

Title: US-09-509-234c-50
Perfect score: 1284
Sequence: 1 acactggaattgaagcttt.....tatgaaattacagagttaa 1284

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

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11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

15: em.ba.*

16: em.fun.*

17: em.hum.*

18: em.in.*

19: em.mu.*

20: em.om.*

21: em.or.*

22: em.ov.*

23: em.pat.*

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29: em.vi.*

30: em.htg_hum.*

31: em.htg_inv.*

32: em.htg_other.*

33: em.htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description

1	1284	100.0	1284	6	A97494	A97494 Sequence 50
2	1233	96.0	1254	1	AF099966	AF099966 Staphyloc
3	628	48.9	1343	1	SHV12874	Y12874 Staphylococ
4	626.4	48.8	1343	6	A97496	A97496 Sequence 52
5	626	48.8	1371	6	A97497	A97497 Sequence 53
6	622.6	48.5	1263	1	SSU66880	U66880 Staphylococ
7	622	48.4	1257	1	AF144663	AF144663 Staphyloc
8	613.8	47.8	1283	6	A97490	A97490 Sequence 46
9	610.8	47.6	1263	1	AF145332	AF145332 Staphyloc
10	610.4	47.5	1350	1	SSV12875	Y12875 Staphylococ
11	606.8	47.3	1254	1	AF099964	AF099964 Staphyloc
12	602.2	46.9	3446	1	SASEMA	X17688 S.aureus fa
13	602	46.9	1266	1	AF144662	AF144662 Staphyloc
14	601.6	46.9	1297	6	A97492	A97492 Sequence 48
15	598.8	46.6	1260	1	AF145333	AF145333 Staphyloc
16	597.4	46.5	303750	1	AP003133	AP003133 Staphyloc
17	597.4	46.4	345900	1	AP003362	AP003362 Staphyloc
18	595.8	46.4	1266	1	AF099967	AF099967 Staphyloc
19	595.6	46.4	1295	6	A97488	A97488 Sequence 44
20	594.2	46.3	1305	6	A97484	A97484 Sequence 40
21	588	45.8	1263	1	AF099962	AF099962 Staphyloc
22	588	45.8	1263	1	SHU23711	U23711 Staphylococ
23	585.4	45.6	1263	1	AF144661	AF144661 Staphyloc
24	584.8	45.5	1280	6	A97486	A97486 Sequence 42
25	584.6	45.5	1260	1	AF099963	AF099963 Staphyloc
26	579	45.1	4434	1	AF269697	AF269697 Staphyloc
27	579	45.1	4434	6	AX145015	AX145015 Sequence
28	578.4	45.0	1263	1	AF099965	AF099965 Staphyloc
29	577.4	45.0	1877	1	SEU23713	U23713 Staphylococ
30	574.4	44.7	1257	6	I32344	I32344 Sequence 1
31	554.2	43.2	1179	6	AX141471	AX141471 Sequence
32	537.6	41.9	1328	6	A97445	A97445 Sequence 1
33	346.8	27.0	1805	1	AF093750	AF093750 Staphyloc
34	330.2	25.7	6528	1	SSU66883	U66883 Staphylococ
35	324.4	25.3	1551	1	AF106849	AF106849 Staphyloc
36	324.4	25.3	1551	1	AF106849	AF106849 Staphyloc
37	324.4	25.3	341350	1	AP003137	AP003137 Staphyloc
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39	322.8	25.1	2598	1	AB000222	AB000222 Staphyloc
40	322.4	25.1	2816	1	AF106851	AF106851 Staphyloc
41	322.4	25.1	4140	1	AB015195	AB015195 Staphyloc
42	317.2	24.7	3115	1	AF269316	AF269316 Staphyloc
43	317.2	24.7	3115	6	AX144636	AX144636 Sequence
44	315	24.5	54064	2	AC090968	AC090968 Staphyloc
45	301.2	23.5	1254	6	AX141473	AX141473 Sequence

ALIGNMENTS

RESULT	1	A97494	1284 bp	DNA	linear	PAT 26-JAN-2000
LOCUS	A97494	Sequence 50 from Patent WO9916780.				
DEFINITION	A97494					
ACCESSION	A97494.1	GI:6780840				
VERSION						
KEYWORDS		Staphylococcus sciuri.				
SOURCE		Staphylococcus sciuri				
ORGANISM		Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/staphylococcus group; Staphylococcus.				
REFERENCE		1 (bases 1 to 1284)				
AUTHORS		Gala, J. and Vannuffel, P.				
TITLE		GENERIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS				
JOURNAL		Patent: WO 9916780-A 50 08-APR-1999;				
FEATURES		GALA JEAN LUC (BE); UNIV LOUVAIN (BE)				
source		Location/Qualifiers				
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.4e-183;
Matches 1284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ACACGGAAATTGAAGCTTTTACAAATAAATGCCGTACGCCATTTTACCAAGCAGTA 60
OY 61 gtaattatgaattaaaaacatctgaagctactcaacacattagtaggggtcaagat 120
Db 61 GGTAAATTATGAATTTAAAACATCTGNAAGTACTTCAACACATTGTAGGGGTAAAGAT 120
OY 121 aatcaagcgaagtagtagcgcgcgtctgtcttaacaagtgtaacagttatgaagaatt 180
Db 121 AATCAAGCGAAGTATAGCTGCGTCTGTCTTAAACAAGTACCGATTATGAAGAAATTT 180
OY 181 aattacttactcaataagagagacagtaatgattatgacaacaagaagaacttgtagc 240
Db 181 AATTACTTTACTCAATAGAGAGACAGTAATGATTATGACAAAGAAGACTGTGGAC 240
OY 241 tttctcttaagaagaatcgtagctatttaaaaagtataaaggattatctttagaatc 300
Db 241 TTTTCTTTAAAGAAATCGTAGCTATTTTAAAAGTATTAAGATTTATCTTTAGAAATC 300
OY 301 gatccttactgcatacatcaataagagatcatgagatggaacataataaaatcatcaac 360
Db 301 GATCCTTACTGCGCATATCAATCAAGATCATGATGCGCAATTAATTAATAATCTTTAC 360
OY 361 cgtgatggtttaattaacaatttgaatcatagtagtaagaacacaaaggtctacaact 420
Db 361 CGTGATGGTTTAAATTAACAATTTGATTCATGTAGTTATGAACACACAGSGTTACAACT 420
OY 421 ggttccacccaatcatcaaatagatgagcattctgtaacttgattagaagatgagac 480
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OY 481 gaaagaagcgtatcaagaacatgacagtttaagaagaagaataactcaaaaaagtccaa 540
Db 481 GAAAGAAGCGCTCATCAAGACATGGAAGAGTTTAAAGAAAAAGAAATCTAAAAAGTTCAA 540
OY 541 aaaaatgggttaaggttcgtttctctcaagaatgaaatccgatatccgtaattc 600
Db 541 AAAAATGGGTTAAGGTCGTTTCTATCTTAAGAGTGAATCCCGATTTCCGCAATTT 600
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Db 601 ATGGAAGATACACAGAGAGAAGAAGATTTCACAGATCGGCGGAGATCTTATTAATAA 660
OY 661 agattaaatacttgaataatgtaagaatccttagcatatataagacttgaactac 720
Db 661 AGATTAAATATCTTGAAATATGTAAGATTCCTTTGATATATAGACTTTGAAACTTAC 720
OY 721 attccacaatttgaagaagaacatgaaacatatacaagaatatgcaaaagctga 780
Db 721 ATTCCACAATTGGAAGAAGAACATGAACATATACAAAGAGATATTGCAAAAGCTG 780
OY 781 gatttgaagaagaacacgataatcaaaaaagataataaataagacaacttaaaaa 840

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Db 781 GATTGAAAGAAACCAGTATATCAAAAAAGATTATATAATAGACACTTAAAAACA 840
OY 841 caaagaagaacaaatgaagcctaataatgaagaagacacttcaactaacaagaacatggt 900
Db 841 CAAGAAGACCAATGAGACTTAATTAAGAGACACTTCAACTACAAAGACATGCT 900
OY 901 gatacataccataagacagctggtttcttataatcaatcattgaagtgtatattat 960
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OY 961 gcaagtggttcacagaaatgaatcgttcaacttgcagtgatgataatcgaatgggaa 1020
Db 961 GCAGTGTTATCATGATGAATGAATATGTCATTTCAGGTAGTATTCATTTCAGTGGAA 1020
OY 1021 atgattataacgcgttataatcaacaacttgcacgttataacttcaatgataagcga 1080
Db 1021 ATGATTAAATACCGCTTAGATCAACAATGACCGTTATTAATCTTATGTATGACGGA 1080
OY 1081 gacttccagaagatgcacctgatgttggttgaatttaaatlaaagaagttacaatgca 1140
Db 1081 GACTTCCAGAAGATGCACCTGATGTGGCTTATTAATTTAAAAAGTTTACATGCA 1140
OY 1141 gatgttatgaatataatggttattcgttgaacaaatlaaataaagaacagcgtacaagca 1200
Db 1141 GATGTTATGATATATTTGTTGATTTTCGTTAAACATTAATTAACACGCGTACAAAGCA 1200
OY 1201 tatacaacataaagaaglatlaaanaataatgatttccagtaagaagaattag 1260
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OY 1261 ataatacgaattcacagagttaa 1284
Db 1261 ATAATATGAATTTACAGAGTTAA 1284

RESULT 2
AF099966      1254 bp      DNA      linear      BCT 02-NOV-1998
LOCUS      AF099966
DEFINITION      Staphylococcus sciuri factor essential for methicillin resistance
VERSION      AF099966
KEYWORDS      AF099966.1 GI:3820631
SOURCE      Staphylococcus sciuri.
ORGANISM      Staphylococcus sciuri
REFERENCE      1 (bases 1 to 1254)
AUTHORS      Vanuifel,P., Heusterspreute,M., Bouyer,M., Philippe,M. and Gala
J.-L.
TITLE      Molecular characterization of fema from Staphylococcus hominis,
Staphylococcus saprophyticus and Staphylococcus haemolyticus and
fema-based discrimination of Staphylococcal species
RESOURCES      Res. Microbiol. (1998) In press
AUTHORS      Vanuifel,P., Heusterspreute,M. and Gala,J.-L.
TITLE      Direct Submission
JOURNAL      Submitted (21-OCT-1998) LBCM, UCL, Clos Chapelle-aux Champs
30/3046, Bruxelles 1200, Belgium
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DRGDDFYNNLKAYFENKIPLAIDFETIYPOLEKHEQYKNDIAKAEKDLKKPNQ
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BASE COUNT 506 a 181 c 207 g 360 t
ORIGIN

Query Match 96.0%; Score 1233; DB 1; Length 1254;
Best Local Similarity 100.0%; Pred. No. 6.1e-176;
Matches 1233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 acattggaattgaagcttttacaaaataaaatgcgtagcgagctttttacacaaagcagta 60
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Qy 61 gtaattatgaattaaacacatctgaagtgacttcaacacacatttagtgggtcaaagat 120
Db 82 GSPAATTATGAATTAACAAATCATGAAGTACTTCAACACATTTAGTAGGGTCAAGAT 141
Qy 121 aatcaagtggaattatagctgctgtctgttaacaaagtgaccagttatgaagaaattt 180
Db 142 AATCAAGGTGAAGTATTAGTGGCTGCTGTGTTAACAAAGTGACCAGTTATGAAGAAATTT 201
Qy 181 aattacttttaacataagagaccagtaagtgtatgatcatgaacaaagacattttgac 240
Db 202 ANTACTTTTACTCAATAGAGACCGATGATGGATTATGACAAAGAACTTTGTTGAC 261
Qy 241 tttttttaaagaatactgtagctattttaaagaattataaaggattattcttttagaatc 300
Db 262 TTTTCTTTAAAGAAATCGTGAGCTATTAAAAAGTTATAAGAGATTATCTTTAGATC 321
Qy 301 gatccttacttgccatacaactaagagatcatgatggcaattataaaataatcattcaac 360
Db 322 GATCCTTACTTGCCATATCACTAAGATGATGATGCGCAATATTAATAAATCATTTCAAC 381
Qy 361 cgtgatggtttaataaacaatttgaatcattagttatgaacacaaagcttcaact 420
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Qy 721 attcaacaattagaagaacatgaacaaatacaacaagaagatttgcagaagctgaaaaa 780
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Qy 781 gattagaaaaaaccagcataatacaaaaaagatttaataaataagacaacttaaaacaa 840
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Qy 841 caaagaagaagcaaatgaagctaaatttagaagaagcacttcaactacaagaagaactgtg 900
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Db 1222 TATACAACACTAAAAAAGTATTAAAAAATAA 1254

RESULT 3
SHY12874
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DEFINITION Staphylococcus hominis fema gene.
ACCESSION Y12874
VERSION Y12874.1 GI:2462667
KEYWORDS fema gene.
SOURCE Staphylococcus hominis.
ORGANISM Staphylococcus hominis.
REFERENCE 1 (bases 1 to 1343)
AUTHORS Vannuffel, P.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1343)
AUTHORS Vannuffel, P.
TITLE Direct Submission
JOURNAL Submitted (30-APR-1997) P. Vannuffel, University of Louvain Medical
School, Laboratoire de Genetique Molculaire, UCL-GEMO-5225, Avenue
E. Mounier 52, Brussels, 1200, BELGIUM
FEATURES
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QY 362 gtgatgtttaattaaacattgtaacatcattagttatgaaacacacagcttcacactg 421
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 QY 422 gtccacccaaatataatgaattagatggcattcgtctcattgattgaaagatgagc 481
 Db 506 GCTTTACCCCAATCTTCAATTAATGATTCCTGTTTGTATTAATGCTGGAACACTG 565
 QY 482 aaaaagcgtccatcaagaacatgacagtttaagaagaataactaaaaagttcaaa 541
 Db 566 CTAAACAGCTACTTATATGATGATGATGATGATGATGATGATGATGATGATGAT 625
 QY 542 aaaaagtggttaagattcgtctcattgaaagatgaaatgcgataatccgataat 601
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 QY 602 tggagatactacacagagaagaattcaacgacatcggtgagatgactctatcaata 661
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 Db 806 ATATACAGATTTAAAGCTGAAACGGAATTTAAAGATTTAAAGATTTAAAGATTT 865
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 Db 926 AACAACTGATTTGAAACCAACAAATTAAGATGAAAGCCTGCTGCTGCTGCTGCTG 985
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RESULT 6
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 LOCUS SSU66880
 DEFINITION Staphylococcus simulans fema (fema) gene, complete cds.
 ACCESSION U66880
 VERSION U66880.1 GI:1762961
 KEYWORDS

SOURCE Staphylococcus simulans.
 ORGANISM Staphylococcus simulans
 Bacteria; Firmicutes; Bacillus/Clostridium group;
 Bacillus/Staphylococcus group; Staphylococcus.
 REFERENCE 1 (bases 1 to 1263)
 AUTHORS Thumm, G. and Goetz, F.
 TITLE Studies on polysaccharide processing and characterization of the
 lysostaphin immunity factor (Lif) of Staphylococcus simulans biovar
 staphylophilus
 JOURNAL Mol. Microbiol. 23 (6), 1251-1265 (1997)
 MEDLINE 97260121
 REFERENCE 2 (bases 1 to 1263)
 AUTHORS Thumm, G. and Goetz, F.
 TITLE Direct Submission
 JOURNAL Submitted (13-AUG-1996) Mikrobielle Genetik, Universitaet
 Tuebingen, Waldhauser Strasse 70/8, Tuebingen 72076, Germany
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Query Match 48.5%; Score 622.6; DB 1; Length 1263;
 Best Local Similarity 69.5%; Pred. No. 2e-84;
 Matches 860; Conservative 0; Mismatches 374; Indels 3; Gaps 1;

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 Db 142 AAAGATNCAATGTCATTTGACGATGTTTACTTACAGCTGCTGCTGCTGCTGCTGCT 201
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 QY 241 ttttctttaaagaacatcgtagcattttaaagaatgataatgataatgataatgata 300
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 QY 361 cgtgatgtttaataaacaattgataatcattagttatgacacacacagcttcacact 420

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 Db 508 GATGTTTAAACGATATGATATTAGTAAAGTAATCTAAAAAGTACAAAAAAT 567
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 Db 868 TTAGCAAGCTATCAACAGAAATATGATGAAGCAACACTTGACGTAACATGGCAAT 927
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 Db 1228 ACGACATTAAGAAATTAATTAATAAATA 1257

RESULT 8
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 LOCUS Sequence 46 from Patent WO9916780.
 DEFINITION A97490
 ACCESSION A97490
 VERSION A97490.1 GI:6780836
 KEYWORDS
 SOURCE
 ORGANISM
 Staphylococcus capitis.
 Staphylococcus capitis
 Bacteria; Firmicutes; Bacillus/Clostridium group;
 Bacillus/Staphylococcus group; Staphylococcus.
 1 (bases 1 to 1283)
 AUTHORS
 Galia, J. and Vanunite, P.
 GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND
 DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS
 Patent: WO 9916780-A 46 08-APR-1999;
 JOURNAL
 GALIA JEAN LUC (BE); UNIV LOUVAIN (BE)
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 Location/Qualifiers

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BASE COUNT 484 a 170 c 224 g 405 t
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Query Match 47.8%; Score 613.8; DB 6; Length 1283;
 Best Local Similarity 68.6%; Pred. No. 4.1e-83;
 Matches 879; Conservative 0; Mismatches 392; Indels 10; Gaps 2;

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 QY 67 tatgataaaaacatctgaagattcttcaacacatttagtaggggtcaagaatacaa 126
 Db 70 TATGAACTTAAAGTTGCTGAAGGTACGATTCACATCTCTAGAAATTAATAATGAC 129
 QY 127 ggtgaagatattagctgctgctgttaacaagtgaccagtttagaagaattatcac 186
 Db 130 AACCAAGATTTGACGAGATTTTAACTGCTGATGATGATGATGATGATGATGAT 189
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 Db 250 TTTAATGAATTAAGTAATATGTAATAAAGCATTAATGCTTTATCAAGATGACCT 309
 QY 307 tacttgccatcaactaagaagatcatgagatgacatataaataatcatcaacggtat 366
 Db 310 TATCTTCTTATCAATCTTAAATCATGACGGTGAATTAATGGAATGCTGGCATGAT 369
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 QY 427 caccacaatacaataatagatggcattcgtactgattagaagaatgagcgaagaag 486
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Best Local Similarity 68.9%; Pred. NO. 1.1e-82;
Matches 853; Conservative 0; Mismatches 382; Indels 3; Gaps 1

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Qy	62	gtaattatgaattaaaacatctgaagtgacctccaacacatttagtaggggtccaagata	121
Db	83	GGAACATGCAATTAATAATTGCCAAGAAGTGACAGAACACACATTTTAGTAGTATAAAAAATA	142
Qy	122	atcaaggtgaagtattagtcgctgtctttaacaagtgaccagttatgaagaatta	181
Db	143	ATGAAAATGAAGTATTTCGACGATGTTTTAATACCTGCTGTACCTGTATAGAAACTACTTTA	202
Qy	182	attacttttactcaaatagaggccagtagtgattatgaaccaacaagaaccttgttgcact	241
Db	203	AATATTTTTATCTAACCGTGGACCGGTAAATAGATTTGAAATAAAGAAACTTGTGCATT	262
Qy	242	ttttctttaaagaatcgtgagctatttaaagaagtataaaggattattctttagaactcg	301
Db	263	ACTTCITTAATGAAATATCAAAATATGTAAGAAACATCGTCGCTTTATTTAAGAGTTG	322
Qy	302	atccttacttgcoatatcaoctaagaagatacatgatggcaattataaaaaatcatccaoc	361
Db	323	ATCCATATTTACCCTTACCAATATCGAATCATGATGGTGATGATTAGAGANNTGCGAGC	382
Qy	362	gtgatgtttaattaaacaatttgaatcattgatttatgaaccaccaaggtctcacactg	421
Db	383	ATGATTTGGATCTTCGTATAGATGAAGCAATTTAGTTTAAACACCAAGGTTCTTAACTG	442
Qy	422	gtttcccaccaatcacatcaaatatagatggcattctgacttattagaagaagtatggacg	481
Db	443	GTTTTTGATCCAGTCGTTCAAATPAAGATTTCACTCAGTATTAGAGTAAAGATTAAGACTG	502
Qy	482	aaagacgcctcatcaagaacatggacgctttagaanaaagaataactaaaaagttccaaa	541
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Qy	542	aaaatgggtttaaagttcgttttctatcaaagatgaatgccgatattccogtcaatta	601
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Qy	602	tggaaagtactacagagaagaagaatttcaacgatcgtggcgatgactcttattacaata	661
Db	623	TGAAAGATACGCTCTGAAACTTAAAGCTTTGGAAGATAGAGACGATAGTTTTCTATTATACT	682
Qy	662	gattaaaaactcttggaaaa--tgtaagattcccttagcatatatagactttgaaactt	718
Db	683	GTTTGGAAATTAATAAATAATCGTGTCTGGTACCGTTGGCATATATGGATTTTGTATGAAT	742
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RESULT	9	
AF145332		
LOCUS	1263 bp	DNA linear
DEFINITION	Staphylococcus gallinarum methicillin resistance protein FemA (femA) gene, complete cds.	
ACCESSION	AF145332	
VERSION	1	GI:5565906
KEYWORDS		
SOURCE	Staphylococcus gallinarum.	
ORGANISM	Staphylococcus gallinarum	
	Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus.	
REFERENCE	1 (bases 1 to 1263)	
AUTHORS	Vannuffel,P., Heusterspreute,M. and Gala,J.-L.	
TITLE	Cloning and characterization of femA genes from Staphylococci	
JOURNAL	unpublished	
REFERENCE	2 (bases 1 to 1263)	
AUTHORS	Vannuffel,P., Heusterspreute,M. and Gala,J.-L.	
TITLE	Direct Submission	
JOURNAL	Submitted (23-APR-1999) LBCM, UCL 3046, Clos Chapelle Aux Champs, 30, Bruxelles 1200, Belgium	
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DB	87	CAAAAGAGTTCGGTCATTTCAGGATTAATGCCAATAGCATTTTACGCCAAGGTTG	146						
QY	62	gtattatgaatlaaacaacatcgtgaagcttcaacacattagtaggggtcaagata	121						
DB	147	GAATTAATGAATTTGAAATTTCCAGAAAGTCAAGAAACACACCTAGTATTAAGAATA	206						
QY	122	atcaagtgtaagctatagctgctgctgttctgtlaacaagtgatccagttatgaagaatta	181						
DB	207	ATGTAATAGAGTAATTCGACATGTTACTTTCACCTGCTTCCTGTTATTAATTCCTCA	266						
QY	182	attacttactaacaatagaggaccagtaatgattatgatgacaacaagaactggtact	241						
DB	267	AGTATTTTATTCATATGAGAGTCGACGTCAATTAATTTTAAATTAAGAACCTGTCAT	326						
QY	242	tttctcttaagaacatcgtagcgtatttaaaagcttataaagaatttctttagaatcg	301						
DB	327	ACTTCTTAACGAATTTAGCAAAATATGTGAAAAAACAATATCCCTTATTTTCAGAGT	386						
QY	302	atccttacttcgcatacactaagaagatcatgcatggtcaataataaaatcatcaacc	361						
DB	387	ATCCGTATCTGTTTATCAATTCGTATATCATGATGAGTGAAGTATTATACCAATCGGGT	446						
QY	362	gtgaagtttaattaaacaattgtaataataggtatgataacccaaggttcaacgt	421						
DB	447	ACGATGTGATTTTGTATTAAGAAAGCAACACCGGTTTAAAGCTGAAAGGTTTTTAACTG	506						
QY	422	gtttccaccaatcatcaaatatgataigcatcttgacttggttttagaagtagaacg	481						
DB	507	GCTTTGACCCAAATCTTCAATTAAGATTCCTCTGTTTAAAGTTTACGTGAAACCTG	566						
QY	482	aaaagaagcctatcaagaacatgtagcagtttaagaanaaagaataactaaagaat	541						
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QY	542	aaaatggtttaaagtcgttttctatctaaagatgaatgcccagatattcgccaatta	601						
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Page 13

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RESULT 14
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LOCUS Sequence 48 from Patent WO9916780.
DEFINITION A97492
ACCESSION A97492.1 GI:6780838
VERSION A97492.1 GI:6780838
KEYWORDS
SOURCE
ORGANISM
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Bacteria; Firmicutes; Bacillus/Clostridium group;
Staphylococcus schleiferi.
Bacillus/Staphylococcus group; Staphylococcus.
REFERENCE
1 (bases 1 to 1297)
AUTHORS
Gala,J. and Vannuffel,P.
GENERIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND
TITLES
DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS
JOURNAL
Patent: WO 9916780-A 48 08-APR-1999;
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LDLKDRTAKVNDMSLRKRNKTKVQKNGVRFLEDELPIFRSFDNDSKDEP
DREDSFYNNRLKYKVRVPLAYMDFEAYIDELKSEREVLSDINKALDKARPEN
KRAYKNENLEKOLIANOOKIDEAKSLOBOHGNELPISAAFFVNVYVYVAGTSN
EFHFAGSFAIQWKNYATDNDIRYNEFYISGDFSEAEADAGVVKFKKGFNADVE
YVGFDFKPKNPKMYKIYIMVGLKDKK"

BASE COUNT 497 a 156 c 233 g 374 t
ORIGIN

Query Match 46.6%; Score 598.8; DB 1; Length 1360;
Best Local Similarity 68.4%; Pred. No. 7.2e-81;
Matches 844; Conservative 0; Mismatches 387; Indels 3; Gaps 1;

Qy 2 cactggaattgaagctttacaaataaaatgcgcagcgcattttcacacagcagtag 61
Db 23 CAAAAGAGTTGGTGCATTTGTTGACCATATGCCAACAGTCATTTTACACAAATGGTAG 82
Qy 62 gtaattatgaattaaacacatctgaaggtacttcaacacatttagtaggggccaagata 121
Db 83 GCATTTAGTGTGAAATTCGAGAGGTACAGAAACACATTTGGTAGCGGTGAAATA 142
Qy 122 atcaagtggaagtattagcgcggtctgtttaaagaagtgtaaccagttatgaagaattta 181
Db 143 ATGAAATCAAGTTATAGACGCTGCTTATTAACCTGCTGTACCGGTTATGAAATATTC 202
Qy 182 attacttttactcaaaatagagaccaggaattgattgattgacacaaagaactgttgact 241
Db 203 AATATTTTATACAAATCGTGACCGGTGATTGATTGCGAAATTAAGACACTGTGCCATT 262
Qy 242 tttctttaacaaatcgtagctattttaaagaagttataaaagattattctttagaatg 301
Db 263 ATTTTTCATGAATTAATAATCTGTAATAATGTAATAATGTAATAATGTAATAATGTA 322
Qy 302 atccttacttgccatcaactaaagagatcatgtaggcaatattataaaatcatcacc 361
Db 323 ATCCATACCTTGCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 382
Qy 362 gtgatgtttaaataaacaattgaatcattgattgacacacacacacacacacacacacac 421
Db 383 ATGATTTGGATTTTCGATAAAATGAAGCAACTTGGATTAATCAATCAATCAATCAATCA 442
Qy 422 gtccac 481
Db 443 GTTTTGATCCAAATTTCAATTAAGATTCACCTCTGTGTTTATAGATTTTAAAGATAAG 502
Qy 482 aaagacgctcatcaagaacatgagacgtttaaagaacacacacacacacacacacacac 541
Db 503 CAAAAGATGCTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 562
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Db 563 AAAATGGTGTGAAGTCAGATTTTAGCGGAAGATGAATTAACCAATTTTCGTTTCGTTT 622
Qy 602 tgaagatcactacagagaagaagatttcaacgacgtggtgacgtggtgacgtggtgacgt 661
Db 623 TGAAGATGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGAT 682
Qy 662 gattaaataactttgaaaa---tgtaagattcccttagcatatatagactttgaaactt 718
Db 683 GACTGAAGTATTATAAGAATCGTGTATTAGTGCCATTATGATGATTTTGAAGCAT 742
Qy 719 acattcccaattagaaaaaagaacatgaacatacaacaagaattatgcgaagctgaaa 778
Db 743 ACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 802
Qy 779 agatttagaaaaaagaacacagataatcaaaaaaacgatttaataaaatagacaacttaaac 838
Db 803 AAGATATAGCAAAACGTCAGAAAAATAAAAGCATATAATAAAAAAGAAAAATTTAGAAA 862
Qy 839 acaaaagagaacaaatgaagctaaatttagaagaagacacttcaactacaacaagaacatg 898

Db 850 CTAGAGCGAATCAAGCTAAATAAAGAGCAGAAACATTCGAATTTAAACACCGGTGAC 909
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Qy 964 ggtgttcacgaatgaatcgtcacttgcaggtaggtattgcaattcagtggaatg 1023
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Qy 1084 ttctcagagatgacactgattggtcggtattataattaaagaagttacaatgcagat 1143
Db 1090 TTTTCAAGATGCAAGAGTGCAGGTGCTGATTAATTAATAAGGCTATATATGAGAA 1149
Qy 1144 gttatgaatatattggtattgtttaaaccacattataaccacagcgtcaaaagcatat 1203
Db 1150 GTAATAGATATGTCGGTATTATTAGCCTATATAACAAACCTGCTATACAGTCTAC 1209
Qy 1204 acaacactaa-----aaaaagattataaaataataaccacagcgtcaaaagcatat 1256
Db 1210 TTAATAATTAAGCAATTAAGAGCAAGATAAAGATATAGATATAGCAAGAGAGGGA 1269
Qy 1257 ttaataatatgaatttaccagagttaa 1284
Db 1270 TTTATGTTGATGAATTTACAGAGTTAA 1297

RESULT 15
AF145333 1260 bp DNA linear BCT 22-JUL-1999
LOCUS
DEFINITION Staphylococcus cohnii subsp. urealyticum methicillin resistance
protein Fema (fema) gene, complete cds.
ACCESSION AF145333
VERSION AF145333.1 GI:5565908
KEYWORDS
SOURCE
ORGANISM Staphylococcus cohnii subsp. urealyticus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
REFERENCE 1 (bases 1 to 1260)
Vannuffel, P., Heusterspreute, M. and Gala, J.-L.
Cloning and characterization of femA genes from Staphylococci
species
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1260)
Vannuffel, P., Heusterspreute, M. and Gala, J.-L.
Direct Submission
TITLE Submitted (23-Apr-1999) LBCM, UCL 3046, Clos Chapelle Aux Champs,
30, Bruxelles 1200, Belgium
FEATURES
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/strain="ATCC49330"
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/db_xref="taxon:94138"
/clone="pfem17"
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1..1260
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side chain of the peptidoglycan"
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/transl_table=11
/product="methicillin resistance protein Fema"
/protein_id="AAD45259.1"
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      923  GTATGATTTACCAATTTCAGCAGCATCTCTTATGCTCAATCCATACGAGTAGTGATT 982
QY      959  atgcaggtggttcacgaatgaatcgcacttcaggttagttatgcattcagtg99 1018
      983  ATCGGGAGGAACATCTAACGAGTTAGACATTGCGAGAGCTATGCAATACAAATGA 1042
QY      1019  aatgattaaatcgcgttagatcacacattgaccgttaacttctatggtatcagcg 1078
      1043  AATGTATTATATGCAATGCAATGATATATGATATGATATGATATGATATGATATG 1102
QY      1079  gaagactctcagaaatgacacctgattgtggttataatataaaaggttacaatg 1138
      1103  GTGATTTTCAGAGAGAGACAGAGATGCGAGTGTGTAAGTTTAAAAAGGATTCAACG 1162
QY      1139  cagaatgttatgaatatattggtgatttgcgttaaaccaattataaacacagcgta 1198
      1163  CTGATGTAGTTGAATATGTTGTTGTTTATTAACCAATCATATAGCCATATGTA 1222
QY      1199  catatacaacactaaaaaaglatataaaaaata 1232
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Db

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Search completed: June 20, 2002, 22:13:15
 Job time: 36605 sec

ALIGNMENTS

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22: /SIDSI/cgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
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24: /SIDSI/cgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

SUMMARY

Result No.	Query			ID	Description
	Score	Match	Length		
1	1284	100.0	1284	20 AAX37803	Staphylococcus sci
2	626	48.8	1371	20 AAX37805	Staphylococcus sap
3	617.6	48.1	1342	20 AAX37804	Staphylococcus hom
4	613.8	47.8	1283	20 AAX37801	Staphylococcus cap
5	601.6	46.9	1237	20 AAX37802	Staphylococcus sch
6	595.6	46.4	1295	20 AAX37800	Staphylococcus xyl
7	594.2	46.3	1305	20 AAX37798	Staphylococcus hae
8	584.8	45.5	1280	20 AAX37799	Staphylococcus lug
8	579	45.1	4434	22 RAH54373	S. epidermidis gen

PI Gala J. Vannuffel P;
 XX WPI: 1999-287521/24.
 DR P-PSDB: AAT08220.
 XX
 PT New Staphylococcus-specific oligonucleotides

XX Claim 25; Fig 11a-D; 48pp; English.

XX This invention describes novel Staphylococcus-specific oligonucleotides
 CC based on the consensus fema nucleotide sequence which are used to
 CC develop products for the identification, detection and therapy of
 CC infections. The oligonucleotides can be used for the genetic
 CC amplification, the identification and/or quantification of various fema
 CC sequences which are specific to known or unknown Staphylococci species.
 CC Since the fema sequence is similar to the femB sequence, the
 CC oligonucleotides can also be used for the molecular genotyping of femB
 CC genes of different Staphylococci species or other gram-positive bacteria.
 CC The fema nucleic acids can also be used in therapeutic applications.
 CC They can also be used to identify inhibitors, e.g. antibodies or
 CC antisense oligonucleotides, for blocking expression of the fema
 CC nucleotide sequences. They can also be used for producing vaccines
 CC against Staphylococci infections.

XX Sequence 1284 BP; 518 A; 181 C; 215 G; 370 T; 0 other;

Query Match 100.0%; Score 1284; DB 20; Length 1284;
 Best Local Similarity 100.0%; Pred. No. 2,5e-220;
 Matches 1284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 acacgcgaattggaagcttttacaataaatccgcgaagcgagattttacacgaacagta 60
 QY 61 ggttaattgaattaaataatctggaagttacttacaacatttagtgaggtcaaat 120
 DB 61 ggttaattgaattaaataatctggaagttacttacaacatttagtgaggtcaaat 120
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 DB 121 aatcaagtggaagtagtagtgcgtctgttaacaagtgtaaccagtttgaagaatt 180
 QY 121 aatcaagtggaagtagtagtgcgtctgttaacaagtgtaaccagtttgaagaatt 180
 DB 121 aatcaagtggaagtagtagtgcgtctgttaacaagtgtaaccagtttgaagaatt 180
 QY 181 aatcaagtggaagtagtagtgcgtctgttaacaagtgtaaccagtttgaagaatt 180
 DB 181 aatcaagtggaagtagtagtgcgtctgttaacaagtgtaaccagtttgaagaatt 180
 QY 181 aatcaagtggaagtagtagtgcgtctgttaacaagtgtaaccagtttgaagaatt 180
 DB 181 aatcaagtggaagtagtagtgcgtctgttaacaagtgtaaccagtttgaagaatt 180
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 DB 241 ttttctttaaagaatcgtgagctatttaagaagtataaaggattattcttgaatc 300
 QY 241 ttttctttaaagaatcgtgagctatttaagaagtataaaggattattcttgaatc 300
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 DB 421 ggtttccacccaatacatcaattagatgagcttctgtacttgatttagaagatgagac 480
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 DB 421 ggtttccacccaatacatcaattagatgagcttctgtacttgatttagaagatgagac 480
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 QY 901 gatacattaccaatagacgctggtttcttattatcaattgaagttgatatat 960
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 DB 1201 tatcaacacataaaaagattataaaaataatgattttcaagtaagagagatttag 1260
 QY 1261 ataataagaatttacaagttaa 1284
 DB 1261 ataataagaatttacaagttaa 1284

RESULT 2

AAK37805 standard; DNA: 1371 BP.

AAK37805;

09-JUL-1999 (first entry)

Staphylococcus saprophyticus Fema DNA.

Fema: identification; detection; therapy; infection; femB; amplification; genotyping; gram-positive bacteria; vaccine; ss.

Staphylococcus saprophyticus.

Key Location/Qualifiers

FT CDS 64..1326 /tag= a /product= "Fema"

W0916780-A2.

08-APR-1999.

28-SEP-1998; 98MO-BE00141.

PP 26-SEP-1997: 97EP-0870146.

XX (BENA-) BELGIAN MIN NAT DEFENCE.
PA (UNIV-) UNIV CATHOLIQUE LOUVAIN.

PA (UYLO-) UNIV CATHOLIQUE LOUVAIN.

XX Gala J. Vannuffel P;

XX
DP
WPT: 1999-287521/24.

P-PSDB: AAY08222;

XX new: staphylococcus-specific oligonucleotides

11 non-conf-1
.XX
20. F10 13. 48pp: English.

XX This invention describes novel *Staphylococcus*-specific oligonucleotides
CC based on the consensus femA nucleotide sequence which are used to
CC develop products for the identification, detection and therapy of
CC infections. The oligonucleotides can be used for the genetic
CC amplification, the identification and/or quantification of various femA
CC sequences which are specific to known or unknown *Staphylococci* species.
CC Since the femA sequence is similar to the femB sequence, the
CC oligonucleotides can also be used for the molecular genotyping of femB
CC genes of different *Staphylococci* species or other gram-positive bacteria.
CC The femA nucleic acids can also be used in therapeutic applications.
CC They can also be used to identify inhibitors, e.g. antibodies or
CC antisense oligonucleotides, for blocking expression of the femA
CC nucleotide sequences. They can also be used for producing vaccines
CC against *Staphylococci* infections.

XX 1371 BP; 545 A; 155 C; 248 G; 423 T; 0 other;

Query Match 48.8%; Score 626; DB 20; Length 1371;
Best Local Similarity 69.0%; Pred. No. 5.3e-103;
Matches 887; Conservative 0; Mismatches 395; Indels 4; Gaps 2;

QY	2	cactggaatttgaaagcttttacaataaaatgcgtacgcgttttttaccacgaagctag	61
Db	86	caaaagagtcgtgcattctacgggacaaatgcgaatagctattttacgcgaatgggtg	145
QY	62	gtaattatgaataaaaacactcgaaggtacttcaacacatttagtaggggtcacaagata	121
Db	146	gaaattatgaattgaaattgcgaaagtcagaaacacacctagtaggtattaagaata	205
QY	122	atcaaggtgaagtattagtcgtgctgtttacaagtgtaaccagttatgagaataatta	181
Db	206	atgataatgaagtaattgcagctgtttacttcacggtctcctgtctgaaattcttca	265
QY	182	atctactttactcaaatagagccagctaagtattgattgacaaacaagaacttggtact	241
Db	266	agtattttttccaatagaggtccagctcagtagatttgaaaaataagaacactgcacatt	325
QY	242	ttttctttaagaagaaactcgtgagctattttaaaagttataaaggattattctttagaatcg	301
Db	326	actcttttcaacgaattagcaaaataatgtaaaaaacataaagtcctttatttcagtagt	385
QY	302	atccttacttgcctatcaactcaagagatcatgatggcaataattaaaaaatcattcaacc	361
Db	386	atccttatctgcttcaataatcgtaatcatgatggtgaagtattagcaaatgcgggttc	445
QY	362	gtgatgggtttaaataacaatttgaatcatttaggtttatgaaccacgaagctttcacagt	421
Db	446	acgattggtattttgataaaatgaacacactcgggtattgaagcatgaaggttttttaactg	505
QY	422	gtttccaccocaatcacataaattagatggcattctcgttatttagtaagaagtatggagcg	481
Db	506	gctttgacccaatcttccaataaagattccattctgttttagatttagctgggaaaaactg	565
QY	482	aaaagcgtcatcaagaacatggacagtttaagaanaagaataactcaaaaagtccaag	541
Db	566	ctaaagacgctacttaatgggtatggatgttttacgttaaagcaatactcaaaaagtacaga	625
QY	542	aaaatgggtgttaaaggttcgttttctctatcaagaatgaataatgcgttcattcgtcaatta	601

Sequence 1342 BP; 544 A; 161 C; 217 G; 420 T; 0 other;

Best Local Similarity	0.99	2
Matches	860;	
Conservative	0;	
Mismatches	364;	
Indels	4;	
Gaps	2	

Db 1290 acaacacttaaaaaattaaaaagagat 1317

AAX37801 standard; DNA; 1283 BP.

DT 09-JUL-1999 (first entry)

XX femb: identification: therapy; infection; femb;

KW FemA; identification; detection; vaccine; ss-
KW amonification; gram-positive bacteria; vaccine; ss-

Staphylococcus capitis.

Key	Location/Qualifiers
AA	
FH	

	/*tag=
CDS	
ET	
ET	

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/notes= "partial sequence, no start or stop codon

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Key	Location/Qualifiers
XX FH Key	1..1297
XX FT CDS	/*tag= a
XX FT	/product= "FemA"
XX FT	/note= "partial sequence, no start or stop codon"
XX PN	W09916780-A2.
XX PD	08-APR-1999.
XX PF	28-SEP-1998; 98NO-BE00141.
XX PR	26-SEP-1997; 97EP-0870146.
XX PA	(BENA-) BELGIAN MIN NAT DEFENCE. (UTLO-) UNIV CATHOLIQUE LOUVAIN.
XX PI	Gala J, Vannuffel P;
XX DR	WPI; 1999-287521/24.
XX DR	P-PSDB; AA08219.
XX PT	New Staphylococcus-specific oligonucleotides
XX PS	Claim 23; Fig 10a-b; 48pp: English.
XX CC	This invention describes novel Staphylococcus-specific oligonucleotides based on the consensus fema nucleotide sequence which are used to develop products for the identification, detection and therapy of infections. The oligonucleotides can be used for the genetic amplification, the identification and/or quantification of various fema sequences which are specific to known or unknown Staphylococci species. Since the fema sequence is similar to the femB sequence, the oligonucleotides can also be used for the molecular genotyping of femB genes of different Staphylococci species or other gram-positive bacteria. The fema nucleic acids can also be used in therapeutic applications. CC They can also be used to identify inhibitors, e.g. antibodies or antisense oligonucleotides, for blocking expression of the fema nucleic acid sequences. They can also be used for producing vaccines against Staphylococci infections.
XX SQ	Sequence 1297 BP; 495 A; 184 C; 249 G; 369 T; 0 other;
Query Match	46.9%; Score 601.6; DB 20; Length 1297;
Best Local Similarity	67.9%; Pred. NO. 1.2e-98;
Matches 874; Conservative	0; Mismatches 404; Indels 10; Gaps 2
QY 7	gaattgaagctttcaataataatgcgtacgacgcatltaacacagcagtagtaat 66
DB 10	gaattggtggtttcagatcaatgaatgcctatagccatttcaacgcaatgvtgagac 69
QY 67	tatgattaaacaacatcgaagcttaacacacattagtaggggtcaagaatacaa 126
DB 70	taagaattaaaggtctgaaggttgaagaacacatcttgcgcattaaagtaacaac 129
QY 127	ggtgaagattagctgcgtcgtctgttaacaagtgatccagttatgaagaatttaac 186
DB 130	aataacgtaacacagagaatgtttactgcgcagcagtgccagtaatgaagttttaaat 189
QY 187	ttttactcaaatagagaccagtaatgtattatgacaacaaagaagactgttgactttc 246
DB 190	ttttattcaaacgcgacacagttcatggtacacgaataaagaagcttcgttcaattc 249
QY 247	tttaagaagaatcgcgagcttttaaaaaggtatataaagattatcttttaagaatgc 306
DB 250	tttaagaagacttcaaaaatglttaagaataatcacgcattgtatttgaagtagacc 309
QY 307	tacttgcatacaacaaagaatgatgtgccaattataaaaatcatcctaaccgtgat 366
DB 310	tatttaccacatgtttaaagcgaacacatgatgtgtaaggttgaagaatgacgagtgac 369

[illegible]

Fri Jun 21 08:38:26 2002

DE XX Staphylococcus xylosus FemA DNA.
KW FemA; identification; detection; therapy; infection; femB;
KW amplification; genotyping; gram-positive bacteria; vaccine; ss.
XX
OS Staphylococcus xylosus.
XX
XX Key Location/Qualifiers
XX 1.1295
FT CDS /tag= a "FemA"
FT /product= "FemA"
FT /note= "partial sequence, no start or stop codon"
XX
XX W09916780-A2.
XX
XX 08-APR-1999.
XX 28-SEP-1998; 98MO-BE00141.
XX 26-SEP-1997; 97EP-0870146.
XX (BENA-) BELGIAN MIN NAT DEFENCE.
XX (UYLO-) UNIV CATHOLIQUE LOUVAIN.
XX Gala J, Vannuffel P;
XX WPI; 1999-287521/24.
XX P-PSDB; AAY08217.
XX
XX New Staphylococcus-specific oligonucleotides
XX Claim 19; Fig 8a-b; 48pp; English.
XX
XX This invention describes novel Staphylococcus-specific oligonucleotides
XX based on the consensus femA nucleotide sequence which are used to
XX develop products for the identification, detection and therapy of
XX infections. The oligonucleotides can be used for the genetic
XX amplification. The identification and/or quantification of various femA
XX sequences which are specific to known or unknown Staphylococci species.
XX Since the femA sequence is similar to the femB sequence, the
XX oligonucleotides can also be used for the molecular genotyping of femB
XX genes of different Staphylococci species or other gram-positive bacteria.
XX The femA nucleic acids can also be used in therapeutic applications.
XX They can also be used to identify inhibitors, e.g. antibodies or
XX antisense oligonucleotides, for blocking expression of the femA
XX nucleotide sequences. They can also be used for producing vaccines
XX against Staphylococci infections.
XX
XX Sequence 1295 BP; 511.A; 156 C; 243 G; 385 T; 0 other;
SQ

Query Match 46.4%; Score 595.6; DB 20; Length 1295;
Best Local Similarity 67.7%; Pred. No. 1.4e-97;
Matches 866; Conservative 0; Mismatches 409; Indels 5; Gaps 2;
QY 10 ttgaaagctttacaaaataaaatccgtacgcattttacacaaagcagtagtaattat 69
DB 13 ttgggtgatttcagataaaatgccaaatagcatttcacgcaaatggtaggaattat 72
QY 70 gaataaaacactcgaaggtacttcaacacatttagtaggggtcacaagataatcaaggt 129
DB 73 gaattgaaattgcagaagtagtcaacacatttagtaggggtcacaagataatgataat 132
QY 130 gaatttagtagctgctgtctgttaacaaagtgtaccaggtatgaagaaatttaattacttt 189
DB 133 gaagtcactgcagctgtgttttaactgcagtcaccagtagtaaaattcttaagtatttt 192
QY 190 tactcaatagagaccagtagtaattgattgatacaacaagaactgtgtgactttttcttt 249
DB 193 tataataagaggtccggttatagattttgaaataaagaattagtgctattcttttc 252
QY 250 aaagaatacgtgagctatttaaaaggtttataaaggtatttcttttagatcgatccttac 309

DB 253 aatgaactatctaaatgtgaaaaaacataatgcgctttatttattaaaggtgacoccttat 312
QY 310 ttgcatatcaactaaagatcatgatggcaataataaaaaatcattcaocogtgatggt 369
DB 313 ttgcatatcaactaaacgttaactcatgatgtgggtattggaaaatcgaggacatgattgg 372
QY 370 ttaattaaacaatttgaatcattagttatgaacacacacaggtcttcaactgtttccac 429
DB 373 atttcgataaaatgaacgagcttgataaaacacacaggtatttttaactgtttcgat 432
QY 430 ccaatcacataaattagatggcattctgtactgtatttagaaagtgtgacgaaagacg 489
DB 433 tcaattatcaaatagttgctccactgtactgtgatttagtagtaaaactgctaaagat 492
QY 490 ctcatcaagaacatgacagtttaagaagaaagaaataactaaaaagttcaaaaaaatggt 549
DB 493 gtactaaatggatggatagtttaacgttaaacgttaataaaaaagttacaaaaaatggc 552
QY 550 gttaaagttcgttttctctataaagatgaatgcgataattccgtcaatttatggaagat 609
DB 553 gtgaagtagaagttcttaaggaagatgagttgccaaattttccgttccattcatggaagat 612
QY 610 actacagagaagaagatttcaacgacgtgcgagatgacttctattacatagattaaaa 669
DB 613 acatcgaaactaaagacttgaagtagagacgtggttttactacaatagattaaagg 672
QY 670 tactttgaaaaat---gtaagattccttttagcatatagactttgaaacttaccatcca 726
DB 673 tattataaagtcgctatttagtaccctctagcttattatgattgaattgaattatgaa 732
QY 727 caattgaaaaagacatgaacatacaacaaagattgtgcaaaagctgaaaaagatttta 786
DB 733 gaattgcaagctgaacgtgaggtgttaagcaagatatcaataaagcagtaaaaaagatac 792
QY 787 gaaaagaacacagatatacaaaaaacgatttaataaataagacaacttaaaacacaaaga 846
DB 793 gagaaaagactgaaaaataaaaaagcataataaaaaaagataactctagagaacaaactt 852
QY 847 gaagcaaatgaagctaaatagaagaagacacttcaactcaacaagaacatggtgtgataca 906
DB 853 atagcgatacaacaaataattgatgaagctaaactcaagaagaagcgtgtaacgaa 912
QY 907 ttaccaatagcagctggtttctttatttaattccattgaagttgtattatgcaggt 966
DB 913 ctaccaatctcagcagcagatatttccatttaacoccttatgaagtagtattatgcgggt 972
QY 967 gtttcagatgaatgaatgcacattgcacgttagttcagttatgcaattcagtggaagatt 1026
DB 973 ggaacgtcaaatgagtttagacattttgctggttagttatccattcaatggaagatt 1032
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DB 1033 aactatgtattgaccataataattatgatagataataattttatgggaattagtgctattt 1092
QY 1087 tcgaagatgcacactgattgctggtttatttaaaattaaaaagtttacaatgcagattt 1146
DB 1093 acagaagatgcagaagatgcggtgttagttaatttaaaaaaggtatttaattcggatgta 1152
QY 1147 tatgaatattggtgatttcgtttaaaccaatttaaacacacgctacaaagcatacata 1206
DB 1153 gtggaatgctggtgatttttaaaccaatttaaaccaatttaaaccaattgataacac 1212
QY 1207 acactaaaaaagt---attaaaaataaatgatttttcogtaagagaggaatttagataa 1264
DB 1213 acattaaagaaaattaaagataaaaaagaaataaacatttaataagaagggaactaagctag 1272
QY 1265 tatgaatttaacagagtttaa 1284
DB 1273 aatgaatttaacagagtttaa 1292

Db	211	ttttatcttcacgagacgagccgttaattgattatgataatagaagcgcttgcatttttc	270
Qy	247	tttaagaacatcgtygcgcatcttaaaagltaaagaattatctttagatgcattcc	306
Db	271	tttaattggttaacaagaagattttaaacagcataatgttcataatgttcgaattgaccc	330
Qy	307	tacttgcatactcaactaagaagatcaatgataatgagcaatatttaaaaaatcattcaacgctgat	366
Db	331	tatttaccatactcaattatctaattatgataatggtgaattatccaggtaatgctgtgtaagtat	390
Qy	367	ggtttaattaaacaattttgaatcatctagttatgtaacgacacaaagccttcacaactggttc	426
Db	391	tggttctttttagtaagatgaagacatcgcgatttgcgaatgaaagcgcttactaagaagtttt	450
Qy	427	caccacatactcaaatatgataatgagcatctgttactgtatttgaagaatgataatgagcgaaaag	486
Db	451	gaccggattaaacaacatccgatatattcttcgttttagatttaaaaaataaacaatcaaa	510
Qy	487	acgctcatcaagaacatgtagcaggttataagaaaaaagaataatcacaaaaaagttccaanaaat	546
Db	511	gatatataatggaatggaatgtagtcttactagcgttaaacgttaatacctcaaaaaagttcaanaaat	570
Qy	547	ggtgttaaatggttcgttttctatcttaagaatgaataagtcgataatccgccaattatgga	606
Db	571	ggtgtgaagaatgtaagttcttcatcagaagaagacattccaattcttcgctcatattgga	630
Qy	607	gatactacagagaagaagaatttcaacagatcgttgcgaatgacttctattacatagatta	666
Db	631	gatacaccgaaacgaaagaagattccagaagttagatgatagtttctattatnaatcgtcat	690
Qy	667	aaatactcttgaat--gtaagaatctcttagcatatagactttgaagaacttaaat	723
Db	691	agaatcttcaagaatcagatcgctgtcttgacacatgctatataatgaatttgaagatcatc	750
Qy	724	ccacaatttagaaaaagaacatgatacaatactcaacaagaatattgcanaaagcgtgaanaagat	783
Db	751	gaagaatttcaacaattgaaacgtaagactttaaataagatgttaataagctttaaagat	810
Qy	784	tttaaaagaagaacggagatcatcaaaaaagatataaanaatagacaacttaaacacaa	843
Db	811	atgaaaaacgacgcgacataaaagaagcaattataaaaaagaaaatcttgaanaacaa	870
Qy	844	agagaagacaaatgaagctaaatattgaagaagcacttccactacacaaagaacatggtat	903
Db	871	ttaggtgcacatacaaaaaattagacgaggtcaaaaaattacaagcgcgaacatggtat	930
Qy	904	acattaccatagcagctggttttcttattatataatcatcttggaagtgtlatatagca	963
Db	931	gaattaccaatttccagcaggttcttcttattatcatccatttggaaagtgttattatgca	990
Qy	964	ggtgttcatcgaatgaatcatcgtcacttttgcagtgagtatgcaattcagtgaggaagt	1023
Db	991	gggtgaagacttcaataataatagacattttgcagagtgatgtatcctaaltgagcaatg	1050
Qy	1024	athtaatacgcgttagatcaacaacatgtagccgttataactctttgttatcagcgagac	1083
Db	1051	attaactatgaaattgtatcatgtaattatgataagataaatttctcaggtatcaggtaat	1110
Qy	1084	tctcagaagatgacacctgattgttgcgttatataattttaaanaaggttacaatgagat	1143
Db	1111	tttagtgaagacgcgtgaaagtgtgtggaatcttaataattttaaanaaggttccaatgagac	1170
Qy	1144	gtttatgaatataatgttggatttgcgttlaaaccaattcaataaacaacgagctacaagcat	1203
Db	1171	gtaattggaatagtttggagacgttttggaaaccttaacaacacttgtlatcagtgat	1230
Qy	1204	acaacactaaanaaagatattaanaaataatgatttccagaagaagaggaatttgata	1263
Db	1231	aagacccctaaagaatttaanaaaga-----tttaattaaagagggaatgagcga	1284
Qy	1264	atatgaaatattcacagattaa	1284

DB	1283	atatgaattacagagtaa	1303
	RESULT	8	
	AA37799		
ID	AA37799	standard; DNA; 1280 BP.	
XX	AA37799;		
XX	09-JUL-1999	(first entry)	
XX	Staphylococcus lugdunensis	FemA DNA.	
DE	FemA; identification; detection; therapy; infection; femB;		
KW	amplification; genotyping; gram-positive bacteria; vaccine; ss.		
KW	Staphylococcus lugdunensis.		
OS	Staphylococcus lugdunensis.		
OS	Key	Location/Qualifiers	
FF	CDS	1..1280	
FT	/*tag= a	/product= "FemA"	
FT	/note= "partial sequence, no start or stop codon"		
FT			
PN	W09916780-A2.		
XX	08-APR-1999.		
PD	28-SEP-1998;	98WO-BE00141.	
PF	26-SEP-1997;	97EP-0870146.	
PR	(BENA-) BELGIAN MIN NAT DEFENCE.		
XX	(UYLO-) UNIV CATHOLIQUE LOUVAIN.		
PA	Gala J, Vannuffel P;		
PI	WPI; 1999-287521/24.		
XX	P-PSDB; AAY08216.		
DR	New Staphylococcus-specific oligonucleotides		
DR	Claim 17; Fig 7a-b; 48pp; English.		
PT	This invention describes novel Staphylococcus-specific oligonucleotide		
PT	based on the consensus femA nucleotide sequence which are used to		
PS	develop products for the identification, detection and therapy of		
PS	infections. The oligonucleotides can be used for the genetic		
XX	amplification, the identification and/or quantification of various femA		
XX	sequences which are specific to known or unknown Staphylococci species		
XX	Since the femA sequence is similar to the femB sequence, the		
XX	oligonucleotides can also be used for the molecular genotyping of femB		
XX	genes of different Staphylococci species or other gram-positive bacteria		
XX	The femA nucleic acids can also be used in therapeutic applications.		
XX	They can also be used to identify inhibitors, e.g. antibodies or		
XX	antisense oligonucleotides, for blocking expression of the femA		
XX	nucleotide sequences. They can also be used for producing vaccines		
XX	against Staphylococci infections.		
SQ	Sequence 1280 BP; 484 A; 197 C; 221 G; 378 T; 0 other;		
	Query Match	45.5%;	Score 584.8; DB 20; Length 1280;
	Best Local Similarity	67.2%;	Pred. No. 1.2e-95;
	Matches 864; Conservative	0;	Mismatches 407; Indels 15; Gaps
OY	2	cactggaattgaagctttacaataaataacccgtacgcagcattttacacaagcagtag	61
DB	5	caaaagtattcggtttccacagatcaaatgccattagtcattttacccaatgacag	64
OY	62	gtaattgaattaaacacactgaaggtacttcaacacattagtaggggtcaagaata	121

Qy	1144	gtttatgaatatattggtgatttcggttaaaccaattataaacacagcgtacaaagcatat	1203
Db	4034	gtttatgaatcgttggtagctttatttaaacctattataaaccaatgtaaacatttat	4093
Qy	1204	acacactacaaaaaagttattataaaaaataaatgattttcagtaagagaggaatttagata	1263
Db	4094	agaacactaaaaaacta-----aagaaatagattttaagaaggggaatttatctaa	4143
Qy	1264	atatgaattttacagaggttaa	1284
Db	4144	ttatgaattttacagaggttaa	4164
RESULT 10			
AAQ78141	AAQ78141 standard; DNA; 1257 BP.		
XX	AC	XX	
AC	AAQ78141:		
DT	19-JUL-1995	(first entry)	
XX	Staphylococcus epidermidis femA gene.		
DE	XX	XX	FemA protein; femA gene; methicillin-resistant bacteria; ds.
KW	XX	XX	
OS	XX	XX	Staphylococcus epidermidis.
XX	Key	Location/Qualifiers	
FH	mat_peptide	1..1257	
FT	FT	/tag= a	
XX	EP625575-A.		
PN	XX	XX	
PD	23-NOV-1994.		
XX	25-APR-1994;	94EP-0302950.	
PF	30-APR-1993;	93US-0057163.	
XX	(ELIL) LILLY & CO ELI.		
PA	Alborn WE, Hoskins JA, Skatrud PL, Unal S, Unal S;		
PI	WPI: 1994-359748/45.		
XX	P-PSDB; AAR63440.		
DR	Isolated femA gene of Staphylococcus epidermidis - used to		
XX	develop agents for inhibiting FemA protein for use in treating		
PT	methicillin-resistant bacteria		
PT	Claim 2; Page 15; 23pp; English.		
XX	AAQ78141 encodes AAR63440 the FemA protein from Staphylococcus		
PS	epidermidis (SE). AAQ78141 can be used in disruption studies in		
XX	SE. These studies can be used to generate an assay for agents		
CC	which inhibit the femA protein, and are therefore useful in		
CC	combination with antibiotics to treat methicillin-resistant		
CC	bacteria.		
XX	Sequence 1257 BP; 485 A; 154 C; 225 G; 393 T; 0 other;		
Qy	7	gaattgaagctttacaaaataaaatgcgcgtacgcgcatttttacacaagcagtaggtaat	66
Db	34	gaatttagtgactttactgacgcgtatgacatatagctattttacacaatggaggtaat	93
Ov	67	tatgaattaaaaacatctgaagggttaacttcacacatttagtagggggtcacaagataatcaa	126
Query Match 44.7%; Score 574.4; DB 15; Length 1257;			
Best Local Similarity 67.4%; Pred. No. 8.4e-94;			
Matches 82%; Conservative 0; Mismatches 396; Indels 3; Gaps 1;			

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Db

4 gaaggtaatatcgaattcaaggctgcgaaagcacccgagccacccccccc-----

QY	118	gataatcaaggatgaattagctgcgtgcgtgttaacaagctgacacagatgaagaagaa	177
Db	64	aataatgatacgaatgcatgtgcagcttggtttatcaacgcgtgcttcgtatgaataa	123
QY	178	tttaattccttaactgaataagaggaccacgaatagatgatgatacgaacaagaactgct	237
Db	124	tttaaatattttatcccatccgcgcgcgcgttaataatgatatataataaaggctgtta	183
QY	238	gaattttctttaagaatctgtgagctatttaaaagttataaagattatcttttga	297
Db	184	catttttctttaatgtaattgttgtaaatatgtlaaaaaataataattgtttatatga	243
QY	298	atcgatccttaactctgcatactcaactaagaatcatgatgatggaatataaanaatcattc	357
Db	244	gttgaccatccatccatccatcaatttaatactatgaaggaggaaataactcgtgaatga	303
QY	358	aaccggaatggttaattaaacaatttgatcatctagttatgatacgaaccaaggcttcaca	417
Db	304	gttcatgatgtgatttttggatgtattagaaggtttagatataaaccgaagaagctcac	363
QY	418	actggttccaccacatatacacaattagatgcatctcgtactgatttgaagaatgac	477
Db	364	aagagatttgatccctgatttacaacatcgatatactcttcttctaatttgcacaacaa	423
QY	478	gacgaanaagcgtccatcaagaacatgagccggtttaagaaagaataatcaacaaagtt	537
Db	424	agtgtcaatgagttttaaanaaacatgtagtgtttaagaagaagctatatacaaaaagtt	483
QY	538	caaaaaatggtgttaaggttcgtttcttcatacaatagaataatgctgatalccgticaa	597
Db	484	aagaaanaatgtagctttaaagcttcgcttttattcttgagaagaagttactatattagtc	543
QY	598	tttatggaagatactacagagaagaagaatttcaacgactgctgagatgactcttatac	657
Db	544	tttatgagagatacctctgaaactaaagaattttgcagataagagaatgattttatcac	603
QY	658	aatagatlaaatactttgaaa---tgtaaagcttctcttgatcatataactatctgaa	714
Db	604	aacagatccaacatataaagaacgctgttttagtatacactagcctatataactttgat	663
QY	715	actaactccacaatttagaanaagaacatgatacaatacaacaagaatttgcanaagct	774
Db	664	gagtatataagagaactaataatagaagaagaatgctgttaataaagttatatataagct	733
QY	775	gaaaagaatttagaanaagaagaacacagatatacatacaaaaogatttaataatgacaacta	834
Db	724	ttaaaagacatttgagaaacgctccagagaataataaanaagcacaatacaaaaaggaattta	783
QY	835	aaacaaacaagaagaacaaatgaatgaagctttaaatttagaagaagcattcaactacatacaaga	894
Db	784	gaacacaacacccgatacgaaatcagaacaaaataatgaagaagcttaaaaacttaaaacagaa	843
QY	895	catgtgtatcatatacacaatagcagctggtttcttatattatataatcatttgaagtgtta	954
Db	844	catgcaatgattatcccatctcgtcgtcttcttataataatccgttttgaagtgtc	903
QY	955	tattatgcaagttgttcacgaatgaatatcgtccacttggcgggtatgtgaactgtacg	1014
Db	904	tactaagctgtgtgaacttaaatcgttatcgtcatcgttcgagggagctatgctgttcaa	963
QY	1015	tgaggaaatgattaatcaggtttagatacacaacatgacggttatataactictatggtac	1074
Db	964	tggaaatgatataactatgaattgaatgaacatggtatcttaacgcgtataattctctgttatt	1033
QY	1075	aggcggaagcttcacagaagaatgcacatgctatgctggttatataaatttaaaaaaggttc	1134
Db	1024	agctgtgactttagtgaagaatgctggaagctgctgctgaatgaattttaaanaaggtcat	1083
QY	1135	aatgcagatgtttatgaatatattgtgtgatttctgttaaccatttaataaacgcgcgtac	1194
Db	1084	gatgcgcagtttatagaatacgttctgtgcttattataacatttaataaaccaatgtat	1144
QY	1195	aaagcatatacaacactaaanaagaatttaaaaaa	1229

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Qy      41  ccgattttacacagcagtagtgattatgatgaataaacaatctgaagtaacttcaaac 100
          ||||| ||||| - ||||| ||||| - ||||| -
Db      4077 ctcatatcacacaacatctgctctcattttgatataagaataacacatcagataaatgtgc 413

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[illegible]

Db 1229 aatattaaggtataattttatggaataacagcgctttagtaataagcgagat 1288
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 Db 1289 ttgtgtcttcaacatttaaaagggttcaatgacatgttgaagaataatgtgtat 1348
 Qy 1165 ttggttaaaccaattataacacagcgtaacagatatacaacactaaagaatata 1224
 Db 1349 ttcataacaccgtaagcacttctatataatttgaacacttttataagtttaa 1408
 Qy 1225 aaaaataaagtatttcagtaagagaggaatttgaataatgaatttaacaggttaa 1284
 Db 1409 ttataagatgtgtgaattgaatttataatcttccacaacacttttactttta 1468

RESULT 15
 AA219882
 ID AA219882 standard; DNA; 1470 BP.
 AC AA219882;
 DT 06-DEC-1999 (first entry)
 XX Staphylococcus aureus femx gene.
 DE Staphylococcus aureus femx gene.
 KW Femx gene; Infection; therapy; diagnosis; vaccine; peptidoglycan;
 OS Staphylococcus aureus.
 FT Key Location/Qualifiers
 CDS 164..1408
 /*tag- a

XX W09947639-A2.
 XX 23-SEP-1999.
 XX 19-MAR-1999; 99WO-US05976.
 XX 20-MAR-1998; 98US-0078682.
 XX 01-APR-1998; 98US-0080296.
 XX 07-MAY-1998; 98US-0084674.
 XX (HUMAN) HUMAN GENOME SCI INC.
 XX (LUDM-) LUDMIG INST CANCER RES.
 XX Simpson AUG, Choi GH;
 XX WPI: 1999-562101/47.
 XX P-PSDB; AAY31817.
 XX New Isolated Staphylococcus nucleic acid molecules, used to develop
 XX products for the diagnosis, prevention and treatment of Staphylococcal
 XX infections
 XX Claim 1; Page 17-18; 102pp; English.

XX This is the nucleotide sequence of Staphylococcus aureus strain
 XX ISB3 (ATCC 202108) genomic DNA including the novel femx gene that
 XX codes for a 414-amino acid protein (see AAY31817) of predicted
 XX mol.wt. 49.1 kDa. The sequence was obtained from overlapping
 XX clones BFEF571 and BFEJ519. The predicted protein product shows
 XX sequence identity with the fema and femb proteins of Staphylococcus
 XX spp., suggesting a role in peptidoglycan interpeptide bridge
 XX biosynthesis. The invention provides 11 novel genes (see AA219882-92)
 XX of S. aureus and the polypeptides they encode (see AAY31817-27). Also
 XX provided are vectors, host cells, antibodies and hybridomas. The
 XX invention further relates to screening methods for identifying
 XX agonists and antagonists of S. aureus polypeptide activity, and to
 XX diagnostic methods for detecting Staphylococcus nucleic acids,
 XX polypeptides and antibodies in a biological sample. Also
 XX provided are novel vaccines for the prevention or attenuation of

CC infection by Staphylococcus. The isolated nucleic acid molecules
 CC are also useful for generating probes and primers, and in the
 CC recombinant production of femx protein.

XX Sequence 1470 BP; 604 A; 146 C; 237 G; 483 T; 0 other;

Query Match 25.1%; Score 322.4; DB 20; Length 1470;
 Best Local Similarity 54.0%; Pred. No. 7.3e-49;
 Matches 681; Conservative 0; Mismatches 576; Indels 3; Gaps 1;

Qy 28 aaatgcggaagcagcattttacacagcagtaggtaattgaattaaacacttga 87
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 Qy 88 ggtacttaacacatttagtaggggtcaagatatcaagatcaagtgtaattagctgt 147
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 Qy 148 ctgttaacaagtgaccagttatgaagaatttaacttacttactcaataagagacca 207
 Db 329 ttattacaagagcagcaatttttaattcacaatatttctacttccatagaagcc 388
 Qy 208 gtaatgattatgacaacaagactgttgacttttctttaaagaactgtgactat 267
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 Qy 268 ttaaaagtttaagaagattatctttagaatacgcacttacttccatcaataaga 327
 Db 449 attataaaatagaagagattattatcttctgttgcacattttaaagaattaa 508
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 Qy 925 tttttattatcatcatttgagttgatatattgcaagttgtgtcatcgatgaat 984

us-09-509-234c-50.rng

Fri Jun 21 08:38:26 2002

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Db 1109 ttatttatgtactgatgatgaagtttatctatctcaagtggtatcaaatccgaatat 1168
QY 985 cgtcaatttgaggtagttatgcaattcagtgaggaaatgattaaatcgcgttagatcac 1044
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QY 1165 ttctgttaaaccaatttaaacccggtacaaagcatatatacacacttaaaaaagtatta 1224
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QY 1225 aaaaaataaatgattttcagtaagaggggaatttagataatataatgaaatttacagagttaa 1284
Db 1409 ttataagratgttggaattgaaatttttaattctttccacatacttttccacttttta 1468

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Search completed: June 20, 2002, 14:46:55
Job time: 18805 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 20, 2002, 12:04:07 ; Search time 208.59 seconds
(without alignments)
1512.026 Million cell updates/sec

Title: US-09-509-234C-50
Perfect score: 1284
Sequence: 1 acactgaattgaagcttt.....taagaaattacagagttaa 1284

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues
Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match		Length	DB ID	Description
		Match	Length			
1	574.4	44.7	1257	1	US-08-330-154-1	Sequence 1, Appli
2	216.2	16.8	453	3	US-08-714-918-9	Sequence 9, Appli
3	216.2	16.8	453	4	US-09-265-315-9	Sequence 9, Appli
4	216.2	16.8	453	4	US-09-265-315-9	Sequence 9, Appli
5	216.2	16.8	453	4	US-09-266-417-9	Sequence 6, Appli
6	194	15.1	410	3	US-08-714-918-6	Sequence 6, Appli
7	194	15.1	410	4	US-09-265-315-6	Sequence 6, Appli
8	194	15.1	410	4	US-09-266-417-6	Sequence 6, Appli
9	139.6	10.9	400	3	US-08-714-918-4	Sequence 4, Appli
10	139.6	10.9	400	4	US-09-265-315-4	Sequence 4, Appli
11	139.6	10.9	400	4	US-09-265-315-4	Sequence 4, Appli
12	139.6	10.9	400	4	US-09-266-417-4	Sequence 4, Appli
13	139.6	10.9	400	4	US-09-266-417-4	Sequence 4, Appli
14	83.8	6.5	5253	3	US-08-714-918-19	Sequence 19, Appl
15	83.8	6.5	5253	4	US-09-265-315-19	Sequence 19, Appl
16	83.8	6.5	5253	4	US-09-265-315-19	Sequence 19, Appl
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19	66.8	5.2	2223	1	US-08-257-073-4	Sequence 4, Appli
20	66.2	5.2	7218	1	US-08-232-463-14	Sequence 14, Appl
21	61.8	4.8	658	4	US-08-998-416-595	Sequence 595, App
22	60.6	4.7	2447	2	US-09-014-969-14	Sequence 14, Appl
23	60.4	4.7	930	4	US-08-936-165A-74	Sequence 74, Appl
24	59.6	4.6	19124	2	US-08-487-826B-13	Sequence 13, Appl
25	57	4.4	6243	4	US-09-056-075-1	Sequence 1, Appli
26	55.8	4.3	1956	4	US-08-559-896B-1	Sequence 1, Appli
27	55.2	4.3	2674	4	US-09-817-180-1	Sequence 1, Appli

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c 29	53.4	4.2	1798	4	US-09-797-906-1	Sequence 1, Appli
c 30	52.8	4.1	1021	3	US-08-714-918-70	Sequence 70, Appl
c 31	52.8	4.1	1021	4	US-09-265-315-70	Sequence 70, Appl
c 32	52.8	4.1	1021	4	US-09-265-315-70	Sequence 70, Appl
c 33	52.8	4.1	1021	4	US-09-266-417-70	Sequence 2, Appli
c 34	52.8	4.1	5852	1	US-07-867-106-2	Sequence 1, Appli
c 35	52	4.0	6152	4	US-08-973-462-1	Sequence 2, Appli
c 36	51.4	4.0	6671	1	US-08-280-443-1	Sequence 1, Appli
c 37	51.4	4.0	6671	1	US-08-457-459-1	Sequence 1, Appli
c 38	51.4	4.0	6671	1	US-08-555-678-1	Sequence 1, Appli
c 39	51.4	4.0	6671	5	PCT-US95-02275-1	Sequence 3, Appli
c 40	51	4.0	6124	4	US-08-213-419B-3	Sequence 10, Appl
c 41	50.8	4.0	1051	4	US-09-245-041-10	Sequence 3, Appli
c 42	50.4	3.9	1891	4	US-08-973-462-3	Sequence 15, Appl
c 43	49.8	3.9	1320	1	US-08-257-073-15	Sequence 41, Appl
c 44	49.8	3.9	1482	4	US-08-098-327E-41	Sequence 45, Appl
c 45	49.8	3.9	1482	4	US-08-098-327E-45	

ALIGNMENTS

RESULT 1
US-08-330-154-1
; Sequence 1, Application US/08330154
; Patent No. 5587307
; GENERAL INFORMATION:
; APPLICANT: Alborn Jr., William E
; APPLICANT: Hoskins, Joann
; APPLICANT: Skatrud, Paul L
; APPLICANT: Unal, Serhat
; TITLE OF INVENTION: FEMA GENE OF STAPHYLOCOCCUS EPIDERMIDIS,
; TITLE OF INVENTION: THE FEMA GENE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Division/AEH
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/330,154
; FILING DATE: 27-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,925
; FILING DATE: 09-MAR-1994
; APPLICATION NUMBER: US/08/057,163
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hamilton, Amy E
; REGISTRATION NUMBER: 33,894
; REFERENCE/DOCKET NUMBER: X-8894
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-3169
; TELEFAX: 317-276-1294
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1257 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS

Fri Jun 21 08:38:26 2002

us-09-509-234c-50.rml

Page 2

LOCATION: 1..1257
US-08-330-154-1

Query Match 44.7% Score 574.4; DB 1; Length 1257;
Best Local Similarity 67.4%; Pred. No. 4.3e-118;
Matches 825; Conservative 0; Mismatches 396; Indels 3; Gaps 1;

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DB 154 AACGAAGTATGACAGCTTGTTTATTAACAGCTTCTGTAATGAATAATTAATAT 213
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DB 214 TTTTATTCGAATCGCGGTCCAGTAAATGATTAATAAAGAGCTTGACATTTTTC 273
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DB 274 TTTTAATGAATAGTAATATGTAATAAATAATTAATTTTATTAATTAAGTTGACCCA 333
QY 307 tacttgccatcaactaagatcatgcatgcaatataaataatcaatcaacgtgat 366
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QY 1204 acacacataaaagaatataaa 1227
DB 1234 AGACACTTAATAAAGTAAAGAA 1257

RESULT 2
US-08-714-918-9
Sequence 9, Application US/08714918
Patent No. 6037123
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Ving
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 613 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,918
FILING DATE: September 13, 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Wardburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 222/005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 453 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-714-918-9

FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 935-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 453 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PS-09-265-315-9

Query Match	16.8%;	Score 216.2;	DB 4;	Length 453;
Best Local Similarity	66.2%;	Pred. No. 2.6e-39;		
Matches 296:	Conservative 0;	Mismatches 151;	Indels 0;	Gaps 0;

[illegible]

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RESULT      4
US-09-265-315-9
; Sequence 9, Application US/09265315
; Patent No. 6187541
; GENERAL INFORMATION:
; APPLICANT: Benton, Bret
; APPLICANT: Lee, Ving J.
; APPLICANT: Malouin, Francois
; APPLICANT: Martin, Patrick K.
; APPLICANT: Schmid, Molly B.
; APPLICANT: Sun, Dongxu
; TITLE OF INVENTION: METHODS OF
; TITLE OF INVENTION: ACTIVE ON S
; TITLE OF INVENTION: TARGET GEN
;

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Query Match	16.8%	Score 216.2	DB 3	Length 453
Best Local Similarity	66.2%	Pred. No. 2.6e-39		
Matches 296	Conservative 0	Mismatches 151	Indels 0	Gaps 0
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DB	67	AGAACTAAACGAGAGCGTGATTTTAAATAAAGATTTAATAAAGCGTTAAGGATAT	126	
QY	786	gaaaagaacacacataatcaaaaaacgattaaataaattagacaacttaaaacacaaga	845	
DB	127	TGAAAAAACGTCCTGAAATTAATAAAGCCATATACAGCGAGATAACTTACAACAACAAT	186	
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DB	307	TGGTACATCAATATGCTTCCGTCATTTTNCGGANGTTATGCTGCAATGGGAAATGNT	366	
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RESULT 3
 US-9-265-315-9
 ; Sequence 9, Application US/09265315
 ; Patent No. 6187541
 ; GENERAL INFORMATION:
 ; APPLICANT: Benton, Bret
 ; APPLICANT: Lee, Ving J.
 ; APPLICANT: Malouin, Francois
 ; APPLICANT: Martin, Patrick K.
 ; APPLICANT: Schmid, Molly B.
 ; APPLICANT: Sun, Dongxu
 ; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
 ; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
 ; TITLE OF INVENTION: TARGET GENES
 ; NUMBER OF SEQUENCES: 111
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/265,315
 ; FILING DATE: March 9, 1999
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/714,918

NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/265,315
 FILING DATE: March 9, 1999
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/714,918
 FILING DATE: September 13, 1996
 APPLICATION NUMBER: 60/009,102
 FILING DATE: December 22, 1995
 APPLICATION NUMBER: 60/003,798
 FILING DATE: September 15, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 240/247
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 453 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-265-315-9

Query Match 16.8%; Score 216.2; DB 4; Length 453;
 Best Local Similarity 66.2%; Pred. No. 2.6e-39;
 Matches 296; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

QY 666 aaataacttgaaatgtaagaattcccttagacatataagacttgaacttgaacttcc 725
 DB 7 AATTTCAGAAAGCGGTGTGAGTATTAATTAATTAATTAATTAATTAATTAATTA 66
 QY 726 acaattagaagaagacttgacacatacaagaagattgcaaaagctgaaagatt 755
 DB 67 AGAAGCTAAAGCAAGAGCGGTGATTTAAATTAATTAATTAATTAATTAATTAATTA 126
 QY 786 agaaagaagaacagatacaaaaagcgttaataaaatagaacacttaaacacaaag 845
 DB 127 TGAATAACGCTCTGAAATTAATAAAGCAATTAACAGAGATTAATTAACACCAACT 186
 QY 846 agaagcaaatgaaagctaaattagaagaagacttcaactcaacaagaagaactggtatc 905
 DB 187 TGATGCAATAGCAAAAGATTGTGANGACGTTAAACGCTTACAGAGANGANGATGTAAAGN 246
 QY 906 attaccatagcagctggttcttattatattacattgaagttgtatatatgacag 965
 DB 247 TTACATATCTCTCTGCTGTTCTCTTATCAATTCNTTGTGANGTGTATATATCTG 306
 QY 966 tggctacatgaatgaaatgcatctgacattggaagtagtatgcaattcaaggggaaatgt 1025
 DB 307 TGTGACATCAAAAGCAGTCCGTCATTTTNCAGGANGTATGCGNGTGAATGGAAATGNT 366
 QY 1026 taaatagcggttagacacaaacttgacgcttataactctatggtatcagcggaagact 1085

DB 367 TAATTTCATTAATTCATGCAATGNCCTATATATNCTATGTTAGTGTAAATT 426
 QY 1086 ctcaagaatgacactgattgagcgt 1112
 DB 427 TNCAGNAGGTGCTGAAGATGCTGCTGT 453

RESULT 5
 US-09-266-417-9
 Sequence 9, Application US/09266417
 Patent No. 6228588
 GENERAL INFORMATION:
 APPLICANT: Benton, Bret
 APPLICANT: Lee, Ying J.
 APPLICANT: Malouin, Francois
 APPLICANT: Martin, Patrick K.
 APPLICANT: Schmid, Molly B.
 APPLICANT: Sun, Dongxu
 TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
 TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
 TARGET GENES
 NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/266,417
 FILING DATE: March 9, 1999
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/714,918
 FILING DATE: September 13, 1996
 APPLICATION NUMBER: 60/009,102
 FILING DATE: December 22, 1995
 APPLICATION NUMBER: 60/003,798
 FILING DATE: September 15, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 240/248
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 453 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-266-417-9

Query Match 16.8%; Score 216.2; DB 4; Length 453;
 Best Local Similarity 66.2%; Pred. No. 2.6e-39;
 Matches 296; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

QY 666 aaataacttgaaatgtaagaattcccttagacatataagacttgaacttgaacttcc 725
 DB 7 AATTTCAGAAAGCGGTGTGAGTATTAATTAATTAATTAATTAATTAATTAATTA 66
 QY 726 acaattagaagaagacttgacacatacaagaagattgcaaaagctgaaagatt 785

Db 67 AGAACTAACGAGAGCGTGATATTTTAAATRAAGATTTAAATAAAGCGTTAAAGGATAT 126
QY 786 agaaaagaaccagataaactcaaaaaacgattataaaaaatagacaacttaaacacaacaaga 845
Db 127 TGAHAACGCTCTCAAAAATAAAAAAGCACATAACAAGCGAGATAAATCTACAACAACAAC 186
QY 846 agaagcaaatgaagctaaattagaagaagcaattcaactcacacaagaacatggtgatac 905
Db 187 TGATGCAAAATGAGCAAAAGATTGAGACGGTAACAGCTCACAGGANGANCATGTTATCN 246
QY 906 attaccaatagcagctggtttcttattattaatccatttgaagttggtattattatcgagg 965
Db 247 TTTACCTATCTCTCTGGTTCTCTTTATCATCAATCCNTTGANGTTGTTATTATGCTGG 306
QY 966 tggttcatcgaaatgaatatcgtccacttgcggtgagttatgcaattcagtgggagaatgat 1025
Db 307 TGGTACATCAAAATGCTTCGGTGATTTTTCGGGANGTTATGNGTGCATGGGAATGAT 366
QY 1026 taatacgggttagatcacacaacattgacggtataactctctatggtatcacgcgagacct 1085
Db 367 TAAATTTGGCATTAAATCATGCGCATGNCGGTTATTAATNCTATGGTGTTAGTGSTNAAT 426
QY 1086 ctcaagaagatgcacctgatggttggcgt 1112
Db 427 TNCAGNAGGTGCTGAAGATGCTGGTGT 453

RESULT 6
US-08-714-918-6
; Sequence 6, Application US/08714918
; Patent No 6037123
; GENERAL INFORMATION:
; APPLICANT: Benton, Bret
; APPLICANT: Lee, Ving
; APPLICANT: Malouin, Francois
; APPLICANT: Martin, Patrick K.
; APPLICANT: Schmid, Molly B.
; APPLICANT: Sun, Dongxu

NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U. S. A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,918
FILING DATE: September 13, 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 222/005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

Page 6

NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Filth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798

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1 APPLICATION NUMBER: 05/09/265,315
2 FILING DATE: March 9, 1999
3 CLASSIFICATION: 435
4 PRIOR APPLICATION DATA:
5 APPLICATION NUMBER: 08/714,918
6 FILING DATE: September 13, 1996
7 APPLICATION NUMBER: 60/009,102
8 FILING DATE: December 22, 1995
9 APPLICATION NUMBER: 60/003,798
10 FILING DATE: September 15, 1995
11 ATTORNEY/AGENT INFORMATION:
12 NAME: Warburg, Richard J.
13 REGISTRATION NUMBER: 32,327
14 REFERENCE/DOCKET NUMBER: 240/247
15 TELECOMMUNICATION INFORMATION:
16 TELEPHONE: (213) 489-1600
17 TELEFAX: (213) 955-0440
18 TELEX: 67-3510
19 INFORMATION FOR SEQ ID NO: 6:
20 SEQUENCE CHARACTERISTICS:
21 LENGTH: 410 base pairs
22 TYPE: nucleic acid
23 STRANDEDNESS: single
24 TOPOLOGY: linear
25 US-09-265-315-6
26
27 Query Match 15.1%; Score 194; DB 4; Length 410;
28 Best Local Similarity 68.2%; Pred. No. 2e-34;
29 Matches 279; Conservative 0; Mismatches 127; Indels 3; Gaps 1

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Db 361 CCGAAGTTATGCGTGAATGGGAATGATTAAATTATGCAATAATCA 409

RESULT 9

US-09-266-417-6

; Sequence 6, Application US/09266417

; Patent No. 6228588

; GENERAL INFORMATION:

; APPLICANT: Benton, Bret

; APPLICANT: Lee, Ving J.

; APPLICANT: Malouin, Francois

; APPLICANT: Martin, Patrick K.

; APPLICANT: Schmid, Molly B.

; APPLICANT: Sun, Dongxu

; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS

; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS

; TITLE OF INVENTION: TARGET GENES

; NUMBER OF SEQUENCES: 111

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/266,417

; FILING DATE: March 9, 1999

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/714,918

; FILING DATE: September 13, 1996

; APPLICATION NUMBER: 60/009,102

; FILING DATE: December 22, 1995

; APPLICATION NUMBER: 60/003,798

; FILING DATE: September 15, 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 240/248

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 410 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-09-266-417-6

Query Match 15.1%; Score 194; DB 4; Length 410;

Best Local Similarity 68.2%; Pred. No. 2e-34;

Matches 279; Conservative 0; Mismatches 127; Indels 3; Gaps 1;

Qy 638 gtggcgatgctcttattacaatgattgataaaatcttctgaaa---tgaagattccctt 694

Db 1 GTAATGACAAATNTAACTACGCTTAAATATTACAAAGACCGGTGTGNAGTACCTT 60

Qy 695 tagcatatagacttgaaacttaccattcccaatttagaataaaagaaacatgaacaataca 754

Db 61 TAGCGTATATCAACTTAAATGAATATTAAGAAGAACTAAACGAGCGGTGATTTTAA 120

Qy 755 acaaaatattcgaacaaactgaataaaatattagaataaaacaaacaaataatcaaaacaa 814

Db 121 ATAAAGATTAAATTAAGCGTTAAAGGATATTGAAAAACGCTCTGAAAAATAAAAGCAC 180

Qy 815 ttaataaaatagacaacttaaaacaacaagaagaagaactgaagctaaattagaagaag 874

Db 181 ATAACAAGCGAGATAACTTACAACAACAACCTTGATGCAAAATGAGCAAAAGATTGAAGAAG 240

Qy 875 cacttcaactacacaagaacatgggtgatacattaccataagcagctgggtttctttatta 934

Db 241 GTAAACGCTACAAGANGAACATGGTAATGAATATACCTATCTCTNCCTGGTTCTNCTTTA 300

Qy 935 ttaatccattgaagtgtattatgcaggtgggttcacgaatgaatgcacattg 994

Db 301 TCAATCCATTGANGTTGTTTATTATGCTGGTGATACATCAATGCAATCCGTCATTTTN 360

Qy 995 caggtagttatgcgaattcagtggaagaatgattaaataacgccttagatca 1043

Db 361 CCGAAGTTATGCGTGAATGGGAATGATTAAATTATGCAATAATCA 409

RESULT 10

US-08-714-918-4/c

; Sequence 4, Application US/08714918

; Patent No. 6037123

; GENERAL INFORMATION:

; APPLICANT: Benton, Bret

; APPLICANT: Lee, Ving

; APPLICANT: Malouin, Francois

; APPLICANT: Martin, Patrick K.

; APPLICANT: Schmid, Molly B.

; APPLICANT: Sun, Dongxu

; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL

; TITLE OF INVENTION: TARGET GENES

; NUMBER OF SEQUENCES: 111

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/714,918

; FILING DATE: September 13, 1996

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/009,102

; FILING DATE: December 22, 1995

; APPLICATION NUMBER: 60/003,798

; FILING DATE: September 15, 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 222/005

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 400 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-714-918-4

Qy 638 gtggcgatgctcttattacaatgattgataaaatcttctgaaa---tgaagattccctt 694

Db 1 GTAATGACAAATNTAACTACGCTTAAATATTACAAAGACCGGTGTGNAGTACCTT 60

Qy 695 tagcatatagacttgaaacttaccattcccaatttagaataaaagaaacatgaacaataca 754

Db 61 TAGCGTATATCAACTTAAATGAATATTAAGAAGAACTAAACGAGCGGTGATTTTAA 120

Qy 755 acaaaatattcgaacaaactgaataaaatattagaataaaacaaacaaataatcaaaacaa 814

Page 8

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1  FILING DATE: September 15, 1995
2
3  ATTORNEY/AGENT INFORMATION:
4
5      NAME:  Walburg, Richard J.
6
7      REGISTRATION NUMBER:  32,327
8
9      REFERENCE/DOCKET NUMBER:  240/247
10
11     TELECOMMUNICATION INFORMATION:
12
13     TELEPHONE:  (213) 488-1600
14
15     TELEFAX:  (213) 955-0440
16
17     TELEX:  67-3510
18
19     INFORMATION FOR SEQ ID NO:  4:
20
21     SEQUENCE CHARACTERISTICS:
22
23         LENGTH:  400 base pairs
24
25         TYPE:  nucleic acid
26
27         STRANDEDNESS:  single
28
29         TOPOLOGY:  linear
30
31
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34
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38
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Oy 202 gaccacglaabgaltatvacaacaagaactgttgcttttctttaaaagacvtg 261
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Db 400 GGCCAGGATGTANTATCAAACTCAGANNCTGTACCTTTTCTTAATAAATATCC 341
| | | | |
Oy 262 agc-tatttaaaaagtataaaggatttccttagaatcgatccctaactggcataca 350
| | | | |
Db 340 AAAAATTTAAAAAACATCGTTGGMCHTACTTCANCANCAATTCANCATATCA 281
| | | | |
Oy 321 actaagagatcatgatvgccaatattaanaaatcatcaaccvgtatggtttaataaca 380
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Db 280 ATACTTGGAATTATCATGCCGACAATTACAGGATATGCTGTATATGATGTCTTTGATTA 221
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Oy      381 atttgaatcattagttgatgaacaccagaagcttcaacatcgtgtttccaccgaatcacca 440
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      220 AATGAGTAACTTAATGAGTATGGAACATNCTGATGTCATTAAGGAGATTTCCTGTCTACA 161
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy      441 aattgaatcagatctcgtactcattatgaagaatgacgacgaagaagcgtcatcaagaa 500
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      160 AATCGCTTTCACCTCACTGATGTGATTAAAGATATAACAGACAGATGACATCATTNAAAA 101
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy      501 catgscagtttaagaanaagaataactcaaaaaagtccaaaaaattgltttaaagttcg 560
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      100 TATGAGTGACTTGGAAAAAGAAACCGGAANNNGTNNAAAAGATGTGTATTAAGTAAAG 41
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy      561 ttctcatcaagaatgaatgcgataatcgcgtcaatt 600
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      40 ATTTTTATCTGAAGNACNACTACCAATTTTATGATATATT 1
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 12
 US-09-265-315-4/c
 : Sequence 4, Application US/09265315
 : Patent No. 6187541
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Benton, Bret
 : APPLICANT: Lee, Ying J.
 : APPLICANT: Malouin, Francois
 : APPLICANT: Martin, Patrick K.
 : APPLICANT: Schmid, Molly B.
 : APPLICANT: Sun, Dongxu
 : TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
 : TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
 : TITLE OF INVENTION: TARGET GENES
 : NUMBER OF SEQUENCES: 111
 :
 : CORRESPONDENCE ADDRESS:
 :
 : ADDRESSEE: Lyon & Lyon
 : STREET: 633 West Fifth Street
 : STREET: Suite 4700
 : CITY: Los Angeles
 : STATE: California
 :
 : COUNTRY: U.S.A.

Fri Jun 21 08:38:26 2002

us-09-509-234c-50. nri

Page 10

Db 160 AATCCGTATACACTGCTGTAGATTAAAGATAAAGACAGACATGACATCTTAAATA 101
Qy 501 catggacagtttaagaanaaagaataactaaagaatcaaaaaatggttttaagttcg 560
Db 100 TATGATGACACTAGAAAAGAAAACAGGANNAGTTTAAAGAAAGTGTGTTAAAGTAA 41
Qy 561 tttctcttaagaatgaatgcgcatattcgctcaatt 600
Db 40 ATTTTATCTGAAGAGNACTTACCAATTTTATGATTATTT 1

RESULT 14
US-08-714-918-19/c
Sequence 19, Application US/08714918
Patent No. 6037123
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Ying
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714, 918
FILING DATE: September 13, 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Wardburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 222/005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 5253 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-714-918-19

Query Match 6.5%; Score 83.8; DB 3; Length 5253;
Best Local Similarity 44.5%; Pred. No. 7.3e-10;
Matches 389; Conservative 1; Mismatches 473; Indels 12; Gaps 1;
Qy 377 aacacattgaatcatataggtatgaacacaggttcacacagttggttccaccacatc 436
Db 2963 AAAATTGAAGCGCTGTGTTTAAACATAAAGAGATTAAAGAGTTTATCAAAAGACT 2904

Qy 437 atcaaatagatggtcattcgtcattgattagaagatgagcgaagaagcgtcatca 436
Db 2903 AATCCACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2844
Qy 497 agaacatgacagtttaagaanaaagaataactaaagaatcaaaaaatggttttaag 556
Db 2843 ATAGTTTGAAGCGGAAATCGTTCAAAAGTGCGCTTTAAAGCGAGGTAGCAGCG 2784
Qy 557 ttcgtttctcctaagaatgaatgcgcatattccgtcattatagaagatgag 616
Db 2783 TAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2724
Qy 617 agagaagaatctcaagatcgtgcgagctcctcattacaatgaatgaatcattg 676
Db 2723 AAGCGATGCTTTTAAAGCGGTATTTAGTTACTTTGAAAATTTTATGATGCTTGC 2664
Qy 677 aaatgtlaagaatcccttaagatataagacttgaacttgaacttcaatcacaattagaa 736
Db 2663 ATGAAATGAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2604
Qy 737 aagaacatgaacatacaacaagaatgcaaaagcgtgaagaagattagaaga--- 793
Db 2603 AAGTAATCAAGATTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 2544
Qy 794 -----aaccagataatacaaaacgattaataatgaacacttaaaacacaa 844
Db 2543 AATCATCTGAAGACACTTAAAGCGCAAAATTTGATTTAAGTGAGCGCAAAATTA 2484
Qy 845 gagaagaatgaagctaaatgaagaagacacttaacatacaagaacatggtgata 904
Db 2483 TTGCTTAAATTTGAATTTTAAAGACGCTTAAAGAGGAAACATCTGAAG 2424
Qy 905 cattacaatgagcgtggttcttattatccattgaagtgtatattatgag 964
Db 2423 GTATTATCTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2364
Qy 965 gtggttcatgcatgatatcgtcacttgcaggtatgcatcagtcagtcagtcagtcag 1024
Db 2363 GTGGCTTTCTTAAATTTGAATTTTAAAGACGCTTAAAGAGGAAACATCTGAAG 2304
Qy 1025 ttaatacgcgttagatcacacacatgacgttataacttcatgtagtcagcgagact 1084
Db 2303 TGAATATGACGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2244
Qy 1085 tctcagaagatgacactgattggtgcgttataatataaagaatgaatgagatg 1144
Db 2243 CAGATTAAGACTGAAACATTTATGATTTATGCGCATTTAAAGGTTGGGAAACAT 2184
Qy 1145 tttaagatatattggttgcgttataaactaataaaccagcgtacaaagcatata 1204
Db 2183 TAAGGAAAAGATTGGAATTTGATTTATGATTTGATTCAGCATGRCATTAATTT 2124
Qy 1205 caaccataaagaatataaagaatgaatgatt 1239
Db 2123 AGCAAGTTAAAGCGCTTTAAAGGATTAAGTAAATTT 2089

RESULT 15
US-09-265-315-19/c
Sequence 19, Application US/09265315
Patent No. 6187541
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Ying J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111

Fri Jun 21 08:38:26 2002

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/265,315
 ; FILING DATE: March 9, 1999
 ; CLASSIFICATION: 435
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 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/714,918
 ; FILING DATE: September 13, 1996
 ; APPLICATION NUMBER: 60/009,102
 ; FILING DATE: December 22, 1995
 ; APPLICATION NUMBER: 60/003,798
 ; FILING DATE: September 15, 1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 240/247
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ;
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5253 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ;
 ; US-09-265-315-19

Query Match 6.5%; Score 83.8; DB 4; Length 5253;
 Best Local Similarity 44.5%; Pred. No. 7.3e-10;
 Matches 389; Conservative 1; Mismatches 473; Indels 12; Gaps 1;

QY	377	aacaattgaatcattaggtatgaacacacaggttcacaaactggtttccaccataac	436
Db	2963	AAATTTGAAGCGCTGGTTTAAACATAAAGGATTTAAAGAGGTTTATCAAAAGACT	2904
QY	437	atcaaatagatggcattctgacttattagaaagttagaagatgacgaagaagacgtc	496
Db	2903	ACATCCAAACCCACCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT	2844
QY	497	agaacatggacagtttaagaaagaaagaaagaaagaaagaaagaaagaaagaaag	556
Db	2843	ATAGTTTGAACGCCGGAATTCCTTCAAAAGTGGCTTGAAGCGGCTGACGACAG	2784
QY	557	ttcgtttctatcattgaagatgaatgcgatacttcggtcaatttatggaagatactac	616
Db	2783	FAGAACGATCTGATGAGAGGTTTAAACATTTGCTGAGTTTAAAGAGGTTTATCAAA	2724
QY	617	agaagaagatttcaacgatcgtgacgtatgacgtatgacgtatgacgtatgacgtat	676
Db	2723	AACGGATGGCTTCTTAACCGGTGATATTAGTTACTTTGAAATATTTATGATGCGTGC	2664
QY	677	aaatgtaagattcccttttagcatatagactttgaaacttacattccacaattagaaa	736
Db	2663	ATGAAGATGGAGATGCTGACATATTTTGAAGTTGGATTCACCAAGAAATATATAGCG	2604
QY	737	agaacatgaac	793
Db	2603	AAATTAATCAAGAAATTAATGAACCTTCATGCGGAATTCCTAAATGGCAGCAGAGATGA	2544

QY	794	-----aacagataatcaaaaaacgattataataaataagacaacttaaaacacaaa	844
Db	2543	AAACATCTGAAAAGCAAGCTAAAAAAGCGCAAAATATGATTAAATGATGCGCAAAATAAA	2484
QY	845	gagaagcaaatgaagctaaattagaagaagcacttcaactacaagaacatggcgata	904
Db	2483	TTGCTAAAAATGAAGATTTAAACGAGACCTAGAAGCTTTAGAAAAGGAACATCCCTGAAG	2424
QY	905	cattaccaatgacgctgggtttcttattattataatccatttgaagttgtattatgcag	964
Db	2423	GTATTTATCTTTCTGGTGCACATNTAATGTTTCTGGCTCAAAATCATATATTACTTATATG	2364
QY	965	gtggttcacgaatgaatcgtcacttcttgcaggttagttatgcaattcagtgggaaatga	1024
Db	2363	GTGCGTCTTCTAATGAATTTAGAGATTTTACCAAAATCATCATATGAGTATACGATGA	2304
QY	1025	ttaatacgcgttagatcaacaacattgacogttataacttcttattggtatcagcggagact	1084
Db	2303	TGAAGTATGACGCTGAACATGGTGCAACAACTTACGATTTGCGTGGTACAGATAAATGATC	2244
QY	1085	tctcagaatgacacgtgattggtggttattataaatttaaaaaaggttacaatgcagatg	1144
Db	2243	CAGATAAAGACTCAGACACATTTATGGATTTATGGCATTTAAAAAAGTGTGGGGAACATACT	2184
QY	1145	tttatgaatatattggtgatttctttaaaccacaaataaaccacgcgtacaaagcatata	1204
Db	2183	TAAGTGAAGAGATTGGTGAATTTGATTTATGTTGATTCAGCCATTTGTRCCATTAATTG	2124
QY	1205	caacactaaaaaagttattataaaaaataaaatgatt	1239
Db	2123	AGCAAGTTAAACCGCGTTTAAACAAAGCTTAAAT	2089

Search completed: June 20, 2002, 12:04:14
 Job time: 20969 sec

Fri Jun 21 08:38:26 2002

us-09-509-234c-50.rni

Page 12

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2002, 14:26:57 ; Search time 8551.36 Seconds
(without alignments)
2026.589 Million cell updates/sec

Title: US-09-509-234c-50
Perfect score: 1284
Sequence: 1 acatggaattgaagcttt.....tatgaattacagaggttaa 1284

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST:*
1: em_estha:*
2: em_esthum:*
3: em_estin:*
4: em_estinu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pin:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	95.8	7.5	990	12	CNS00601
C 2	94.2	7.3	982	12	AQ325799 nxb0021B
C 3	91.2	7.1	1042	12	CNS0148K
C 4	90.8	7.1	1059	12	AL103838 Drosophila
C 5	90.4	7.0	879	12	AL147405 Anopheles
C 6	90.4	7.0	1101	12	CNS01JRG
C 7	88.6	6.9	788	3	BI645011
C 8	88.6	6.9	910	10	BM415636
C 9	87.4	6.8	614	12	CNS0152H
C 10	87.4	6.8	796	9	AL524807
C 11	87.4	6.8	804	12	AG077527
C 12	87	6.8	1101	12	CNS001T2
C 13	86.8	6.8	1101	12	CNS000SX
C 14	86.4	6.7	1025	12	CNS014J2
C 15	86.4	6.7	1036	12	CNS00599
C 16	86	6.7	974	12	CNS001TT
C 17	84.8	6.6	1101	12	CNS0153V

18	84.4	6.6	778	12	AG058257
C 19	84.4	6.6	1101	12	CNS017V2
C 20	84	6.5	966	10	BM415686
C 21	83.8	6.5	934	12	AZ184244
C 22	83.8	6.5	967	12	CNS0772W
C 23	83.8	6.5	1101	12	CNS017Y0
C 24	83.6	6.5	830	3	BI645072
C 25	83.4	6.5	968	12	AQ687544
C 26	83.2	6.5	796	12	CNS0118D
C 27	83.2	6.5	875	12	AZ184435
C 28	83	6.5	1885	10	BE420745
C 29	82.8	6.4	922	12	AZ548363
C 30	82.6	6.4	834	12	BI2387
C 31	82.6	6.4	855	12	AZ183849
C 32	82.6	6.4	907	12	CNS021J4
C 33	82.6	6.4	1101	12	CNS012JN
C 34	82.4	6.4	688	9	AL514901
C 35	82.4	6.4	763	12	AG040720
C 36	82.4	6.4	850	12	AZ186328
C 37	82.4	6.4	1101	12	CNS00LJT
C 38	82.2	6.4	737	12	CNS008BU
C 39	82.2	6.4	833	12	CNS007X3
C 40	82	6.4	1135	12	CNS033GQ
C 41	81.8	6.4	773	3	BI644474
C 42	81.8	6.4	781	12	AG171177
C 43	81.8	6.4	947	10	BM416081
C 44	81.6	6.4	942	12	CNS018GS
C 45	81.6	6.4	963	12	CNS00A4L

ALIGNMENTS

RESULT 1
CNS00601/c
LOCUS
DEFINITION

CNS00601 990 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BAC14J23 of RPC1-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

AL065624
AL065624.1 GI:4944693
GSS:
fruit fly.

ORGANISM

Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

AUTHORS

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPC1-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

COMMENT

FEATURES

source

1. .990
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPC1-98"

Page 2

Query Match	7.58;	Score 95.8;	DB 12;	Length 990;
Best Local Similarity	41.48;	Pred. No. 0.00013;		
Matches 325;	Conservative 56;	Mismatches 401;	Indels 3;	Gaps 2

KEYWORD	VERSION	GI:4117649
ORGANISM	Oryza sativa	
AUTHORS	Wing R.A. and Dean R.A.	
TITLE	A BAC End Sequencing Framework to Sequence the Rice Genome	
JOURNAL	Unpublished (1998)	
COMMENT	Contact: Ming RA Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288 Fax: 864 656 4293 Email: rwing@clemson.edu Seq primer: GCGAACACTGATGACATG Class: BAC ends High quality sequence start: 4 High quality sequence stop: 123. Location/Qualifiers	
FEATURES	1. 982	
source	/organism="Oryza sativa" /strain="Japonica" /cultivar="Nipponbare" /db_xref="taxon:4530" /clone="hbx0021814" /clone_lib="CGI Rice BAC Library" /tissue_type="leaf" /lab_host="E. coli DH10B" /note="Vector: pbelBAC11; Site_1: HindIII; Site_2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arunagathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."	
BASE COUNT	141 a 69 c 43 g 674 t 55 others	
ORIGIN		
Query Match	7.3%; Score 94.2; DB 12; Length 982;	
Best Local Similarity	42.6%; Pred. No. 0.00023;	
Matches 324; Conservative	0; Mismatches 437; Indels 0; Gaps 0;	
Oy	153 aacaagctgcacagctatgaagaattacttacttactcaaatgagaccgatat 212	
Db	888 AAGAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 829	
Oy	213 ggattatgacacaagaactgttgacttttctttaagaagaatcgtagcatttaa 272	
Db	828 AAAATTAATTAATTTTAAATAATTAATTAATTAATTAATTAATTAATTAAT 769	
Oy	273 aagttataaaggattatctttagaactcgatccctacttgcacatatacaagaagata 332	
Db	768 AATTAAATTAATTAATTTTAAATTAATTAATTAATTAATTAATTAATTAAT 709	
Oy	333 tgatggaatattaaataatcatccaacgctgtagtggcttaactaacaattgacatt 392	

399 AAAN 340
 Db 690 tccttagcatatagacttgaaacttaccacattgaaagaaagaaacatgaaca 749
 QY 339 AA 280
 Db 750 atacaagaagattgcaaaagctgaaagatttagaagaaagaaacagataatcaaaa 809
 QY 279 AA 220
 Db 810 aacgatttaataatagacacttaaacacaaagagaagaaacaaatgaactaaattaga 869
 QY 219 AA 160
 Db 870 agaagcacttcaactacacaaagaca 896
 Db 159 AA 133

RESULT 6
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 LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #
 DEFINITION BACR05N11 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
 ACCESSION AL061936
 VERSION AL061936.1 GI:4940214
 KEYWORDS GSS.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 1101)
 Genoscope.
 Direct Submission
 TITLE Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
 COMMENT - Web : www.genoscope.cns.fr)
 Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pictet de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's PI and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
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 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone_lib="RPCI-98"
 /clone="BACR05N11"
 /note="end : TET3"
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 Matches 320; Conservative 32; Mismatches 411; Indels 1; Gaps 1;
 QY 510 tttaagaaagaaatactaaagtgtaaaagtggttaagtgctgtttctatc 569
 Db 102 TTTAATTAAAKAKNDTAATAAATAAANHAHAHAHAHAHAHAHAHAHAHAHAHAHAHAHAHA 161

570 taaagatgaatgccgattccgtcaatttgcgaagatgactacacagagaagaagattt 629
 Db 162 AA 221
 QY 630 caacgactggtggagtgactcttattacaatagatttaaaactcttgaaatgtaagat 689
 Db 222 AA 281
 QY 690 tccttagcatatagacttgaaacttaccacattgaaagaaagaaacatgaaca 749
 Db 282 AA 341
 QY 750 atacaagaagattgcaaaagctgaaagatttagaagaaagaaacagataatcaaaa 809
 Db 342 AA 401
 QY 810 aacgatttaataatagacacttaaacacaaagagaagaaacaaatgaactaaattaga 869
 Db 402 AA 461
 QY 870 agaagcacttcaactacacaaagaca 896
 Db 462 AA 521
 QY 930 tattattaatccattgaaagtggttattatgcagtggtgttcgaatgaatcgcga 989
 Db 522 TAWTTTTTWTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 581
 QY 990 cttgcaggtagttatgcattcagtggaagattgaatgaatgcagtggtgtttctt 1049
 Db 582 ATTTAATAAATAAATTTTAAATTAATAAATAAATAAATAAATAAATAAATAAATAA 640
 QY 1050 tgacggtataactctatggtatgcagcgagacattctcagaagatgcacgtggtgg 1109
 Db 641 TTTTWTATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 700
 QY 1110 cgttataataataaaagggttacaatgcagtggtttatgaatataattggtgattcgt 1169
 Db 701 WTTTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 760
 QY 1170 taaacaaatttaaacacagcgtcaagacatacaacacatacaacatacaacatacaaaa 1229
 Db 761 AWAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 820
 QY 1230 ataaatgatttcagtagagagaatttagaataatgaatt 1273
 Db 821 AAWAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 864

RESULT 7
 BI645011/c standard; RNA; EST; 798 BP.
 ID BI645011
 AC BI645011;
 XX BI645011;
 XX BI645011.1
 XX 13-SEP-2001 (Rel. 69, Created)
 DT 13-SEP-2001 (Rel. 69, Last updated, Version 1)
 XX
 DE OP2810 Mixed Stage EST's from Globodera pallida, the potato cyst nematode
 DE Globodera pallida cDNA, mRNA sequence.
 XX
 KW EST.
 XX
 OS Globodera pallida
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
 OC Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
 XX
 RN [1]
 RP Heer J., Sosinski B., Pokrzywa R.M., Wary A., Opperman C.;
 RA "Mixed Stage EST's from Globodera pallida, the potato cyst nematode";
 RT

Unpublished.

CC Contact: Opperman, C
CC Center for the Biology of Nematode Parasitism
CC NC State University; IACR-Rothamsted
CC Campus Box 7616; Raleigh, NC 27695, USA
CC Tel: 919.515.6699
CC Fax: 919.515.9500
CC Email: warthog@unity.ncsu.edu
CC No homology found. ; GT11-6PCN_F_D07_PCN_6_F_058.abl.seq.screen.

Key Location/Qualifiers

1. 788
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/note="Vector: lambda GT11; This is a collaborative effort
between IACR-Rothamsted and North Carolina State
University. The library was constructed from mixed stage G.
pallida in lambda GT11 by Paul Burroughs,
IACR-Rothamsted."
/organism="Globodera pallida"
/clone.lib="Mixed Stage EST's from Globodera pallida, the
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Sequence 788 BP; 68 A; 24 C; 8 G; 613 T; 75 other;

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Best Local Similarity 41.9%; Pred. No. 0.0015;
Matches 323; Conservative 0; Mismatches 444; Indels 3; Gaps 1;

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DB 778 AAAAAAAAAAAAAAAAAAGTATTAATAAAAAAAAAAAAAAAAAAATAAG 719
QY 573 agatgaatgcgaatccgtcaattatggaagatcagcaggaagaagattc 632
DB 718 AAGATAAAG 659
QY 633 cgcgtgagcagatctctatcagaatgaaatcttgaatgtaagattcc 692
DB 658 AAAAAAAAAAAAAAAAAAGATTAAGATAAATAAAAAAAAAAAAAAAAAA 599
QY 693 ttgaatataagacttgaactcattccacatgaaagaacatgacata 752
DB 598 AATAAATA 539
QY 753 caacaagaatctgaaagcgtgaagaattgaaagaacccgataatcaaaac 812
DB 538 AA 479
QY 813 gattataaataagcaacttaaacacagaagaacgaatgaattgaaga 872
DB 478 AAAAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 422
QY 873 agacttcaactcaacaagaacatggtatcaccatagcagctgtttctat 932
DB 421 AATAAATA 362
QY 933 tattaatcattggaattgtatattatgcaagtggtcattgaatcgtcact 992
DB 361 AAAAAAAAAAAAAAAAAATAAATAAATAAATAAATAAATAAATAA 302
QY 993 tgcaggtatgcaatcagtggaatgaatgaatcgcgttgaatcacaat 1052
DB 301 AAAAAAAAAAAAAAAAAATAAATAAATAAATAAATAAATAAATAA 242
QY 1053 cgttataactctatgcatcagcgaagactctcagaagatgacatg 1112
DB 241 NNTNNNTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTT 182
QY 1113 tattaattaaaaagtgcaatgacagatgttataatattgtgtttcgttaa 1172

DB 181 TTTTTCCTCCAAAAAAAAAAAAAAAAAGGCGGCGGTCTTTTAA 122

QY 1173 accaattaataacagcgtcaagaatatacaacactaaagaattataaata 1232

DB 121 AA 62

QY 1233 aatgattcagtaagagagattgataatgaattacagatt 1282

DB 61 AAGCT 12

RESULT 8
BMA15636/C 910 bp mRNA linear EST 28-JAN-2002

LOCUS OP20714 Mixed Stage EST's from Globodera pallida, the potato cyst
nematode Globodera pallida cDNA, mRNA sequence.

DEFINITION BMA15636
VERSION BMA15636.1 GI:18382435

KEYWORDS EST.
SOURCE Globodera pallida.

ORGANISM Globodera pallida.
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchinae;
Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.

REFERENCE 1 (bases 1 to 910)
Heer, J., Sosinski, B., Pokrzywa, R.M., Wary, A. and Opperman, C.
Mixed Stage EST's from Globodera pallida, the potato cyst nematode

JOURNAL Unpublished (2001)
CONTACT: Opperman, C
CENTER for the Biology of Nematode Parasitism
NC State University; IACR-Rothamsted
Campus Box 7616; Raleigh, NC 27695, USA
Tel: 919.515.6699
Fax: 919.515.9500
Email: warthog@unity.ncsu.edu
GT11-6PCN_F_D07_PCN_6_F_058.abl.

FEATURES
Location/Qualifiers

1. 910
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/clone.lib="Mixed Stage EST's from Globodera pallida, the
potato cyst nematode"
/note="Vector: lambda GT11; This is a collaborative effort
between IACR-Rothamsted and North Carolina State
University. The library was constructed from mixed stage
G. pallida in lambda GT11 by Paul Burroughs,
IACR-Rothamsted."

BASE COUNT 72 a 28 c 11 g 724 t 75 others

ORIGIN
Query Match 6.9%; Score 88.6; DB 10; Length 910;
Best Local Similarity 41.9%; Pred. No. 0.0014;
Matches 323; Conservative 0; Mismatches 444; Indels 3; Gaps 1;

QY 513 aagaaagaataaataaagttcaaaagttggttaagttcgtttctatctaa 572
DB 900 AAAAAAAAAAAAAAAAAAGTATTAATAAAAAAAAAAAAAAAAAAATAAG 841
QY 573 agatgaatgcgaatccgtcaattatggaagatcagcaggaagaagattc 632
DB 840 AATAAATA 781
QY 633 cgcgtgagcagatctctatcagaatgaaatcttgaatgtaagattcc 692
DB 780 AAAAAAAAAAAAAAAAAAGATTAAGATAAATAAAAAAAAAAAAAAAAAA 721
QY 693 ttgaatataagacttgaactcattccacatgaaagaacatgacaata 752
DB 720 AAAAAAAAAAAAAAAAAATAAATAAATAAATAAATAAATAAATAA 661
QY 753 caacaagaatctgaaagcgtgaagaattgaaagaacccgataatcaaaac 812
DB 660 AA 601

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Query Match      6.8%; Score 87.4; DB 12; Length 614;
Best Local Similarity 49.8%; Pred. No. 0.0023;
Matches 215; Conservative 9; Mismatches 205; Indels 3; Gaps 1;

QY 813 gattaataaataagacacttaaaacaagaagaagcaaaatgaagctaaattagaaga 872
DB 600 AAAAAAANAATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 544
QY 873 agcacttcacacacaagaacatggtgtatcattaccatgcgcgtggtcttcttat 932
DB 543 AANANANANANANANANANANANANANANANANANANANANANANANANANANAN 484
QY 933 tattaatccattggaagttgtattatgcaggtggttcacgcgaagaatcgctcatt 992
DB 483 ATAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 424
QY 993 tgcaggtgattgacattcagtggaagattgaataacgcgttagatcacacattga 1052
DB 423 AANANANANANANANANANANANANANANANANANANANANANANANANANANAN 364
QY 1053 ccgttataacttctatggtatcagcgagagacttctcagaagatgcacctgatgtg 1112
DB 363 NNTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTT 304
QY 1113 tattaaatttaaaaggttacaatgcagatggttattgaatatattggtatttcgttaa 1172
DB 303 TTTTTCCTCCCAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 244
QY 1173 accaattataaccagcgtcacaaagcatatatacacactaaataaagattataaataaata 1232
DB 243 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 184
QY 1233 aatgatttccagtaagaggaatttagataatgaaattttacagagatt 1282
DB 183 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 134

RESULT 9
CNS0152H 614 bp DNA linear GSS 26-JUL-1999
LOCUS Drosophila melanogaster genome survey sequence SP6 end of BAC
DEFINITION BACN12N03 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL104915
VERSION AL104915.1 GI:5616929
KEYWORDS fruit fly.
SOURCE Drosophila melanogaster
ORGANISM Drosophila melanogaster
REFERENCE 1 (bases 1 to 614)
AUTHORS Karyota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
TITLE Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
JOURNAL Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.
FEATURES
source Location/Qualifiers
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/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN12N03"
/note="end : SP6"
BASE COUNT 553 a 0 c 0 g 41 t 20 others
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http://fulllength.invtrogen.com" 63 others

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clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
location/Qualifiers

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FEATURES
source
location/Qualifiers
1. .804
/...ism"Pan tron]advtes"

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BASE COUNTY
ORIGIN

Best Local
Matches 22

[illegible]

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Qy	926	tctttatttcaatccattggaattggtatattgacggtgctcatcgaatgaatc	985
Db	425	NAANN	484
Qy	986	gtcactctgcagtgatgtaatgacatcagtyggaatgatataacgctgtgatccaa	1045
Db	485	NN	544
Qy	1046	acattgacgctataactctatagtcacgacggagacctctcagaagctcacctgacg	1105
Db	545	AAAAANNNANNN	604
Qy	1106	ttggcgttatctaatttaaaaaggttacatgcagatggttataatgatatgtgtagt	1165
Db	605	NNAAAAANNN	664
Qy	1166	tcgtttaaaccaatataaacacgcggtacaaagcatatacacacataaaaaagattaa	1221
Db	665	NNAAAAANNN	724
Qy	1226	aaaaataatgattcttcgtaagaaggaattgaatataatgaatttacga	1279

[illegible]

BASE COUNT	148 a	88 c	6 g	522 t	261 others
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Query	248 ttaagaacatcgtagcatatttaaaagttaagaagattactttagaatcattccctt 307				
Db	780 KTGCAAAAARTRTRTGTGTAAAAAATATGRTGRTAAATTAATTRTKKKTGATG 721				
Qy	308 acttgccatatacctaagaagatcatgtgtgcchatttaaaatcttaaccgtygat 367				
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Qy	428 acccaatatacctaatactgacatggtctgtactgtatttagaagtagtgacgaaga 487				
Db	600 KKTWTKKTTTTRAAWAAAGRGCTGKAGKAGTRRDWMAAAAAAATAAAAAAAGG 541				
Qy	488 cgcctcatcaagaacatgagacagtttagaataaagaataacttaaaagtccaataaag 547				
Db	540 GGTGADADAAAAAGDAAARADAGWMAAAARATTAATGTGTTKKTGTACTAGTAAGAT 481				
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Db	120 AATATTCNNCMAATACCTTTTATASMTTNNNNNNNAANATATWNTANNNNNNNNNNG 61				
Qy	968 gtcca 972				
Db	60 NNNNA 56				
RESULT 15	CNS00599/c 1036 bp DNA linear GSS 03-JUN-1999				
LOCUS	Drosophila melanogaster genome survey sequence TET3 end of BAC #				
DEFINITION	BAC11116 of RCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.				
ACCESSION	AL057797				
VERSION	AL057797.1 GI:4932579				
KEYWORDS	GSS				
SOURCE	fruit fly.				

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BASE COUNT	64 a 56 c 41 g	701 t 174 others
ORIGIN		

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Query Match      6.7%; Score 86.4; DB 12; Length 1036;
Best Local Similarity 43.6%; Pred. No. 0.0027;
Matches 181; Conservative 38; Mismatches 196; Indels 0; Gaps 0;

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Db 647 MAAAAAAGYSTSYACATRAAAAANRRRAAAARVMAAAAAAARAAAAAATKCGAAMAGA 588

QY 542 aaatggtgttaaggttcgtttctctctaaagatgaatccgcatctccgcgaattta 601
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 587 ANMAAGAGCTAAATAAYAGYAATGAKAWATAWAAKAAAGTSTRAAATATWAKAAAGAA 528

QY 602 tggagaatactacagagaagaagatttcaacgatcgtggcgatgcctctctattacaata 661
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Db 527 NAKAGRTDGAKAAAAAANAATATDRAAAAAAANAANAANAANAANAANAANAANAANA 468

QY 662 gattaaataactttgaaaatgtaaaagattccottgcagcatatagacatttgaaccttaca 721
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Db 467 RAGADAMWAKGDSGRGAAGKWCXAGWATAAAATTAATGTTATAAAACWATKKKAPAGAA 408

QY 722 ttccacattatgaaaaagacatgacaatacaacaaagatttgcaaaagctgaaaaag 781
   : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 407 KAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 348

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Db 347 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 288

QY 842 aaagaagacaaatgaagctaattagaaagcagcacttcaactacaaacaagaaca 896
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Db 287 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 233

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Search completed: June 20, 2002, 14:27:04
Job time: 17734 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2002, 22:12:45 ; Search time 12428.6 Seconds
(without alignments)
2183.803 Million cell updates/sec

Title: US-09-509-234C-48
Perfect score: 1297
Sequence: 1 acgacgcgaattgtgc.....tatgaattacagagtaa 1297

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: gb.htg.*

3: gb.in.*

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29: em.vi.*

30: em.htg_hum.*

31: em.htg_inv.*

32: em.htg_other.*

33: em.htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
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RESULT 1
A97492 A97492 1297 bp DNA linear PAT 26-JAN-2000
LOCUS Sequence 48 from Patent WO9916780.
DEFINITION A97492
ACCESSION A97492
VERSION A97492.1 GI:6780838
KEYWORDS Staphylococcus schleiferi.
SOURCE Staphylococcus schleiferi.
ORGANISM Staphylococcus schleiferi
Bacteria; Firmicutes; Bacillus/Clostridium group;
Staphylococcus group; Staphylococcus.

REFERENCE 1 (bases 1 to 1297)
AUTHORS Gala, J. and Vannuffel, P.
TITLE GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS
JOURNAL Patent: WO 9916780-A 48 08-APR-1999;
GALA JEAN LUC (BE); UNIV LOUVAIN (BE)

FEATURES
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1. .1297
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3	825.6	63.7	1266	1	AF144662	AF144662 Staphyloc
4	722.6	55.7	1371	6	A97497	A97497 Sequence 53
5	722.4	55.7	1350	1	SSV12875	Y12875 Staphylococ
6	704.4	54.3	1257	1	AF144663	AF144663 Staphyloc
7	703.4	54.2	1295	6	A97488	A97488 Sequence 44
8	700.2	54.0	1260	1	AF145333	AF145333 Staphyloc
9	699.6	53.9	1263	1	SSD66880	U66880 Staphylococ
10	698.8	53.9	1263	1	AF099965	AF099965 Staphyloc
11	684.8	52.8	1263	1	AF145332	AF145332 Staphyloc
12	681	52.5	1343	1	SHV12874	Y12874 Staphylococ
13	681	52.5	1343	6	A97496	A97496 Sequence 52
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16	672.4	51.8	1877	1	SEU23713	U23713 Staphylococ
17	670.6	51.7	1283	6	A97490	A97490 Sequence 46
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23	652.6	50.3	1305	6	A97484	A97484 Sequence 40
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26	648.2	50.0	1263	1	AF144661	AF144661 Staphyloc
27	645.6	49.8	1280	6	A97486	A97486 Sequence 42
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29	635	49.0	1179	6	AX141471	AX141471 Sequence
30	601.6	46.4	1284	6	A97494	A97494 Sequence 50
31	596.6	46.0	1254	1	AF099966	AF099966 Staphyloc
32	589.2	45.4	1328	6	A97445	A97445 Sequence 1
33	386	29.8	3115	1	AF269316	AF269316 Staphyloc
34	386	29.8	3115	6	AX144636	AX144636 Sequence
35	347.8	26.8	1551	1	AF106849	AF106849 Staphyloc
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QY 961 tctatgcagcggcgcacagcagaacgatttcgcatcttcgctggaagtcagcagtgcaa 1020
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DB 1261 agaagggagattattggtgatgaattacagagttaa 1297
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RESULT 2
AF099967      1266 bp      DNA      linear      BCT 02-NOV-1998
LOCUS      Staphylococcus schleiferi factor essential for methicillin
DEFINITION      resistance fEma (fema) gene, complete cds.
ACCESSION      AF099967
VERSION      AF099967.1
KEYWORDS      GI:3820633
SOURCE      Staphylococcus schleiferi.
ORGANISM      Bacteria; Firmicutes; Bacillus/Clostridium group;
      Bacillus/Staphylococcus group; Staphylococcus.
REFERENCE      1 (bases 1 to 1266)
AUTHORS      Vannuffel, P., Heusterspreute, M., Bouyer, M., Philippe, M. and Gala
      J.-L.
TITLE      Molecular characterization of fema from Staphylococcus hominis,
      Staphylococcus saprophyticus and Staphylococcus haemolyticus and
      fema-based discrimination of staphylococcal species
JOURNAL      Res. Microbiol. (1998) In press
REFERENCE      2 (bases 1 to 1266)
AUTHORS      Vannuffel, P., Heusterspreute, M. and Gala, J.-L.
TITLE      Direct Submission
JOURNAL      Submitted (21-OCT-1998) IBCN, UCL, Clos Chapelle-aux Champs
      30/3046, Bruxelles 1200, Belgium
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Query Match 96.2%; Score 1248; DB 1; Length 1266;
Best Local Similarity 100.0%; Pred. No. 4, 6e-204;
Matches 1248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 acgagcgctgaatttgctgtttacagatcaaatgccatatagccatttcacgcaaatg 60
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QY 61 gtagggaactatgaattaaagggtgtcgaaggtttgaacacacattctgtcgccattaaa 120
DB 79 GTAGGGAATATGAATTAAGAGTGTCTGAAGGTGTTGAACACATCTTGTGCGCATTA 138
QY 121 gatacaacaataactagcagcagctgttactgacagcagcagcagcagcagcagcagc 180
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QY 181 tttaaatatttttatacaaccgagcagcagcagcagcagcagcagcagcagcagcagc 240
DB 199 TTTAATATTTTATCAACCGGAGCAGTCAATGAGTCAATGAGTCAATGAGTCAATG 258
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QY 301 gtagcccttatttaccatgtttaagcgaacacatgatgagtgagtgagtgagtgagtgag 360
DB 319 GTAGCCCTTATTTACCAATGTTAAAGCGAACCATGATGTTGAAGTGAATGAAGATAC 378
QY 361 ggcagtgactggtttttgataaaatgctgaattaaacttggaacatgaagtgattcaca 420
DB 379 GCGAGTGACTGTTTGTATATAATGGCTGAATTAACCTTTGAACATGAAGTGTTCACA 438
QY 421 actgggtttgatacaataaggcaaatcgttttcattctgtcgtcgtcgtcgtcgtcgtcgt 480
DB 439 ACTGGGTTTGATACATATAGGCAATTCGTTTTCATTCTGCTGATGTTGAAATATAA 498
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DB 499 ACATCAAAAGACATCTTAATCAATGGAATTTAAGGAAGAAGAAATACGAAAAGTA 558
QY 541 cagaaaatggttgaaagtcgctcatcaaaagagatgaattacattatttcgctcgtcgt 600
DB 559 CAGAAAATGTTGTAAGTCCGCTATCTTAACGAGATGAATTAACATATTTCCGTTCC 618
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QY 661 catcgtatgaataactataagatcgtccgctaccatagcagcagcagcagcagcagcagc 720
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QY 721 gcatatttagcagagcctcaactgaagcagcagcagcagcagcagcagcagcagcagcagc 780
DB 739 GCATATTTAGCAGACTCAACACTGAAGCGCAAGACTTTTAAAAAGAAATTCGAAAAGCA 798

RESULT 3
AF144662 1266 bp DNA linear BCT 01-JUN-1999
LOCUS Staphylococcus intermedius factor essential for methicillin
DEFINITION resistance (femA) gene, complete cds.
ACCESSION AF144662
VERSION AF144662.1 GI:4929300
KEYWORDS Staphylococcus intermedius.
SOURCE Staphylococcus intermedius.
ORGANISM Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
REFERENCE 1 (bases 1 to 1266)
AUTHORS Vannuffel, P., Heusterspreute, M. and Gala, J.-L.
TITLE Cloning and characterization of femA genes from Staphylococci
JOURNAL species
REFERENCE 2 (bases 1 to 1266)
AUTHORS Vannuffel, P., Heusterspreute, M. and Gala, J.-L.
TITLE Direct Submission
JOURNAL Submitted (21-APR-1999) LBCM, UCL 3046, Clos Chapelle-aux-Champs,
30, Bruxelles 1200, Belgium
FEATURES
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BASE COUNT 484 a 183 c 237 g 362 t
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Query Match 96.2%; Score 1248; DB 1; Length 1266;
Best Local Similarity 100.0%; Pred. No. 4, 6e-204;
Matches 1248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 acgagcgctgaatttgctgtttacagatcaaatgccatatagccatttcacgcaaatg 60
DB 19 ACAGCGCTGAATTTGGTGGCTTTACAGATCAATGCGCATATAGCCATTTACGCAATG 78
QY 61 gtagggaactatgaattaaagggtgtcgaaggtttgaacacacattctgtcgccattaaa 120
DB 79 GTAGGGAATATGAATTAAGAGTGTCTGAAGGTGTTGAACACATCTTGTGCGCATTA 138
QY 121 gatacaacaataactagcagcagctgttactgacagcagcagcagcagcagcagcagc 180
DB 139 GATAACACAATAACGCTAGCAGCACTGTTTACTGACAGCAGTGCAGTGAATGAAGTT 198
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DB 259 CATTTCTTTTAAATGAATTTCAAAATATGTTAGAATATATCAGCAGTGTATTGAGA 318
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QY 421 actgggtttgatacaataaggcaaatcgttttcattctgtcgtcgtcgtcgtcgtcgtcgt 480
DB 439 ACTGGGTTTGATACATATAGGCAATTCGTTTTCATTCTGCTGATGTTGAAATATAA 498
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DB 499 ACATCAAAAGACATCTTAATCAATGGAATTTAAGGAAGAAGAAATACGAAAAGTA 558
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BASE COUNT 458 a 208 c 258 g 342 t
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 Best Local Similarity 78.8%; Pred. No. 7.3e-132;
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 DB 139 GATTAATCAAAACCAAGTATTAGCTGCTTTATTACCTGCGTACAGCATGAAGTG 198
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RESULT 4
 A97497 1371 bp DNA linear PAT 26-JAN-2000
 LOCUS A97497
 DEFINITION Sequence 53 from Patent WO916780.
 ACCESSION A97497
 VERSION A97497.1 GI:6780844
 KEYWORDS
 ORGANISM
 Staphylococcus saprophyticus.
 Staphylococcus saprophyticus
 Bacteria; Firmicutes; Bacillus/Clostridium group;
 Bacillus/Staphylococcus group; Staphylococcus.
 REFERENCE
 1 (bases 1 to 1371)
 Gata,J. and Vannunfel,P.
 GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND
 TITLE
 PATENT: WO 9916780-A 53 08-APR-1999;
 JOURNAL
 GALA JEAN LUC (BE); UNIV LOUVAIN (BE)
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 Best Local Similarity 73.2%; Pred. No. 2.9e-114;
 Matches 949; Conservative 0; Mismatches 339; Indels 6; Gaps 1;
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Qy 10 gaatttgctgcttttacagatcaaatgccatatagccatttcacgcgaatcggtgaggaac 151

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0y	1210	ttaaataaagcaatataaagacaagataaaagaataagatatagcaaga	1261
Db	1292	ACGACATTGAAAAAATTAAGATATAAAAGAAATTAACATTAATAGAAAGGA	1343

1253

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Oy	553	gtgaagtcgcgcatalcaacgaagatgaattacatatttcogttcgitttgtgaagat	612
Db	553	GTGAAGAATGCTTTAGGGAAGATGATGCCAATTTTCCGTCATCATCAGAAAT	612
Oy	613	aacatcgacaacaagaatttgtagtaagagatggcagatttttatcatcgltgaa	672
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Oy	1153	atagaatgtcgtggtatttattataagacctataaacaacitgcctatacgttactta	1212
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Oy	1273	atgtgtgtaatttacagattaa	1297
Db	1268	GCTAGAAATGAATTTACAGATTTAA	1292
RESULT 8			
AF145333	API45333	1260 bp DNA linear BCT 22-JUL-1999	
LOCUS	Staphylococcus cohnii subsp. urealyticus methicillin resistance		
DEFINITION	protein fema (fema) gene, complete cds.		
ACCESSION	AF145333		
VERSION	AF145333.1 GI:5565908		
KEYWORDS	Staphylococcus cohnii subsp. urealyticus.		
SOURCE	Staphylococcus cohnii subsp. urealyticus		
ORGANISM	Bacteria; Firmicutes; Bacillus/Clostridium group;		

[illegible]

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 Db 979 TATTATGCAAGTGTAGTACGGAATGAATACCTCAGTTCGGGAGTATG 1038
 Qy 1021 tgggaatgattcaatgactgatttcaatccaaagataacttattgact 1080
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 Db 1099 AGCGACACTTACTGAGAGCGCTGAGAGGCGGCTGTGAAGTTCAAAA 1158
 Qy 1141 aatgcaagaatgataatgctgctgatttatttaagcctataaacaac 1200
 Db 1159 AACGCAATGATTAATGATGTTGAGACTTATGACCGATTAATGAAG 1218
 Qy 1201 acagctacttaaaatgaagaactaaagaagaataa 1242
 Db 1219 AACCTTATACAGCTTAAAGAAATCAAGATGATTAAC 1260

RESULT 10
 AF099965 1263 bp DNA linear BCT 02-NOV-1998
 LOCUS Staphylococcus xylosus factor essential for methicillin resistance
 DEFINITION fema (fema) gene, complete cds.
 ACCESSION AF099965
 VERSION AF099965.1 GI:3820629
 KEYWORDS Staphylococcus xylosus.
 SOURCE Staphylococcus xylosus
 ORGANISM Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus.
 REFERENCE 1 (bases 1 to 1263)
 AUTHORS Vannuffel, P., Heusterspreute, M., Bouyer, M., Philippe, M. and Gala, J.-L.
 TITLE Molecular characterization of fema from Staphylococcus hominis, Staphylococcus saprophyticus and Staphylococcus haemolyticus and fema-based discrimination of staphylococcal species
 JOURNAL Res. Microbiol. (1998) In press
 REFERENCE 2 (bases 1 to 1263)
 AUTHORS Vannuffel, P., Heusterspreute, M. and Gala, J.-L.

TITLE Direct Submission
 JOURNAL Submitted (21-OCT-1998) LBCM, UCL, Clos Chapelle-aux Champs
 30/3046, Bruxelles 1200, Belgium
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 source Location/Qualifiers
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 KKAVKNDNLEKOLLANOOK IDEAKTLOEHGNEHPIISAAYFIINPEVYVYAGTSH
 EFRFPASTYIOMKMINIAYIDHINDFNFIISGFTEDADGAVVFKFGNADVVE
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 BASE COUNT 496 a 151 c 236 g 380 t
 ORIGIN

Query Match 53.98; Score 698.8; DB 1; Length 1263;
 Best Local Similarity 73.04; Pred. No. 3.4e-110;
 Matches 898; Conservative 0; Mismatches 332; Indels 0; Gaps 0;

Db 13 ttgtgctgttcaacagataaagccatagcattccacgcaaatggttaggaact 72
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 Qy 73 gaattaaagcttcgaagtggttgaagaacacatctgtcgcattaaagaaca 132
 Db 91 GAATGAAATTCGAAAGATGCTGAACACATTTGATGATGATGATGATGAT 150
 Qy 133 aacgtactagcagcatgttactgacagcagtgccagtaagaagttttaatat 192
 Db 151 GAAGTCATTCGACCTGTTTATTATACAGTACAGTATGATGATGATGATTT 210
 Qy 193 taltcaaacgcgagccagctatgacatcagaataaagaagcgttcattccttt 252
 Db 211 TATACTAATAGAGTCCGCTGTATGATTTGAAAATTAAGAAATTTAGTCA 270
 Qy 253 aatgacttttaaaatgtaagaataatcaacgcatctgattgagaagacct 312
 Db 271 AATGAACTATCTTAATATGTAAGAAATCAATGCGTTATTTAAGGTTGAT 330
 Qy 313 ttacaatggttaagcgcaaacatgtagtgagtgatgaaagattacagcgag 372
 Db 331 TTAGCATATCAATACCGTAAATCATGATGATGATGATGATGATGATGAT 390
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[illegible]

Fri Jun 21 08:38:22 2002

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 Db 922 GAACAGCAATTAAGAACGACGACGACGACGACGACGACGACGACGACGACGACGAC 981
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RESULT 13
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 LOCUS Sequence 52 from Patent WO916780.
 DEFINITION A97496
 ACCESSION A97496
 VERSION A97496.1 GI:6780842
 KEYWORDS
 SOURCE Staphylococcus hominis.
 ORGANISM Staphylococcus hominis
 Bacteria; Firmicutes; Bacillus/Clostridium group;
 Bacillus/Staphylococcus group; Staphylococcus.
 1 (bases 1 to 1343)
 Galla, J. and Vanuifel, P.
 REFERENCES
 AUTHORS Staphylococcus hominis
 TITLE GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND
 DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS
 JOURNAL Patent: WO 916780-A 52 08-APR-1999;
 GALLA JEAN LUC (BE); UNIV LOUVAIN (BE)
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Query Match 52.5%; Score 681; DB 6; Length 1343;
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 Db 202 AATAAGATTAATGAAGTCATTTGCTGCTGTGTGTAACATCTGTACCCGTTATGAAAATT 261
 Qy 181 tttaataattttattcaaacgcgcgcacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 240
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 Db 622 CAATAAATGCTGTTAAAGTAAAGTTCCTTACTAAAGAAAGAAATTAACCTATTTCAGATCA 681
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RESULT 14
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LOCUS Staphylococcus epidermidis strain sri clone step.1017f06 genomic
DEFINITION sequence.
ACCESSION AF269697
VERSION AF269697.1 GI:9623592
KEYWORDS
SOURCE Staphylococcus epidermidis.
ORGANISM Staphylococcus epidermidis
          Bacillus/Clostridium group;
          Bacteria; Firmicutes; Bacillus/Staphylococcus.
REFERENCE 1 (bases 1 to 4434)
AUTHORS Kimmerly,W.J., Taylor,J.David., Nelson,A.J., Godlevski,M.M.,
          Rudino,M.A., Nelson,F.J., Rivers,P.R., Torrella-Miller,I.,
          Listenebee,S., Ashanti,C., Altschuler,G., Mammo,L., Shepherd,N.S.,
          Fuchs,R., Fleming,T., Guan,X., Du,L., Cain,D.H., Miller,G.S. and
          Furdon,P.J.
TITLE Transposon-mediated sequencing of the Staphylococcus epidermidis
      genome
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4434)
AUTHORS Taylor,J.David., Kimmerly,W.J., Nelson,A.J., Godlevski,M.M.,
          Rudino,M.A., Nelson,F.J., Rivers,P.R., Torrella-Miller,I.,
          Listenebee,S., Ashanti,C., Altschuler,G., Mammo,L., Shepherd,N.S.,
          Fuchs,R., Fleming,T., Guan,X., Du,L., Cain,D.H., Miller,G.S. and
          Furdon,P.J.
TITLE Direct Submission
JOURNAL Submitted (22-MAY-2000) Departments of Genomic Sciences and
      Bioinformatics, Genetics Directorate, Glaxo Wellcome, Inc., 5 Moore
      Drive, Research Triangle Park, North Carolina 27709-3398, USA
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Best Local Similarity 71.2%; Pred. No. 4,7e-106;
Matches 890; Conservative 0; Mismatches 360; Indels 0; Gaps 0;

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Search completed: June 20, 2002, 22:13:00
 Job time: 36590 sec

RESULT 15
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 LOCUS Sequence 3737 from Patent WO0134809.
 DEFINITION
 AX145015
 ACCESSION
 VERSION AX145015.1 GI:14283580
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM
 1. (bases 1 to 4434)
 Kimmerly, W.J.
 AUTHORS Staphylococcus epidermidis nucleic acids and proteins
 TITLE Patent: WO 0134809-A 3737 17-MAY-2001;
 JOURNAL GLAXO GROUP LIMITED (GB)
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 Best Local Similarity 71.2%; Pred. No. 4.7e-106;
 Matches 890; Conservative 0; Mismatches 360; Indels 0; Gaps 0;
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 QY 370 tggttttttgataaaatggcgtgaattaaactttgaacatgaaggttttcacaaactgggttt 429
 DB 3254 TGGATTTTGTGATTAAGAGTGTAGGATATAAACACAGAGGATCCCAAGGATTT 3313
 QY 430 gatacaataaaggcaaatctgttttcttctgctgctgctgctgctgctgctgctgctgctgct 489
 DB 3314 GATCTGTATTAACAAATCCGATATCATCTCTTCTTAATTTAGCAAAACAAAGTGTAAAT 3373
 QY 490 gacatcttaaatcaaatgataatttaagggaagaaataacgaaaaaggtacagaaaaat 549
 DB 3374 GATGTTTTAAAAAATGAGTGGTTTAAAGAACGCTAATACATAAAGATTTAAGAAAT 3433
 QY 550 ggtgtgaagtcgcgtatctataaacgaagatgaattacatatatttccgttcgttttatgaa 609
 DB 3434 GGAGTTAAAGTCCGCTTTTATCTGAAAGAGGTACTTATATTTAGGTTCATTTATGGAG 3493
 QY 610 gatacatctgaacaaaagattttgttagatagagatgacgattttttattatcatcgatg 669
 DB 3494 GATACCTCTGAACATAAGATTTTGCAGATAGAGAAGATAGTTTTTATTAACACAGATTC 3553

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us-09-509-234c-48.rge

Fri Jun 21 08:38:22 2002

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2002, 14:46:22 ; Search time 1139.49 Seconds
(without alignments)
1954.241 Million cell updates/sec

Title: US-09-509-234C-48
Perfect score: 1297
Sequence: 1 acgacggctgaattgggtgc.....tatgaattacagagtaa 1297

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1736436 seqs, 858457221 residues 3472872
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802.*
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20: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	1297	100.0	1297	20 AAX37802	Staphylococcus sch
2	722.6	55.7	1371	20 AAX37805	Staphylococcus sap
3	703.4	54.2	1295	20 AAX37800	Staphylococcus xyl
4	674	52.0	4434	22 AAH54373	S. epidermidis gen
5	672.2	51.8	1342	20 AAX37804	Staphylococcus hom
6	670.6	51.7	1283	20 AAX37801	Staphylococcus cap
7	666.4	51.4	1257	15 AAQ78141	Staphylococcus epi
8	652.6	50.3	1305	20 AAX37798	Staphylococcus hae
9	645.6	49.8	1280	20 AAX37799	Staphylococcus lug

10	635	49.0	1179	22 AAH52400	S. epidermidis ope
11	601.6	46.4	1284	20 AAX37803	Staphylococcus sci
12	589.2	45.4	1328	20 AAX37797	Staphylococcus sp.
13	386	29.8	3115	22 AAH53994	S. epidermidis gen
14	322.8	24.9	3821	18 AAH74615	Staphylococcus aur
15	310	23.9	6528	21 AAZ49723	Staphylococcus sim
16	282.8	21.8	1470	20 AAZ22843	Staphylococcus aur
17	282.8	21.8	1470	20 AAZ19882	Staphylococcus aur
18	281.2	21.7	1245	23 AAH55125	Staphylococcus aur
19	280.8	21.6	3271	18 AAH74747	Staphylococcus aur
20	256	19.7	1260	23 AAH54419	Staphylococcus aur
21	254	19.6	1257	23 AAH51636	Staphylococcus aur
22	252.8	19.5	1260	20 AAH07088	Staphylococcus aur
23	252.8	19.5	1260	20 AAH07091	Staphylococcus aur
24	250	19.3	1254	22 AAH52401	S. epidermidis ope
25	234.6	18.1	2453	22 AAH55015	Staphylococcus epi
26	221.8	17.1	453	21 AAH26858	S. epidermidis gen
27	221.8	17.1	453	22 AAH08009	Essential Staphylo
28	221.8	17.1	453	22 AAH08009	Staphylococcus aur
29	221.8	17.1	453	22 AAH08009	Staphylococcus aur
30	206.4	15.9	410	21 AAH26855	Essential Staphylo
31	206.4	15.9	410	22 AAH08006	Staphylococcus aur
32	206.4	15.9	410	22 AAH08006	Staphylococcus aur
33	193.6	14.9	514	18 AAH89751	Synthetic DNA frag
34	185.8	14.3	420	20 AAH89751	Essential Staphylo
35	170	13.1	400	21 AAH26853	Staphylococcus aur
36	170	13.1	400	22 AAH08004	Staphylococcus aur
37	170	13.1	400	22 AAH08004	Staphylococcus aur
38	147.2	11.3	795	23 AAH50508	Staphylococcus aur
39	144	11.1	543	22 AAH71123	C. glutamicum SRT
40	143.6	11.1	1221	18 AAH74940	Staphylococcus aur
41	137.2	10.6	1281	23 AAH52835	Enterococcus faeca
42	127.4	9.8	10194	20 AAX13028	Enterococcus faeca
43	91	7.0	1266	23 AAH54453	Staphylococcus aur
44	90.2	7.0	1263	23 AAH51692	Staphylococcus aur
45	89.6	6.9	289	18 AAH75592	Staphylococcus aur

ALIGNMENTS

RESULT 1
AAX37802
ID AAX37802 standard; DNA; 1297 BP.
XX AAX37802;
AC AAX37802;
XX 09-JUL-1999 (first entry)
XX Staphylococcus schleiferi FemA DNA.
XX Staphylococcus schleiferi FemA DNA.
XX FemA: identification; detection; therapy; infection; femB;
XX amplification; genotyping; gram-positive bacteria; vaccine; ss.
XX Staphylococcus schleiferi.
OS Staphylococcus schleiferi.
XX Key Location/Qualifiers
XX 1..1297
XX CDS /*tag= a
XX /*product= "FemA"
XX /*note= "partial sequence, no start or stop codon"

PN WO9916780-A2.
XX PD 08-APR-1999.
XX PF 28-SEP-1998; 98WO-BE00141.
XX PR 26-SEP-1997; 97EP-0870146.
XX PA (BENA-) BELGIAN MIN NAT DEFENCE.
XX PA (UYLO-) UNIV CATHOLIQUE LOUVAIN.

PI Gala J, Vannuffel P;
 XX WPI: 1999-287521/24.
 DR P-PSDB: AAY08219.
 XX
 PT New Staphylococcus-specific oligonucleotides
 XX
 PS Claim 23: Fig 10a-b; 48pp; English.
 XX
 CC This invention describes novel Staphylococcus-specific oligonucleotides
 CC based on the consensus fema nucleotide sequence which are used to
 CC develop products for the identification, detection and therapy of
 CC infections. The oligonucleotides can be used for the genetic
 CC amplification, the identification and/or quantification of various fema
 CC sequences which are specific to known or unknown Staphylococci species.
 CC Since the fema sequence is similar to the molecular genotyping of fema
 CC oligonucleotides can also be used for the molecular genotyping of fema
 CC genes of different Staphylococci species or other gram-positive bacteria.
 CC The fema nucleic acids can also be used in therapeutic applications.
 CC They can also be used to identify inhibitors, e.g. antibodies or
 CC antisense oligonucleotides, for blocking expression of the fema
 CC nucleotide sequences. They can also be used for producing vaccines
 CC against Staphylococci infections.
 XX
 SQ Sequence 1297 BP: 495 A; 184 C; 249 G; 369 T; 0 other;

Query Match 100.0%; Score 1297; DB 20; Length 1297;
 Best Local Similarity 100.0%; Pred. No. 3.6e-255;
 Matches 1297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 acgagcgctgaatttggtggtgttacaagatcaaatgacattccacgcaaatg 60
 QY 61 gtgagggaactgaattgaatgaatggtggtgttgaacacattcttcgcat 120
 DB 61 gtgagggaactgaattgaatgaatggtggtgttgaacacattcttcgcat 120
 QY 121 gatacaacaataacgctactagcagcatttactgacagaagcagcaatgaat 180
 DB 121 gatacaacaataacgctactagcagcatttactgacagaagcagcaatgaat 180
 QY 181 tttaatt 240
 DB 181 tttaatt 240
 QY 241 cattctcttt 300
 DB 241 cattctcttt 300
 QY 301 gtaagacctatt 360
 DB 301 gtaagacctatt 360
 QY 361 ggcagtgacgtgttttttttttttttttttttttttttttttttttttt 420
 DB 361 ggcagtgacgtgttttttttttttttttttttttttttttttttttttt 420
 QY 421 actgggttt 480
 DB 421 actgggttt 480
 QY 481 acatcaaaagacatcttaataatcaatgataatttaagaaagaaatcgaa 540
 DB 481 acatcaaaagacatcttaataatcaatgataatttaagaaagaaatcgaa 540
 QY 541 cagaanaaatggtgtaagtcgctatcttaacgaaagatgaatttttttt 600
 DB 541 cagaanaaatggtgtaagtcgctatcttaacgaaagatgaatttttttt 600
 QY 601 ttatctgaagatacatctgaaacaaagattttgagatgagatgacattttat 660
 DB 601 ttatctgaagatacatctgaaacaaagattttgagatgagatgacattttat 660

DB 601 ttatctgaagatacatctgaaacaaagattttgagatgagatgacattttat 660
 QY 661 catcgtatgaataactataaagatggttcggtgacccactgcatatgtttat 720
 DB 661 catcgtatgaataactataaagatggttcggtgacccactgcatatgtttat 720
 QY 721 gatattgagagagctcaaacactgaagcgaagactttaaagaatttcgaa 780
 DB 721 gatattgagagagctcaaacactgaagcgaagactttaaagaatttcgaa 780
 QY 781 gataagaacatcgacaagcgctctgaaatcagaagccataaataaagaat 840
 DB 781 gataagaacatcgacaagcgctctgaaatcagaagccataaataaagaat 840
 QY 841 gagcaacaactagagaggaatcaagtaataaagaagcagaacattgcaat 900
 DB 841 gagcaacaactagagaggaatcaagtaataaagaagcagaacattgcaat 900
 QY 901 cagcgtgacacattacccgatttcggtgattttattatccatttgaag 960
 DB 901 cagcgtgacacattacccgatttcggtgattttattatccatttgaag 960
 QY 961 tattatgcagcgcgacagcaagcaatcttgcattttgtgaaagctacgca 1020
 DB 961 tattatgcagcgcgacagcaagcaatcttgcattttgtgaaagctacgca 1020
 QY 1021 ttgggaatgatttaattatgcatgatttattcaattccaagataaattat 1080
 DB 1021 ttgggaatgatttaattatgcatgatttattcaattccaagataaattat 1080
 QY 1081 agtggatatttttcgaaagatgcagaagatgcaggtgataaatttaaa 1140
 DB 1081 agtggatatttttcgaaagatgcagaagatgcaggtgataaatttaaa 1140
 QY 1141 aatgcagaagtaataatgataatgctggtgatttatttaagcctataa 1200
 DB 1141 aatgcagaagtaataatgataatgctggtgatttatttaagcctataa 1200
 QY 1201 acatctacttaataatgaagcaatttaagaacagataaagaatagata 1260
 DB 1201 acatctacttaataatgaagcaatttaagaacagataaagaatagata 1260
 QY 1261 agaagggattttatggtatgaatttcagagttaa 1297
 DB 1261 agaagggattttatggtatgaatttcagagttaa 1297

RESULT 2
 AAX37805 standard; DNA; 1371 BP.
 ID AAX37805
 XX
 AC AAX37805;
 XX
 DT 09-JUL-1999 (first entry)
 XX
 DE Staphylococcus saprophyticus Fema DNA.
 XX
 KW FemA; identification; detection; therapy; infection; fema;
 amplification; genotyping; gram-positive bacteria; vaccine; ss.
 XX
 OS Staphylococcus saprophyticus.
 XX
 FH Key Location/Qualifiers
 FT CDS 64..1326
 FT /*tag= a
 FT /product= "FemA"
 PN W09916780-A2.
 XX
 PD 08-APR-1999.
 XX
 PF 28-SEP-1998; 98WO-BE00141.

[illegible]

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OY		553	gtgaagaatccgctaactcaagaataatgaatcatatttcggttggttatygaagt	612
Db		553	gtgaagaatgaagttctttaaggagaatgagttgcgaatttcggttaattcaygaagt	612
OY		613	aacttcgaaaacaaaattttgttagatagagatgacgatattttatcatcgtatgaaa	672
Db		613	aacatcgaaaccaagaaccttgacgtatagagacgatgacctttactacaatagattaag	672
OY		673	tactataaagatcytgtccgcgtacacactagcgtatatttgattttaacgcatattnga	732
Db		673	tattataaagatcgcgtattagtagtacctagcttactgattatgatttcaagatatattgaa	732
OY		733	gaagctcaacatcggaagcgcgaagactttaaaaaagaaatgycaaaagcagataaagaacat	792
Db		733	gaattgaaagcgtgaacgctgaggtgttttaagcaaaagatccaataaagcagataaagaatcatc	792
OY		793	gacacgcttcctgnaaatcagaagaagccataataaaaaagaaaatttagacacaaacta	852
Db		793	gagaaaagacctgnaaatlaaaaaagcctaataaaaaagataactctagagaacaactt	852
OY		853	gaagcgaatcaagctbaataataaaagcagaacatgycgaacttaaacacgtgacaca	912
Db		853	atagagatcaacaaaaaatltgaggaagcctaaabctcaagaagaaagatgltacgaa	912
OY		913	ttaccgattccgctggtgattcttattatcatccatttgaggtgtgtttattatcgagc	972
Db		913	ctaccacatccagcagcatatttccatcaacttaaccccttagaagtagtattatcggggt	972
OY		973	ggcacagcaaaacgaatttcgattttgctggagagctacgcagtcgaatgygaatygat	1032
Db		973	ggagcgtcaaatgagtttagacattttgctgtagtatagtatgccattcaatgygaatygat	1032
OY		1033	aattatgcgatttgatttccaattccaagatatnaactttatgtgcattagtggtgattt	1092
Db		1033	aactatgcatcttgccctaatatgatatgatataattttatgagatttagtgctattt	1092
OY		1093	tccgaagatgcagagaatgycaggtgtgtataaatttaaaaaagcgtacatgycagaagta	1152
Db		1093	acagaaagatgcagagaatgycgcggtgtgatttaatttaaaaaagatatttaagcgaagta	1152
OY		1153	atgaaataatgctggtgattttattaaagcctataacacaacctgacctatacgttcta	1212
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Db		1213	acattaaag-----aaaattaaagataaaagaataaacatttaataagaggaactaa	1267
OY		1273	attgtagaataaattacagattaa	1297
Db		1268	gctagaatgaatttccagagttaa	1292
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ID	AAH54373 standard; DNM: 4434 BP.			
XX	AAH54373;			
AC				
XX	03-SEP-2001 (first entry)			
DT				
XX	S. epidermidis genomic polymucleotide sequence SEQ ID NO:3737.			
DE				
XX	Staphylococcus epidermidis SRI strain; infection; diagnosis;			
KW	vaccination; endocarditis; ds.			
XX				
OS	Staphylococcus epidermidis.			
XX				

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3254 tggatttttgatgaattagagagtttagatataaacacgaagattccacaaagattt 3313
 430 gatacaataagcgaattcgtttcattctgtcgtcgtgttgaaataaacaacacaa 489
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 730 gcagagctcaacacgtgaagcgaagccttttaaaagaaatttgcacaaagcgataa 789
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 1210 ttaaaataagcgaataaagacgaataaagacgaataaagacgaataaagacgaata 1299
 4094 agaactcttaaaactaaagaaatagatttttaagaaggaattatctaa 4143

RESULT 5
 AAX37804
 ID AAX37804 standard; DNA; 1342 BP.
 AC AAX37804;
 DT 09-JUL-1999 (first entry)
 XX Staphylococcus hominis Fema DNA.
 XX Fema; identification; detection; therapy; infection; femB;
 XX amplification; genotyping; gram-positive bacteria; vaccine; ss.
 XX Staphylococcus hominis.

PN W0200134809-A2.
 XX 17-MAY-2001.
 XX 09-NOV-2000; 2000WO-US30782.
 XX 09-NOV-1999; 99US-0164258.
 XX (GLAX) GLAXO GROUP LTD.
 PA Kimmerly WJ;
 PI WPI; 2001-316495/33.
 XX Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
 XX useful for vaccinating against infections, e.g. endocarditis -
 PT Claim 8; Page 1358-1360; 2188pp; English.
 XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
 CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
 CC (I) and (II) can have antibacterial activity and therefore can be used
 CC in vaccination. The nucleic acids (I) may be used to produce the
 CC S. epidermidis polypeptides (II) via the production of vectors
 CC containing them which are used to produce hosts cells which express the
 CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
 CC used to vaccinate subjects and to raise antibodies against the bacteria.
 CC The polypeptides may also be used to assay for other inhibitors of their
 CC activity and therefore identify compounds that may be used for the
 CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
 CC AAH55090 represent specifically claimed S. epidermidis genomic DNA
 CC polynucleotide sequences from the present invention. AAH55091 to
 CC AAH55098 represent oligonucleotide sequences and primers which are used
 CC in the exemplification of the present invention.
 CC N.B. The present invention specifically claims all the polynucleotide
 CC sequences given in the sequence listing of the present specification,
 CC however the sequence listing only goes up to SEQ ID NO:4454 so even
 CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
 CC no sequences are present for SEQ ID NO:4455 to 4464.
 XX Sequence 4434 BP; 1676 A; 554 C; 819 G; 1385 T; 0 other;

Query Match 52.0%; Score 674; DB 22; Length 4434;
 Best Local Similarity 71.2%; Pred. No. 3 5e-128;
 Matches 890; Conservative 0; Mismatches 360; Indels 0; Gaps 0;
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Db	501	acaggattctgcataattacaattcaaatctgcgtccattccagttttaatttaaggataa	560
Oy	481	acatacaagaacatcttaataatgtataattttaagaaagaagaatacgaanaagta	540
Db	561	actcgttaagaatgtatttaattggaatgtatgtattctgcgaagaagaataactaaaaagtc	620
Oy	541	cagaataaagtgtcgaagtcgcgtcatctaaacgaagatgaattacatatcttcgctgc	600
Db	621	caaaaaagtggtttaagtaagtaattcttactcaagaagaattccattttcagatca	680
Oy	601	ttatgtgaagaatacctcgtgaacaaagattttgtatgataagatgaacgatttttat	660
Db	681	ttatgtgaagaatacctcagagataaagaatttctcgtatgagagatagttttactat	740
Oy	661	catcgtatgaataactataaagaatcgtgcgcgcgtaccactagcgtatatgtattat	720
Db	741	aatgatttgcattcaatttaagaatagattatgtactctcgcataataaatttgat	800
Oy	721	gcattatgacagagctcacaactagaacgcgcgaagactttaaaaaaattgcgaaga	780
Db	801	gaatatcttgaaagactcttcacgcagaacgtcgcagacataaataagactttaacaagct	860
Oy	781	gataaagactcgcgaacgcgcctgataatcagaagaagccaataaanaagaataatca	840
Db	861	ctaaaaagatatctgaaaaaagcccgataaacaanaaagacaanaataaanaataatctta	920
Oy	841	ggacacaacactgaagcgaatacgaactaaataaagaagaagaagaacatggaacttaa	900
Db	921	ggacgcgaactaaagaacatgagcaanaaatgtatgaagaacacaacttaattgaa	980
Oy	901	caacgttgacacattaccggttcgcgtcggaattcttattatcaattccatttgaagttgt	960
Db	981	catgttaacgnaattaccaatctgcgcggtctctcttatttaaccatttgaattgtta	1040
Oy	961	tatttgcaagcgcgcacacgaacgaatttcgctcattttgctggaacgcagcagtgcaa	1020
Db	1041	tatttgcaaggttggaagcgtcaataataatagaacacttcgcgtgaagttctgcagttcaa	1100
Oy	1021	tgggaagaatataattatgtggaattgattatccaattccaagataaactttatgtgcatt	1080
Db	1101	tggactatgataatatacgaattgtatcatgactgcagcgttaataattttatgysatt	1160
Oy	1081	agcgtggaattctcagaagaatgcgaagaatgcagtggtatataaattttaaaaagcatt	1140
Db	1161	agcgtgcattttaacgagtgtgcgtgaagatgcagtggtgtgttaaatttaaaaagattt	1220
Oy	1141	aatgcgaagaataatgaatatgtcgtgtgtttttttaagcctataaacaacatgcctat	1200
Db	1221	aatgcgaatgaattatgaatatgttcgtgtgtttctgttaacctataaataacccaagtat	1280
Oy	1201	acagctacttaaatataaagcattaaagaacagaataaagaataagtaag	1249
Db	1281	tcactatatacaacacttaaaaaaatttaaaaagagattgattaaagag	1329
RESULT	6		
AAK37801			
ID	AAK37801	standard; DNA; 1283 BP.	
XX	AAK37801:		
XX	09-JUL-1999	(first entry)	
DE		Staphylococcus capitis FemA DNA.	
XX		FemA: identification; detection; therapy; infection; femB:	
KW		amplification; genotyping; gram-positive bacteria; vaccine; ss.	
XX			

Staphylococcus capitis...
OS XX Key Location/Qualifiers
FH 1..1283
FT CDS /tag- a
FT /product- "femA"
FT /note- "partial sequence, no start or stop codon"
XX
XX W09916780-A2.
XX PN 08-APR-1999.
XX PD 28-SEP-1998; 98WO-BE00141.
XX PF 26-SEP-1997; 97EP-0870146.
XX PR (BENA-) BELGIAN MIN NAT DEFENCE.
XX PA (UYLO-) UNIV CATHOLIQUE LOUVAIN.
XX PI Gala J, Vannuffel P;
XX DR WPI: 1999-287521/24.
XX DR P-PSDB: AAY08218.
XX XX New Staphylococcus-specific oligonucleotides
XX PT Claim 21; Fig 9a-b; 48pp; English.
XX PS
XX CC This invention describes novel Staphylococcus-specific oligonucleotides
XX CC based on the consensus femA nucleotide sequence which are used to
XX CC develop products for the identification, detection and therapy of
XX CC infections. The oligonucleotides can be used for the genetic
XX CC amplification, the identification and/or quantification of various femA
XX CC sequences which are specific to known or unknown Staphylococci species.
XX CC Since the femA sequence is similar to the femB sequence, the
XX CC oligonucleotides can also be used for the molecular genotyping of femB
XX CC genes of different Staphylococci species or other gram-positive bacteria.
XX CC The femA nucleic acids can also be used in therapeutic applications.
XX CC They can be used to identify inhibitors, e.g. antibodies or
XX CC antisense oligonucleotides, for blocking expression of the femA
XX CC nucleotide sequences. They can also be used for producing vaccines
XX CC against Staphylococci infections.
XX SQ Sequence 1283 BP; 484 A; 170 C; 224 G; 405 T; 0 other;

Query Match 51.7%; Score 670.6; DB 20; Length 1283;
Best Local Similarity 71.6%; Pred. No. 1.4e-127;
Matches 880; Conservative 0; Mismatches 349; Indels 0; Gaps 0;
QY 10 gaatttggtggttcaagatcaaatgcatatagccatttcacgcaaatgtaggaac 69
DB 10 gaatttggtggttcaagatcaaatgcatatagccatttcacgcaaatgtaggaac 69
QY 70 tatgaattaaaggtgctgaaggtgttgaaacacatctgtgcgcatttaagaatacaac 129
DB 70 tatgaattaaaggtgctgaaggtgttgaaacacatctgtgcgcatttaagaatacaac 129
QY 130 aataacgtactagcgatgttttactgacagcagtgccagtaagtatttaaatat 189
DB 130 aataacgtactagcgatgttttactgacagcagtgccagtaagtatttaaatat 189
QY 190 ttttattcaaacggcgacgtatggtactgacgcaataaagagctgcttattcttt 249
DB 190 ttttattcaaacggcgacgtatggtactgacgcaataaagagctgcttattctttc 249
QY 250 ttttaataacgtttcaaaaatgttaagaataatcacgcattgtatttgagagtagacct 309
DB 250 ttttaataacgtttcaaaaatgttaagaataatcacgcattgtatttgagagtagacct 309
QY 310 tatttacaattgtaagcgaaacccatgattggaagtattgaaagatacgcgagtgac 369
DB 310 tatttacaattgtaagcgaaacccatgattggaagtattgaaagatacgcgagtgac 369

RESULT 7
AAQ78141
ID AAQ78141 standard; DNA; 1257 BP.
XX AC AAQ78141;
XX AC 19-JUL-1995 (first entry)
XX DE Staphylococcus epidermidis femA gene.
XX KW femA protein; femA gene; methicillin-resistant bacteria; ds.

```

XX Staphylococcus epidermidis.
OS
XX Key Location/Qualifiers
FH mal_peptide 1.1257
FT /tag- a
XX
XX EP625575-A.
XX PD 23-NOV-1994.
XX PF 25-APR-1994; 94EP-0302950.
XX PR 30-APR-1993; 93US-0057163.
XX (EHLIL ) LILLY & CO ELI.
PA Alborn WE, Hoskins JA, Skatrud PL, Unal S, Unal S;
PI WPI; 1994-359748/45.
PI P-PSDB; AAR63440.
DR
XX Claim 2; Page 15; 23pp; English.
XX
XX AAO78141 encodes AAR63440 the FemA protein from Staphylococcus
XX epidermidis (SE). AAO78141 can be used in disruption studies in
XX SE. These studies can be used to generate an assay for agents
XX which inhibit the FemA protein, and are therefore useful in
XX combination with antibiotics to treat methicillin-resistant
XX bacteria.
XX
XX Sequence 1257 BP; 485 A; 154 C; 225 G; 393 T; 0 other:
SQ
Query Match 51.48; Score 666.4; DB 15; Length 1257;
Best Local Similarity 71.68; Pred. No. 1e-126;
Matches 874; Conservative 0; Mismatches 346; Indels 0; Gaps 0;
QY 10 gaattggtggtttacagatcaatgacatagcattccagcaaatggtggagac 69
D6 34 gaattggtggtttacagatcaatgacatagcattccagcaaatggtggagac 93
QY 70 tatgaattaaaggttgcgtgaaggtgtggaacacactctgtgcgcatlaaagaataaac 129
D6 94 taagaattaaaggttgcgtgaaggtgtggaacacactctgtgcgcatlaaagaataaac 153
QY 130 aataagctactagcagcatgttactgcagcagcagtcgacagatgaagattttaaatat 189
D6 154 aacgaagtgatgcagcgtgttactgcagcagcagtcgacagatgaagattttaaatat 213
QY 190 ttattatcaaacgcgcgcagcgcagtcagtcagcagcaataaagcgtcgttattctt 249
D6 214 ttattatcaaacgcgcgcagcgcagtcagtcagcagcaataaagcgtcgttattctt 273
QY 250 tttaagaactttcaaaatagttgaagaataatcagcagcgttattgaagtagagcct 309
D6 274 tttaagaactttcaaaatagttgaagaataatcagcagcgttattgaagtagagcct 333
QY 310 taattacaaatgttaagcgaacacatgagtgagtgagtgagtgagtgagtgagtgag 369
D6 334 taacttccatatacatatttaataatcagcagcagcagcagcagcagcagcagcagc 393
QY 370 tgggtttttgataaagcgtgaattgaactttgaacacagaggtttcaacactgggtt 429
D6 394 tggattttttgataaagcgtgaattgaactttgaacacagaggtttcaacactgggtt 453
QY 430 gatacaataaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 489
D6 454 gatctgtattcaaaatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 513

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QY 490 gacatcttaataatgataatgataaggaagaagaataatcagcaaaatgacagcaaaat 549
D6 514 gatgttttaaaaacatgacgttataagaagcgttaataaataaagaagttagaanaat 573
QY 550 ggtgtgaagtcctgcgtatcacaagcagatgaaatctacatttccgttccgttattgaa 609
D6 574 ggaattaaagtcctgcgttattcagaagaaggtttaccatttttaagtcattttagag 633
QY 610 gatacatgaaacaaagattttgtatagatagatgacagcagttttatttctcgtatg 669
D6 634 gataccctgaacaaataagattttgcagatagagaagatgatttttatttacaacagc 693
QY 670 aaatactataaagatcgttcgcgtaccagcagcagcagcagcagcagcagcagcagc 729
D6 694 aaacattataagccgtgttttagtaccagcagcagcagcagcagcagcagcagcagc 753
QY 730 gcaagcgtcaacacgtgaagcgaagcagcagcagcagcagcagcagcagcagcagc 789
D6 754 gaggaaactaaatgaagaagaatgtgcttaataaagattataaagcgtttaaagac 813
QY 790 atcgaagcgtcctgtaaaatcagaagcagcagcagcagcagcagcagcagcagcagc 849
D6 814 attggaagcgtccagagaataaagaacacatacaaaaaggaatttgaacacaa 873
QY 850 ctagaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 909
D6 874 ctgagatgaacacagcaaaaataatgaagcagcagcagcagcagcagcagcagcagc 933
QY 910 acattacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 969
D6 934 gaattacacacacacacacacacacacacacacacacacacacacacacacacacac 993
QY 970 ggcgcgaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1029
D6 994 ggtgcgaacacacacacacacacacacacacacacacacacacacacacacacacac 1053
QY 1030 attaatatgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1089
D6 1054 attaatatgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1113
QY 1090 tttaagaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1149
D6 1114 tttaagaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1173
QY 1150 gtaataaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1209
D6 1174 gtaataaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1233
QY 1210 ttaaatataagcaattaa 1229
D6 1234 agaacacttaaaaactaa 1253

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RESULT 8
 AAX37798
 ID AAX37798 standard; DNA; 1305 BP.
 XX
 AC AAX37798;
 DE 09-JUL-1999 (first entry)
 XX
 DE Staphylococcus haemolyticus FemA DNA.
 XX
 KW FemA; identification; detection; therapy; infection; femB;
 KW amplification; genotyping; gram-positive bacteria; vaccine; ss.
 OS Staphylococcus haemolyticus.
 XX
 XX Key Location/Qualifiers
 FT CDS 4..1305
 FT /tag- a
 FT /product- "FemA"

XX 09-JUL-1999 (first entry)
DT
XX
XX
XX
DE Staphylococcus lugdunensis FEMa DNA.
XX
XX FEMa; identification; detection; the
KW amplification; genotyping; gram-posi
KW
XX
XX Staphylococcus lugdunensis.
OS

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XX Key Location/Qualifiers
FH CDS 1..1280
FT /tag= a
FT /product= "FemA"
FT /note= "partial sequence, no start or stop codon"
XX
XX MO9916780-AZ.
XX
XX 08-APR-1999.
XX
XX 28-SEP-1998; 98MO-BE00141.
XX
XX 26-SEP-1997; 97EP-0870146.
XX
XX (BENA-) BELGIAN MIN NAT DEFENCE.
XX (UYLO-) UNIV CATHOLIQUE LOUVAIN.
XX
XX Gaia J, Vannuffel P;
XX WPI; 1999-287521/24.
XX P-PSDB; AAY08216.
XX
XX New Staphylococcus-specific oligonucleotides
XX
XX Claim 17; Fig 7a-b; 48bp; English.
XX
XX This invention describes novel Staphylococcus-specific oligonucleotides
XX based on the consensus femA nucleotide sequence which are used to
XX develop products for the identification, detection and therapy of
XX infections. The oligonucleotides can be used for the genetic
XX amplification, the identification and/or quantification of various femA
XX sequences which are specific to known or unknown Staphylococci species.
XX Since the femA sequence is similar to the femB sequence, the
XX oligonucleotides can also be used for the molecular genotyping of femB
XX genes of different Staphylococci species or other gram-positive bacteria.
XX The femA nucleic acids can also be used in therapeutic applications.
XX They can also be used to identify inhibitors, e.g. antibodies or
XX antisense oligonucleotides, for blocking expression of the femA
XX nucleotide sequences. They can also be used for producing vaccines
XX against Staphylococci infections.
XX
XX Sequence 1280 BP; 484 A; 197 C; 221 G; 378 T; 0 other:

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Query Match 49.83; Score 645.6; DB 20; Length 1280;
Best Local Similarity 70.18; Pred. No. 1.7e-122;
Matches 867; Conservative 0; Mismatches 369; Indels 0; Gaps 0;

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OY 9 tgattgtgtgtgtttacagatcaaatgcatatagccatttcacgaagaatgtaggaa 68
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 9 tgaattcgtgtgtttcacagatcaaatgcatatagccatttcacgaagaatgtaggaa 68
OY 69 ctatgataaaggtgtgtgaaggtgtgtgaacacatctgtcgcatataagaagaa 128
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 69 ctataatttaaaagttgcgaaaaaacaagaacacatttattgtgtttaaataaa 128
OY 129 caataaagctactagcagatgtttactgacagcagtgccaaatgaatgttttaata 188
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 129 taagaagatgactgacgtgtttactgacagcagtgccaaatgaatgttttaata 188
OY 189 ttttattcaaacgcgcagcagtcagtcagtcagtcagtcagtcagtcagtcagtc 248
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 189 ctttaacgaataagagccagtcagtcagtcagtcagtcagtcagtcagtcagtc 248
OY 249 tttaatagaattcaaatatgttaagaataatcgcagatgttagtgagtagacc 308
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 249 ctttaagagctaaccaaatatttaaaaagataactgtctcattgtccgcatagatc 308
OY 309 ttatttccaatgttlaagcgaacatgtatgtgtgaagtgtatgaagatacgca 368
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 309 attacttactatcaataatagacacatgacgtgttaataaagcaaatgtcgcaatga 368

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OY 369 ctgggtttttgataaagtgtgaattaaacttgacatgaaggtttccacactggtt 428
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 369 ttggttttcaataaagtgaacaactgcgataccatcctatgtgtcttcaacagatatt 428
OY 429 tgatacaataaggaacttcgttttcttcgtcgcgtatgtgtgaataataaacacaa 488
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 429 tgatccaatattcaaatatgaatccattctattcttattttaaagtagacagctaa 488
OY 489 agacatcttaaatcaaatgtataatttaaggaanaaanaatcgaanaaagtacaagaaa 548
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 489 agatgttttaataataatgtatgtatgtatgtatgtatgtatgtatgtatgtatgt 548
OY 549 tgggtgtgaagtcgcgtatcctaagagatgtatgtatgtatgtatgtatgtatgtat 608
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 549 tggagtcagaagtaaaagttccttaccgaaagaactcctaccccttcgtttattatga 608
OY 609 agatcacatcaaacgaagaattctgtatagatgaatgtatgtatgtatgtatgtat 668
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 609 gcagagctcagaatacctaagaattctcgtatagagacgacacatttatacaatcggt 668
OY 669 gaatactataaagatgtgtcgcgtatccactagcgtatgtatgtatgtatgtatgtat 728
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 669 taagtactataaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 728
OY 729 agcagagctcaacatgaagcgaagaacttaaaaagaatgtcaaaagcagaataaga 788
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 729 agagaagactcaacgaatgaacgaacactttagaanaaagatttagcgaagcactaa 788
OY 789 catcgacagcgtcttgaataatcagaagcctaataataaagaataatttaggcagaca 848
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 789 catcggaagcagcagacagatacaaaaagctataataaagcagaacacttaacacaca 848
OY 849 actagaagcgaatcagaactaataaagaagcagaacacacttaacacacaggttga 908
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 849 actcagatgcacatcaacaaaagttaaatgagctatcattgtatcaacgcgaacaggt 908
OY 909 cacattacgattcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 968
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 909 tgggttactatcttcgtcggtttcttatttattatcgttttgaagttgttatacgc 968
OY 969 agcagcagcagaacgaatttgcattttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1028
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 969 tggagtgaccgttaataatcgtcatcttgcagtgatgtgtgtgtgtgtgtgtgtgt 1028
OY 1029 gatttaattgcattgtatcaaatccaaatataactttatgtgcaatgtgtgtga 1088
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1029 gatttaattgcattgcagacgcgcagcatagacagatataatttcaacgcatgtgtga 1088
OY 1089 ttttcagaagatgcagagaatgtcaggtgtgtataaatttaaaaagcatalaagcaga 1148
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1089 ctctcagatgagctgcagagcaggtgtcattcgttttaaaaagcatalaagcaga 1148
OY 1149 agtaataatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1208
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1149 agtattgttaatagttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1208
OY 1209 cttaaatataagcaatataaagaacagataaag 1244
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1209 ttcaagtttaaacgattcacaataaagcatalagag 1244

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RESULT 10
AAH52400
ID AAH52400 standard; DNA; 1179 BP.
XX
XX AAH52400;
XX
XX 03-SEP-2001 (first entry)
XX
XX S. epidermidis open reading frame nucleotide sequence SEQ ID NO:193.
XX
XX Staphylococcus epidermidis SRI strain; infection: diagnosis;
XX
XX vaccination; endocarditis; ds.
XX

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XX Staphylococcus epidermidis.
OS WO200134809-A2.
XX 17-MAY-2001.
XX 09-NOV-2000; 2000WO-US30782.
XX 09-NOV-1999; 99US-0164258.
XX (GLAX) GLAXO GROUP LTD.
XX Kimmerly WJ;
XX WPI: 2001-316495/33.
XX P-PSDB; ANG81550.
XX Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
XX useful for vaccinating against infections, e.g. endocarditis.
XX Claim 8; Page 95; 2188pp; English.
XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
XX (II), given in ANG81550 to ANG83120, from Staphylococcus epidermidis.
XX (I) and (II) can have antibacterial activity and therefore can be used
XX in vaccination. The nucleic acids (I) may be used to produce the
XX S. epidermidis polypeptides (II) via the production of vectors
XX containing them which are used to produce hosts cells which express the
XX polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
XX used to vaccinate subjects and to raise antibodies against the bacteria.
XX The polypeptides may also be used to assay for other inhibitors of their
XX activity and therefore identify compounds that may be used for the
XX treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
XX AAH55090 represent specifically claimed S. epidermidis genomic DNA
XX polynucleotide sequences from the present invention. AAH55091 to
XX AAH55098 represent oligonucleotide sequences and primers which are used
XX in the exemplification of the present invention.
XX N.B. The present invention specifically claims all the polynucleotide
XX sequences given in the sequence listing of the present specification,
XX however the sequence listing only goes up to SEQ ID NO:4454 so even
XX though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
XX no sequences are present for SEQ ID NO:4455 to 4464.
XX Sequence 1179 BP; 456 A; 144 C; 212 G; 367 T; 0 other;
Query Match 49.08; Score 635; DB 22; Length 1179;
Best Local Similarity 71.2; Pred. No. 2.5e-120;
Matches 839; Conservative 0; Mismatches 340; Indels 0; Gaps 0;
QY 58 atgtaaggaactatgaattaaaggtgtcgaaggtgttgaaacacacatcttgcgcatt 117
DB 1 atggaaggttaatacgaattaaaggtgtcgaaggtaccgagtcacatttagttgaatt 60
QY 118 aaagataacacataaagctactagcgcgtgtttactgacagcagtcgcagtaaggaag 177
DB 61 aaaaataatacgaaggtgttcgagctgtttattacacagctgttcctgtaacgaaa 120
QY 178 ttttttaaaatatttttcaaacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 237
DB 121 atatttaaatatttttcccatcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 180
QY 238 gtcaattcttttttaataaactttcaaaatattgttaagaataatcagcgcattgtttg 297
DB 181 gtacatttttttttaataaactttcaaaatattgttaagaataatcagcgcattgtttg 240
QY 298 agagttagacccttattacacatgttaagcgaacacatgagtggtgaagtgattgaaga 357
DB 241 agagttgaccatccatccatcaatatttaataatcagtgaggggaaataactggaat 300
QY 358 taaggcagtgactggttttttgaataaagtgctgaattaaactttgaacatgaaggttc 417

Db 301 gcaggcatgattggtatttttgatgaattagagagtttaggataataaacacgaagattc 360
QY 418 acaactgggtttgatcaataaaggcaaatcgttttcattctgtcgtcgtgtaaat 477
Db 361 cacaaggattgactctgtattacaatccgatactattctgttcttaatttagcaac 420
QY 478 aaacatcaaaaagacatcttaataatcaaatgataatttaaggaagaaataacgaaaaa 537
Db 421 aaagtgtctatgttttaaaaacatggatgggttttaagaaagcgttaactaaaaa 480
QY 538 gtacagaaaaatggtgtgaagtcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 597
Db 481 gtttaagaaaaatggagttaaagtcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 540
QY 598 tcggtttatggaagatcacatctgaacacaaaagattttgtatagatagagatgagattttat 657
Db 541 tcatttatggaggttaactctgaactaaagattttgcagatagagagatagttttat 600
QY 658 tatcatcgtatgaataactataaagatcgtgtccgcgtaccactcgtatattgatttt 717
Db 601 tacaacagattcaaacattataaagacgcgttttagtaccactcgtatattgatttt 660
QY 718 aatgcattatttagcagagctcaactcgaagcgaagcatttaaaaaaagaaatgcacaa 777
Db 661 gatgatatatagaggaactaaataatgaagaaatgtcttaataaagattataataa 720
QY 778 gcagataaagacatcgcagc 837
Db 721 gctttaaaagacattggaagacgtccagagataaaaaagcacaatacaaaaaggaaaa 780
QY 838 tttagacaaactagaagcgaatcaagctaaataaaaaagacagacacattgcacatt 897
Db 781 tttagacaaactagaagcgaatcaagctaaataaaaaagacagacacattgcacatt 840
QY 898 aaacacgggtgacacattaccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 957
Db 841 gaacatggcaatgaattaccatctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 900
QY 958 gttattatgcaggc 1017
Db 901 gttaccacgc 960
QY 1018 caatgggaatgatattatgc 1077
Db 961 caatgggaatgatattatgc 1020
QY 1078 attagtggtatttttcagaagatgcagagatgcaggtgtgtgataaaaaatttaaaagcgc 1137
Db 1021 attagtggtatttttcagaagatgcagagatgcaggtgtgtgataaaaaatttaaaagcgc 1080
QY 1138 tataatgcagaagataatagatgt 1197
Db 1081 tatgatgc 1140
QY 1198 tatacagtcctactaaataaagcaattaaagacaaag 1236
Db 1141 tatacatttatagaacacttaaaaaactaaagaataag 1179

RESULT 11
AAH537803
ID AAX37803 standard; DNA; 1284 BP.
XX
XX AAX37803;
XX 09-JUL-1999 (first entry)
XX Staphylococcus sciuri FemA DNA.
XX
XX FEMa; Identification; detection; therapy; infection; femB;
KW amplification; genotyping; gram-positive bacteria; vaccine; ss.
XX
OS Staphylococcus sciuri.

XX Key Location/Qualifiers
 FH CDS 1.1284
 FT /tag="a"
 FT /product="Fema"
 FT /note="partial sequence, no start or stop codon"
 XX MO9916780-A2.
 XX 08-APR-1999.
 XX 28-SEP-1998; 98MO-BE00141.
 XX 26-SEP-1997; 97EP-0870146.
 XX (BENA-) BELGIAN MIN NAT DEFENCE.
 XX (OULO-) UNIV CATHOLIQUE LOUVAIN.
 XX Gala J, Vannuffel P;
 XX WPI: 1999-287521/24.
 XX P-PSDB: AAY08220.
 XX New Staphylococcus-specific oligonucleotides
 PS Claim 25; Fig 11a-b; 48pp; English.
 XX This invention describes novel Staphylococcus-specific oligonucleotides
 CC based on the consensus fema nucleotide sequence which are used to
 CC develop products for the identification, detection and therapy of
 CC infections. The oligonucleotides can be used for the genetic
 CC amplification, the identification and/or quantification of various fema
 CC sequences which are specific to known or unknown Staphylococcal species.
 CC Since the fema sequence is similar to the femB sequence, the
 CC oligonucleotides can also be used for the molecular genotyping of femB
 CC genes of different Staphylococcal species or other gram-positive bacteria.
 CC The fema nucleic acids can also be used in therapeutic applications.
 CC They can also be used to identify inhibitors, e.g. antibodies or
 CC antisense oligonucleotides, for blocking expression of the fema
 CC nucleotide sequences. They can also be used for producing vaccines
 CC against Staphylococcal infections.
 XX Sequence 1284 BP; 518 A; 181 C; 215 G; 370 T; 0 other:

Query Match 46.48; Score 601.6; DB 20; Length 1284;
 Best Local Similarity 67.98; Pred. No. 1.6e-113;
 Matches 874; Conservative 0; Mismatches 404; Indels 10; Gaps 2;

QY 10 gaattgctgcttacagatcaatgcatatagcatttcacgcaaatgtaggaac 69
 DB 7 gaattcaagctttacaataataaagtcgtagcgcatattacaagaagtaggaat 66
 QY 70 tatgaataaagctgcgaaggtcgtgaagaacacatctgtgcgcattaagaagaac 129
 DB 67 tatgaataaagaacatcgaagtagtactcaacacatctgtgcgcattaagaagaac 126
 QY 130 aatacgcgtagcagatgcttactgacagcagtcgccaagtaagaattttaaat 189
 DB 127 ggtggaatattagctgcgtcgtctgttaacaagtgaccagttatgaagaatttaaac 186
 QY 190 ttatttcaaacgcggaacgtagtactgactacgaaataagaagctgttcctt 249
 DB 187 ttatttcaaatagagcaggaatgattatgacacaagaacattgttgaacttttc 246
 QY 250 tttaatagaacttcaaatatgttaagaataatcacacattgatttagagtagaacct 309
 DB 247 tttaagaataatgtagcatttaaaagttataaagaattatctttagatagatgcct 306
 QY 310 tatttaacagttaagaacgaacatgtagtgaagtagtgaagaagtagcagatgac 369
 DB 307 tacttgcatacaactaagaagatcatgtgccaattttaaaatcattcaaccgtagat 366

QY 370 tggtttttgataaaatgctgaatttaactttgaacatggaaggttcacaactgggtt 429
 DB 367 ggttaatttaaacatttgaatcatttagttagaacacaaaggttcacaactgtttc 426
 QY 430 gatcaataaaggcaaatctgtttcattcgtcgtcgtcgtgaataaataacataaa 489
 DB 427 caccacaatacacaattagatgtagcattcgttagcttagttagaagtagtagcgaag 486
 QY 490 gacatttaaatcaatggataatttaaggaaaagaataacgaaaagaatgaagaataat 549
 DB 487 acgctcacaagaacactgtagcagtttaagaaaagaataatcaaaaagttcaaaaat 546
 QY 550 ggtggaagatcgctcattcctcaaacgaagtagaattatatttcctgttattgga 609
 DB 547 ggtgtaaaagtcgttcttctatcaataagaatgaatgcgcatatccgccaatttagaa 606
 QY 610 gataactcgaacaaaagaattttagatagagatgacgattttattatcatcgtatg 669
 DB 607 gatactacagaagaagaagatttcaacgacgtgtagatgacttcatatcaatagatta 666
 QY 670 aataactaagaagatcgtcgcgtacacacagtagatattttagatttaagcatatta 729
 DB 667 aataacttgaaaa---tgtaagattcctttagacatataatgacttgaacttaactatc 723
 QY 730 gcagagctcaacactggaagcgaagctttaaaaagaattgcaaaagcagataaagac 789
 DB 724 ccaaatatgaaaaagaacatgatacacaataaagaatttgcaaaagctgaaaaagat 783
 QY 790 atcgaagaagctctgtaaaatcagaagccataaataaagaataatttagagaacaa 849
 DB 784 ttgaaaagaagaacagatatacaaaaacgatttaataatagacacttaaaaacaa 843
 QY 850 ctgaagcgaatcaacagctcaaaataaagaagaagaacatgcaacttaaacagtgac 909
 DB 844 agaaagaacaaatgaagctcaaaatagaagaagccttcaacacaaagaacatgtgat 903
 QY 910 acattaccgattcgtcgtgattcttattatbaatcattgaggtgtttattatga 969
 DB 904 acattaccgaatgcgcgtgttcttattatbaatcattgaggtgtttattatga 963
 QY 970 ggcgacagcagaacgaatttcgcatctgtgcggaagctacgagcagatgggaatg 1029
 DB 964 ggtgttcacgaaatgaatatacgtacacttcgcaggtagtagttagcattcgtggaaatg 1023
 QY 1030 attaatatgcgattatattatcaaatccaaagatataactttatgcatatgtgat 1089
 DB 1024 attaatatgcgattatattatcaaatccaaagatataactttatgcatatgtgat 1083
 QY 1090 tttaagaagaatcagaagatcaggtgtgtataaatttaaaaaggtataatgacaa 1149
 DB 1084 ttctcagaagatgcacactgtatgttgcgttatttaaatcttaaaaaggtataatgacaa 1143
 QY 1150 gtaatagaatattgcgtgatttttaagcctataaacaacgtgactatagacgtc 1209
 DB 1144 gttatgaataatattgtgtatttcgttaaccacaatttaaaacagcgctlaaagaacat 1203
 QY 1210 ttaaaatnaagcaatbaaagaagaagaataaagaataagaatagtagaagaaggga 1269
 DB 1204 acaaacctaa-----aaaagttatlaaaaataaataatgatttcagtagaagggaat 1256
 QY 1270 ttatattgtagaattttacagattaa 1297
 DB 1257 tttagaatatgaattttacagattaa 1284

RESULT 12
 AAX37797 standard; DNA: 1328 BP.
 ID AAX37797
 AC AAX37797;
 XX 09-JUN-1999 (first entry)
 XX

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DE Staphylococcus sp. FemA consensus DNA sequence.
 XX FemA: identification; detection; therapy; infection; femB;
 KW amplification; genotyping; gram-positive bacteria; vaccine; ss.
 KK
 XX
 OS Synthetic.
 OS Staphylococcus sp.
 XX
 XX W09916780-A2.
 PN
 XX
 XX 08-APR-1999.
 XX
 XX 28-SEP-1998; 98WO-BE00141.
 XX
 XX 26-SEP-1997; 97EP-0870146.
 PR
 XX (BENA-) BELGIAN MIN NAT DEFENCE.
 XX (UYLO-) UNIV CATHOLIQUE LOUVAIN.
 PA
 PA
 PI Gala J, Vannuffel P;
 XX
 XX WPI; 1999-287521/24.
 DR
 XX
 XX
 XX New Staphylococcus-specific oligonucleotides
 PT
 XX
 XX Claim 1; Fig 3; 48pp; English.
 PS
 XX This invention describes novel Staphylococcus-specific oligonucleotides
 CC based on the consensus femA nucleotide sequence which are used to
 CC develop products for the identification, detection and therapy of
 CC infections. The oligonucleotides can be used for the genetic
 CC amplification. The identification and/or quantification of various femA
 CC sequences which are specific to known or unknown Staphylococci species.
 CC Since the femA sequence is similar to the femB sequence, the
 CC oligonucleotides can also be used for the molecular genotyping of femB
 CC genes of different Staphylococci species or other gram-positive bacteria.
 CC The femA nucleic acids can also be used in therapeutic applications.
 CC They can also be used to identify inhibitors, e.g. antibodies or
 CC antisense oligonucleotides, for blocking expression of the femA
 CC nucleotide sequences. They can also be used for producing vaccines
 CC against Staphylococci infections. This sequence represents a femA
 CC consensus DNA sequence composed from Staphylococcus sp. sequences.
 XX
 XX Sequence 1328 BP; 304 A; 78 C; 146 G; 227 T; 573 other;
 SQ
 Query Match 45.4%; Score 589.2; DB 20; Length 1328;
 Best Local Similarity 50.5%; Pred. No. 5.4e-111;
 Matches 655; Conservative 0; Mismatches 636; Indels 6; Gaps 1;
 Qy 1 acgagcggtgaattggtggtttacagatcaaatgcccataagcatttcacgcaaatg 60
 Db 35 acngnaganagtntnnnnntcngannnnatnncnannagcatttnaancanann 94
 Qy 61 gtagggaactatgaattgaagggtgtggaaggtgtggaacacacattgtgcgcaataa 120
 Db 95 nnnngnnantanganntnaanttgcnannnnnnnnngnncncaantagtgngnatnaa 154
 Qy 121 gatacaacaataacgtactagcagcatttactgacagcagtcgagcagtaagattt 180
 Db 155 aanaannataangnangntatgngcngntnnntnncngndtccngntnatgaaatn 214
 Qy 181 tttaataatttttataaaccgagcagcagtcagtcagtcagtcagtcagtcagtcagtc 240
 Db 215 tnaaantattttatcnaannngnccngntnatgntatnnaannnagcngntgn 274
 Qy 241 cattctcttttttaagaacttcaaatatgttaagaataatcacgcattgtattgaga 300
 Db 275 cantnttctttaangntnnnaantatnnaannnnnnnnnnnnnnnnnnnnnnnnnnnn 334
 Qy 301 gtagacccttatttaccatgttaagcggaacacacacacacacacacacacacacacac 360
 Db 335 ntngancocntannntnctatcaatannnnnaatcatgngngannntnnnnnnnnaatgcn 394

Qy 361 ggcagtgactggttttttgataaaaatggctgaattaaaactttgaacatgaaggtttcaca 420
 Db 395 ggnnangattggtntngatnann 454
 Qy 421 actggtgttgatacaataaaggcaaatgcttttcatctgtgctgctgctgctgctgctgct 480
 Db 455 aunggtttgancnntnnnncaaatngntnnccntngntnnccntngntnnccntngntnn 514
 Qy 481 acatcaaaaagacatcttaataatgaataaattgaagaaagaaatacagaaagaaagta 540
 Db 515 annncnnanganntnnnaannnnatggtngntnnngnnaannngnaannnaaanaaaagtn 574
 Qy 541 cagaaaaatggtgaaagtcgctctatctaaacgaagatgaattacattatttccgttgcg 600
 Db 575 nanaanaatggtgaaagtcgctctatctaaacgaagatgaattacattatttccgttgcg 634
 Qy 601 tttatggaagatcacatctgaacaaagaatttttagatagatagacgattttattat 660
 Db 635 ttnatggangatacnnccnann 694
 Qy 661 catcgatgaataactataaagatcgctccgctaccactagctatattgatttttaatt 720
 Db 695 aanngtntnnnnnnattnnaaagannnnngcnnngntnnngntnnngntnnngntnnnn 754
 Qy 721 gcattatgagagctcaacactgaagcgaagactttaaaaaaagaaataatgcagaaagca 780
 Db 755 gantntnnnnngaanntnn 814
 Qy 781 gataaagacatcgacacgctcctgaaatacgaagcgcataataaagaaataaattta 840
 Db 815 ntnaanganatnganaaangcngnanaanaaaangcnnnnnnnnnnnnnnnnnnnnnnnn 874
 Qy 841 gagcaacactagaagcgaatcaagctcaaaataaagaagcagacacattgcacactaaa 900
 Db 875 naanacaantnnngcnaann 934
 Qy 901 caggtgacacattaccgcttccgctggtggtttatttatttatttatttatttatttatt 960
 Db 935 catgnaangaattaccnatnctcngnnntcttntnnnnnnnnnnnnnnnnnnnnnnnn 994
 Qy 961 tattatcagcggcgacacaaagaaatttcgctatttctgctggaagtcagcagtgcaa 1020
 Db 995 tantangnggtggnacntcnaatnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 1054
 Qy 1021 tgggaaatgattattatgcgattgattatcaaatcccaagataataacttttattgcatt 1080
 Db 1055 tggnnnngatttaantatgcnntnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 1114
 Qy 1081 adgtgtgattttcagaagatgcagacagtcagagtcaggtgtgataaaattttaaaggctat 1140
 Db 1115 agnggtntantnnngannngcngagatgngngntnnnnnnnnnnnnnnnnnnnnnnnn 1174
 Qy 1141 aatgcagaagtaataagatgtcggtgattttatttatttatttatttatttatttatt 1200
 Db 1175 natcgannntnnngantngtngngntnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 1234
 Qy 1201 acagtctacttaataaagcgaatcaaaagcaagataaagataagataagataagcaag 1260
 Db 1235 nnn 1288
 Qy 1261 agaaggggtttattggtgataaatttacagagattaa 1297
 Db 1289 nann 1325

RESULT 13
 AAH53994/c
 ID AAH53994 standard; DNA; 3115 BP.
 XX
 XX AAH53994;
 XX
 XX 03-SEP-2001 (first entry)
 DT

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PI Rosen CA;
XX WPI: 1997-374922/35.
DR polynucleotide(s) and proteins derived from *Staphylococcus aureus*
PT stored on computer readable medium and used in the production of
PT anti-S.aureus vaccines
XX
XX Claim 1; Page 1139-1141; 3271pp; English.
XX This sequence represents one of 5191 *Staphylococcus aureus* DNA sequences
CC of the invention. The DNA sequences are recorded on a computer readable
CC medium, preferably selected from a floppy or hard disk, random access
CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
CC the S.aureus DNA sequences allows putative functions to be assigned so
CC that protein-encoding or regulatory regions of commercial, therapeutic or
CC industrial importance can be obtained. Specifically, sequences which are
CC likely to encode antigens have been identified and these polypeptides can
CC be used in a vaccine composition against *S.aureus* infection. The
CC polypeptides can also be used in a kit for the immunodetection of
CC *S.aureus* in a sample. *S.aureus* is implicated in numerous human diseases,
CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
CC skin and surgical wound infections, scalded skin syndrome, toxic shock
CC syndrome, etc. Organisms transformed with the DNA sequences can be used
CC for recombinant production of the polypeptides. The new DNA sequences
CC (and their fragments) are useful as primers or probes for isolating
CC homologues of any of the *S.aureus* DNA sequences contained on the
CC computer readable medium.
XX
XX Sequence 3821 BP; 1233 A; 548 C; 673 G; 1245 T; 122 other;
SQ

Query Match 24.9%; Score 322.8; DB 18; Length 3821;
Best Local Similarity 52.5%; Pred. No. 1.2e-56;
Matches 624; Conservative 1; Mismatches 563; Indels 0; Gaps 0;

QY 36 gccatattgcttcacgcaaatggtgagggaactgaattaaaggttgcgtgaagtggt 95
DB 3820 GCATTTTCACATTACACAAATCAGCTATTCTTACACATAGAGTTGATTTAAAGG 3761

QY 96 tgaacacattcttgcgcattaaagataacacaaataagctactgagcgatgttact 155
DB 3760 CGATGTCATCTGTAGGGGTTAAAGATGCAATGCTCAAGTGTTCAGGATGCTTTATT 3701

QY 156 gacagcagtcgcsagtaaggtttttaaataatttttcaaacgcggaccagtcac 215
DB 3700 GACAGAGCAGCGCACACTTAAATTTTCAAAATATTTTATACATCGCGGCCAGTGAT 3641

QY 216 ggactacgaaaaataaagagcgttcgttcattttttttaaataagcttttcaaaatgttaa 275
DB 3640 GGATATACAAATCAATCATATTAGTAGCATTTTCTTTAAAGCATTAACGTCATATTAA 3581

QY 276 gaaatcacgcattgtatttgagagtagacocctttttaccacaaatgttaagcgaaacca 335
DB 3580 GAAACACAAATGTTTATATGCTCTGTAGATCCATATTAAATGAAATTTACGCAATGC 3521

QY 336 tgatggtgaagtgtgaaagatacgcgagtgactggtttttttgataaaatggctgaatt 395
DB 3520 AGACGGTGAATTTGTTAAATCTTATGATTAACCGAGCATTTGTTAGAACAAATGGATAAT 3461

QY 396 aaactttgacatgaagtttccaaactgggtttgtatcacataaaggcaaatcttttca 455
DB 3460 AGGTTATAACACACACAGGTTTCCCTGTAGTTTATGATCAATGAGCAAAATCCGTGGCT 3401

QY 456 ttctgtgctcgatgttgaaataaataacacataacacatacttaataatcgaataatt 515
DB 3400 GTCAAGTTAGATTATTAAGATAAGACTGAAGACCACTTTTAAAGAAATGGATTATCA 3341

QY 516 aaggaataagaaatacagaataagacagaataatggtgtgaaagtcgcgtatcacaaga 575
DB 3340 AACGAGACGTAATTTAAATAAACATATGATTTGTTGTCATAAACTAAACAGTTAACGAT 3281

QY 576 agatgaattacatatttccgttcgttttatggaagatacatctgaaacaaaagatttgt 635

Db 3280 TGATGAACGCAAACTTTTTCGACTTATTCATATGGCTGAGGAAAGCAGCGTTTCAA 3221
QY 636 agatagatgacgattttttattatcatcgtatgaataactataaagatcgttcgcggt 695
Db 3220 ATTCCGTGAGTTACATACATCTTTGAGAAATGCAAAAGTTTATAGATGACCGCATGTT 3161
QY 696 accactgactatattttatgcatatttagcagagctcaacactgaagcgcaaga 755
Db 3160 AAAAGTTGGCGTATATGTTTAAACGAGTATTAAACACGTTTCAATTAAGCAACACACA 3101
QY 756 ctttaaaaaaagaattgcaaaagcagataaaacacacagcagcgtcctgaaatcagaa 815
Db 3100 ATTAACAGCTGAACCTCTCAGGTGTTGAAGAAGCATTTGGAAGAAGTCTCTTAATCAAGAA 3041
QY 816 agccataataaaaaaagaatttagcgaacaaactagaagcgaatcaagcgtcaaaaaa 875
Db 3040 AATAAAACGAAACGACACACAGCTAGAACACAGCTAAATAGCAATAAGCGTAAATCGA 2981
QY 876 agaagcagaacattgcaacttaaacacgcggtgacacattaccgatttcggtggtatt 935
Db 2980 CAATACATAGAACAAATTTGAACAAGATGGTGCAGTCTTAAACATTAGCTTCTCTTATT 2921
QY 936 tattattaatccatttgaggtttgtttattatgcagggcgacagcaaacgaattcgta 995
Db 2920 TATCTACAATGAGCATGAAGTTTATTCTTATCTAGTGTTCAAACCCCTAAATATATGC 2861
QY 996 ttttgcggaagcagcagtcgcaatgggaatgatttaattgattgattgattcaaat 1055
Db 2860 TTATATGGGTCCTACCACTTTCAGTGGGAAATGATTAAGTTTGTCTAAAGCGCATCAT 2801
QY 1056 tccaaagataaacttttgcgttagtggtgatttttcagaagatgcagaagatgcagg 1115
Db 2800 TGATCGCTATATTTTATGTTTATGCTATTACCGGTGACTTTTCAGATCATCAGAAGACTATGG 2741
QY 1116 tgtgataaatttaaaaaagcgtataatgcagaagtaagataatgctggtgatttat 1175
Db 2740 CGTCCAAACAATTTCAAAAAGGTTTAAACGCACATGTAGAANNNNNNNNNNNNNNNN 2681
QY 1176 taagcctataaacaacacgtcctatacagctcacttaacttaaaattaaagca 1223
Db 2680 NNN 2633

RESULT 15
AA249723
ID AA249723 standard; DNA; 6528 BP.
XX
XX AA249723;
AC
XX 18-APR-2000 (first entry)
XX
XX *Staphylococcus simulans* lysostaphin gene allelic variant-3.
XX Lysostaphin; antibiotic; anti-staphylococcal; endopeptidase;
KW gene therapy; mastitis; staphylococcal infection; ruminant; cow;
KW transgenic animal; allelic variant; altered lysostaphin gene; ds.
XX *Staphylococcus simulans*.
OS
XX
XX Location/Qualifiers
FH complement (2329..3810)
FT /tag=a
FT /product="Lysostaphin"
FT /trans_except= (pos:3808..3810, aa:Met)
XX
XX WO9967381-A1.
PN
XX
XX 29-DEC-1999.
PD
XX
XX 22-JUN-1999; 99WO-US14073.
PF
XX
XX 22-JUN-1998; 98US-0090175.
PR

PR 21-JUN-1999; 99US-0337079.
 PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
 PI Bramley JA, Plaut KI, Kerr D;
 XX WPI: 2000-147208/13.
 DR P-PSDB: AAY44648.
 XX
 PT Treatment of Staphylococcal infections, such as mastitis, in ruminant
 PT animals, especially cows -
 PS Disclosure: Fig 16; 61pp; English.
 XX
 CC The present sequence is an allelic variant of *S. simulans*
 CC lysostaphin gene cloned by Thumm and Goltz et al., supra and encodes a
 CC lysostaphin protein. Lysostaphin is an anti-staphylococcal protein
 CC having endopeptidase activity. The present sequence is used in the
 CC production of altered genes which allow expression and preferably
 CC secretion of active protein in mammalian cells/tissues. The
 CC modifications include operably linking the lysostaphin coding
 CC sequence to mammalian expression signals, removing two
 CC glycosylation sites in the wild type gene and preferably linking
 CC a mammalian signal peptide. The modified sequence
 CC is used in gene therapy to treat staphylococcal mastitis infections in
 CC ruminants, e.g. goats, sheep, and cows. It is also used to produce
 CC transgenic animals which are resistant to staphylococcal infections.
 CC
 SO Sequence 6528 BP; 2195 A; 1034 C; 1058 G; 2241 T; 0 other;
 Query Match 23.9%; Score 310; DB 21; Length 6528;
 Best Local Similarity 53.9%; Pred. No. 5.1e-54;
 Matches 637; Conservative 0; Mismatches 545; Indels 0; Gaps 0;
 QY 46 catttaacgaatgtaggaggaactgtaataagggttgctgaaggttggaacaacat 105
 DB 4079 catttaacgaatgtaggaggaactgtaataagggttgctgaaggttggaacaacat 105
 QY 106 ctgtcgacataaagaatacaacaataagctactagcagatgttactgacagcagtg 165
 DB 4139 ctgtcgacataaagaatacaacaataagctactagcagatgttactgacagcagtg 165
 QY 166 ccagtaatgaagtttttaatttttttttaacacggcgagacagctacgacagaa 225
 DB 4199 cgtgtttaaagttcttaaatatttcttaacacgcgcgcgcagcagcagcatttaa 4258
 QY 226 aataaagctcgttcattcttttttaagtaacttcaaatatgtttaagaataacac 285
 DB 4259 gaacatagatgtagcagatgttttttatgaaacattacgacctatctaaagaacaaac 4318
 QY 286 gcatgtatttgagtagagacctatttaccatgtaataagcgaaacatgatgtgaa 345
 DB 4319 tgcttaatagttttaacgagaccttaccctgttgaanaatattcgaatgttgacggaagaa 4378
 QY 346 gtgattgaagaatgagcagtgactggttttttgataaataagtcgtaataactttgaa 405
 DB 4379 atccctgaacctatgatacgaacactttatgaacgtagatgaattattaggttacggt 4438
 QY 406 catgaagtttcaacaactggttgatacaataagcgaaatcgtttcattctgtgtc 465
 DB 4439 catgaagtttcaacaactggtttatccaacaagtcagatcagatgtgtcgttcta 4498
 QY 466 gatgttgaataataacatcaagaacatcttaatacgaatgataatttaagaaaga 525
 DB 4499 aacctaagaataataagataaatacaatgtttaaagaataagattatcaaacacgcgt 4558
 QY 526 aatacgaataaagatacagaataatgtgtgaagtcgcgtatctaaacgaagaatgaat 585
 DB 4559 aatacgaataaagatacagaataatgtgtgaagtcgcgtatctaaacgaagaatgaat 585
 QY 586 catatttcggttcgtttatggaagatacatcgaacaaagaattttagatagaagat 645

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 Job time: 18789 sec

us-09-509-234c-48.rng

Fri Jun 21 08:38:22 2002

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ALIGNMENTS

RESULT 1
 1 Sequence 1, Application US/08330154-1
 2 Patent No. 5587307
 3 GENERAL INFORMATION:
 4 APPLICANT: Alborn Jr., William L
 5 APPLICANT: Hoskins, Joann
 6 APPLICANT: Skatrud, Paul L
 7 APPLICANT: Unal, Serhat
 8 TITLE OF INVENTION: FEM A GENE O
 9 TITLE OF INVENTION: FEM A PROTEI
 10 TITLE OF INVENTION: THE FEM A GE
 11 NUMBER OF SEQUENCES: 4
 12 CORRESPONDENCE ADDRESS:
 13 ADDRESSEE: Patent Division/AE
 14 STREET: Lilly Corporate Center
 15 CITY: Indianapolis
 16 STATE: Indiana
 17 COUNTRY: USA

ZIP: 46285
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/330,154
 FILING DATE: 27-OCT-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/208,925
 FILING DATE: 09-MAR-1994
 APPLICATION NUMBER: US/08/057,163
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Hamilton, Amy E
 REGISTRATION NUMBER: 33,894
 REFERENCE/DOCKET NUMBER: X-6894
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 317-276-3169
 TELEFAX: 317-276-1294
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1257 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS

GenCore version 4.5

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Run on: June 20, 2002, 12:04:01 ; Search time 208.59 Seconds
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US-09-509-234C-48
1297

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 38353 seqs, 122816752 residues 767066

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, Σ is the sum of the total score distribution.

SUMMARIES

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2	221.8	17.1	453	3	US-08-714-918-9	Sequence 9, Appli
3	221.8	17.1	453	4	US-09-265-315-9	Sequence 9, Appli
4	221.8	17.1	453	4	US-09-265-315-9	Sequence 9, Appli
5	221.8	17.1	453	4	US-09-266-417-9	Sequence 9, Appli
6	206.4	15.9	410	3	US-08-714-918-6	Sequence 6, Appli
7	206.4	15.9	410	4	US-09-265-315-6	Sequence 6, Appli
8	206.4	15.9	410	4	US-09-266-417-6	Sequence 6, Appli
9	206.4	15.9	410	4	US-08-714-918-4	Sequence 4, Appli
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11	170	13.1	400	4	US-09-265-315-4	Sequence 4, Appli
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13	170	13.1	400	4	US-09-266-417-4	Sequence 4, Appli
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NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/265,315
 FILING DATE: March 9, 1999
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/714,918
 FILING DATE: September 13, 1996
 APPLICATION NUMBER: 60/009,102
 FILING DATE: December 22, 1995
 APPLICATION NUMBER: 60/003,798
 FILING DATE: September 15, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Maiburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 240/247
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 453 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-265-315-9

Query Match 17.1%; Score 221.8; DB 4; Length 453;
 Best Local Similarity 66.7%; Pred. No. 6.9e-44;
 Matches 301; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

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RESULT 5
 US-09-266-417-9
 Sequence 9, Application US/09266417
 Patent No. 6228588
 GENERAL INFORMATION:
 APPLICANT: Benton, Bret
 APPLICANT: Lee, Ving J.
 APPLICANT: Malouin, Francois
 APPLICANT: Martin, Patrick K.
 APPLICANT: Schmid, Molly B.
 APPLICANT: Sun, Dongxu
 TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
 TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
 TITLE OF INVENTION: TARGET GENES
 NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/266,417
 FILING DATE: March 9, 1999
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/714,918
 FILING DATE: September 13, 1996
 APPLICATION NUMBER: 60/009,102
 FILING DATE: December 22, 1995
 APPLICATION NUMBER: 60/003,798
 FILING DATE: September 15, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Maiburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 240/248
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 453 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-266-417-9

Query Match 17.1%; Score 221.8; DB 4; Length 453;
 Best Local Similarity 66.7%; Pred. No. 6.9e-44;
 Matches 301; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

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Fri Jun 21 08:38:23 2002

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-714-918-6

Query Match 15.9% Score 206.4; DB 3; Length 410;
Best Local Similarity 68.6% Pred. No. 2.9e-40;
Matches 279; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

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RESULT 7
US-09-265-315-6
Sequence 6, Application US/09265315
Patent No. 6187541
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Ving J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315

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RESULT 6
US-08-714-918-6
Sequence 6, Application US/08714918
Patent No. 6037123
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Ving
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,918
FILING DATE: September 13, 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 222/005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

Page 6

Query Match	15.98;	Score 206.4;	DB 4;	Length 410;
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				Gaps 0;

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1 RESULT 8
2 US-09-265-315-6
3 ; Sequence 6, Application US/09265315
4 ; Patent No. 6187541
5 ;
6 ; GENERAL INFORMATION:
7 ;
8 ; APPLICANT: Benton, Bret
9 ;
10 ; APPLICANT: Lee, Ying J.
11 ;
12 ; APPLICANT: Malouin, Francois
13 ;
14 ; APPLICANT: Martin, Patrick K.
15 ;
16 ; APPLICANT: Schmid, Molly B.
17 ;
18 ; APPLICANT: Sun, Dongxu
19 ;
20 ; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
21 ;
22 ; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
23 ;
24 ; TITLE OF INVENTION: TARGET GENES

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NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/265,315
 FILING DATE: March 9, 1999
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/714,918
 FILING DATE: September 13, 1996
 APPLICATION NUMBER: 60/009,102
 FILING DATE: December 22, 1995
 APPLICATION NUMBER: 60/003,798
 FILING DATE: September 15, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 240/247
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 410 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-265-315-6

Query Match	15.9%	Score 206.4	DB 4	Length 410
Best Local Similarity	68.6%	Pred. No. 2.9e-40		
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			Gaps	0
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Oy	764	aagaattgcgaagcagatagaagaatcgacaagcgcctccgtaaatcaagaacatata	823	
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Oy	884	aaactatgcaacttaaacacagcgggtgaacattacggaattcgctgattctttattata	943	
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Oy	944	atcaattgagtgattgtattattatcaggcggcgaacgcaaacgaattcgatatttgctg	1003	
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Fri Jun 21 08:38:23 2002

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RESULT 10
US-08-714-918-4/C
; Sequence 4, Application US/08714918
; Patent No. 6037123
; GENERAL INFORMATION:
; APPLICANT: Benton, Bret
; APPLICANT: Lee, Ving
; APPLICANT: Malouin, Francois
; APPLICANT: Martin, Patrick K.
; APPLICANT: Schmid, Molly B.
; APPLICANT: Sun, Dongxu
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
; TITLE OF INVENTION: TARGET GENES
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California

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FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-265-315-4

Query Match 13.1%; Score 170; DB 4; Length 400;
Best Local Similarity 64.8%; Pred. No. 1,1e-31;
Matches 259; Conservative 0; Mismatches 140; Indels 1; Gaps 1

OY 205 ggaacagtcattgagctacgaataaagaagctgcgttattctttttaagactt-c 263
DB 400 GGTCCAGATGTGANTATGAATAAACAAGNACTCGTACACTTTTNCATTAAATGATTAACC 341
OY 264 aaataatgttaagaataatatacgcattgatttggagtgagaccttaatacaatgtt 323
DB 340 AAAAATNTTTTAAAAAATCATCGTTGCTACTATACCTACATATNGCATCCATTTACATATCA 281
OY 324 aaaggaacacacgatcgtggaagtgaattgaagaacatagcgaagtgactggtttttgata 383
DB 280 ATACTTGATATGATGATGCGGAGATTACAGGTAAATCGTAAATGATGGTCTTTGATATA 221
OY 384 aatgctgaattaaactttgaacatgaagttccacacggtgttggatacaataagga 443
DB 220 AATGAGTAACTTAGATGATTTGAACATCTGATTCATTAAGATTTGATCTGTGCTAACA 161
OY 444 aattgctttatctcgtcgtcgtatgltgtaaaataaacaacataaagaacatttaataca 503
DB 160 AATCCCTTATACCTCAAGTGTAGATTTTAAAGATTAATAACACAGATGACATCATTTAAAA 101
OY 504 aatggaataattgaagaaagaataacgaataaagaagtaagaataaagtgtgtgaagtcgg 563
DB 100 TATGATGTGACTTAGAAAAAAGAACACGGAANNAGTTTAAAAAGATGTGTAAAGTAAG 41
OY 564 ctatctaagcagaatgaattacataatttcggttcgttt 603
DB 40 ATTTTATCTGAAGAGNACTCAATTTTATGATTAATT 1

RESULT 12
US-09-265-315-4/c
Sequence 4, Application US/09265315
Patent No. 6187541
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: lee, Vling J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.

```

APPLICANT: Benton, Bret
 APPLICANT: Lee, Ying J.
 APPLICANT: Malouin, Francois
 APPLICANT: Martin, Patrick K.
 APPLICANT: Schmid, Molly B.
 APPLICANT: Sun, Donxuu
 TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
 ACTIVE ON STAPHYLOCOCCUS AUREUS
 TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
 TITLE OF INVENTION: TARGET GENES
 NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/266,417
 FILING DATE: March 9, 1999
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/714,918
 FILING DATE: September 13, 1996
 APPLICATION NUMBER: 60/009,102
 FILING DATE: December 22, 1995
 APPLICATION NUMBER: 60/003,798
 FILING DATE: September 15, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 240/248
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 400 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

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Query Match      13.1%; Score 170; DB 4; Length 400;
Best Local Similarity 64.8%; Pred. No. 1.1e-31;
Matches 259; Conservative 0; Mismatches 140; Indels 1; Gaps 1;

205 ggaccagtcaggactacgaaataaagagcgtgttcattctttttaaagtgaacttt-c 263
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
400 GGTCCAGTGATTGANTATGAAATCAAGNACTCGTACATTTTNCITTAATGAATTATCC 341
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
264 aaaaatttgaagaataatcacgcattgtattggagagtagaccctattttaccaatggt 323
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340 AAAAATATGTTAAAAACATCGTGNCTATACCTACATPANGCATCATATTTACCATACA 281
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
324 aaagcgaaacccaatgatgtgaagtgatgaagatacggcagtgactggttttttgataa 383
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
280 ATACTTGAATCATGATGCGGAGATTACAGTAAATCGCTGGTAAATGATGGTCTTTGTATA 221
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
384 aatggcgtgaattcaaacctttgaacatgaaggtttccaacactgggttttgatacaataaggca 443
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220 AATGAGTACTTTAGGATTTGAACATATCTGGATTCCATAAAGGATTGTATCTTGTGCTTACA 161
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
444 aattcgttttctattctgtgcgatgttgaaaaataaaacatcaaaagacattttaaatca 503
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[illegible]

Query Match	13.1%	Score 170	DB 4	Length 400
Best Local Similarity	64.1%	Pred. No. 1	le-31	
Matches	259	Conservative	0	Mismatches 140; Indels 1; Gaps 1
QY	205	gacacgcatgactacacaaataaagagctcgtgttcattcttttttaatgaactt-c	263	
DB	400	GGTCCAGTGATGATGAAATCAAGNACTCGTACACTTTCNTTATGAATATCC	341	
QY	264	aaaatagttaaagaataacagctattattigagtagacaccttattaccaatgtt	323	
DB	340	AAAATATGTTAAAAAACAATCGTTGNCATACCTACATFACNGATCCATATTACCATATCA	281	
QY	324	aaagcgaacctatggtgaaagtattgaaagatacgcgcagtgactcgttttttgataa	383	
DB	280	ATATCTTCATCATGATGGCGAGATTACAGGTAATGCTGGTAATGATTGGTCTTGATAA	221	
QY	384	aatggctgaattaaactttgaaacatgaaggtttcacaactgggtttgatacaataagcca	443	
DB	220	AATGAGTAACCTTAGGATTGAAACATACTGGATTCCATAAAGGATTTGATCTGTGTACA	161	
QY	444	aattcgttttcattcgtcgtcgtattgaaataaaacatacaaaagacatcttaaatca	503	
DB	160	AATCCGTTATCATCTCAGTGTGTAGNTTTAAAGATAAAACAGACATGACATCATTTAAAA	101	
QY	504	aatggataaatttaaagaaaagaataacgaaaaaaatgcacaaaatcgtgtgaaagtcgcg	563	
DB	100	TATGGATGACCTTAGAAAAAAGAAACAGCGAANNAGTTTAAAGAATGGTGTAAAGTAAG	41	
QY	564	ctatctaaacagagatgaattcacatatattttccgttcgtt	603	
DB	40	ATTTTATCTCAGAGGAGNACTPACCAATTTTATGATTATT	1	

RESULT 13
US-09-266-417-4/C
; Sequence 4, Application US/09266417
; Patent No.. 6228588
GENERAL INFORMATION.

RESULT 14
 US-08-714-918-19/C
 ; Sequence 19, Application US/08714918
 ; Patent No. 6037123
 ;
 ; GENERAL INFORMATION:
 ; APPLICANT: Benton, Bret
 ; APPLICANT: Lee, Yung
 ; APPLICANT: Malouin, Francois
 ; APPLICANT: Martin, Patrick K.
 ; APPLICANT: Schmid, Molly B.
 ; APPLICANT: Sun, Dongxu
 ; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
 ; TITLE OF INVENTION: TARGET GENES
 ; NUMBER OF SEQUENCES: 111
 ;
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/714,918
 ; FILING DATE: September 15, 1996
 ; CLASSIFICATION: 424
 ;
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/009,102
 ; FILING DATE: December 22, 1995
 ; APPLICATION NUMBER: 60/003,798
 ; FILING DATE: September 15, 1995
 ;
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 37,327
 ; REFERENCE/DOCKET NUMBER: 222/005
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 488-1600
 ; TELEFAX: (213) 955-0440
 ;
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5253 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ;
 ; TOPOLOGY: linear

RESULT 15
 US-09-265-315-19/c
 Sequence 19, Application US/09265315
 Patent No. 6187541
 GENERAL INFORMATION:
 APPLICANT: Benton, Bret
 APPLICANT: lee, Vling J.
 APPLICANT: Malouin, Francois
 APPLICANT: Martin, Patrick K.
 APPLICANT: Schmidt, Molly B.
 APPLICANT: Sun, Dongxu
 TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
 TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
 TITLE OF INVENTION: TARGET GENES
 NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/265,315
 FILING DATE: March 9, 1999
 CLASSIFICATION: 435
 PRIOR APPLICATION NUMBER: 08/714,918

us-09-509-234c-48.rni

Fri Jun 21 08:38:23 2002

FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 5253 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-265-315-19

Query Match 6.8%; Score 87.8; DB 4; Length 5253;
Best Local Similarity 49.2%; Pred. No. 6.9e-12;
Matches 284; Conservative 1; Mismatches 288; Indels 4; Gaps 2;

QY 701 tagctattgatttaattgcatatttagcagagctcacaactgaagcgaagcgaacttta 760
DB 2636 TAGTAAGTTGGATCCCAAGAAATATAGCGAAAGTAATCAAGAAATTGAATGAATTC 2577
QY 761 aaaaagaattgcgaagcagataaagacatcgacaagcgt---cctgaaatcagaag 817
DB 2576 ATCCGAAATTGCTAAATGGCAGCAGAGATGAAACATCTGAAAGCAAGCTAAAAAG 2517
QY 818 cctaataaaaaaagaataatttagcgaacactagaagcgaatcgaagcgaatcgaagcgaag 877
DB 2516 CGCAAAATATGATTATGATGCGCAAAATAAATTTGCTFAAAATGAAGATTTAAACGAG 2457
QY 878 aagcagaacattgcaacttaaacacggtgacacattaccgatttggcgtgattctta 937
DB 2456 ACCTAGAGCTTTAGAAAAGGACATCCTGAAGGTATTATCTTTCTGTGTCACATTAA 2397
QY 938 ttattaatcattgaggtgtttattattgagcgccgacagcaaacgaatttcgtcatt 997
DB 2396 TGTGTTGCTGCTCAAAATCATATTACTTATGTTGCGCTCTCTAATGAATTTAGAGATT 2337
QY 998 ttgctgaagctacgcagtgcaatgggaatggaatggaatggaatggaatggaatggaatc 1057
DB 2336 TTTTACCAATATCATATGTCAGTATACGATGATGAAGTATGACGTCAGTGAACATGGTGCA 2277
QY 1058 caagataaactttttagcattagtggtgattttcagaagatgcagaagatgcaggtg 1117
DB 2276 CAACCTAGATTTCGGTGTACAGATAATGATCCAGATTAAGACTCAGACATTATGGAT 2217
QY 1118 tgataaaatttaaaaggctataatgcagaagtaataagaatagatgctggtgatttt-att 1176
DB 2216 TATGGCATTTTAAAAAAGTGTGGGACACATCTTAAGTGAAAAGATTGGTGAATTTGATT 2157
QY 1177 aagcctataaacaacctgcttatcacagtcacttaaaattaaagcaagcaag 1236
DB 2156 ATGTATTGAATCAGCCATTGTRCAATTAATTGAGCAAGTTAAACCGGCTTTACAAAG 2097
QY 1237 ataaaagaatagatatagcaagaagaggggattta 1273
DB 2096 CTAAATTAATAATCTCGTAAATTAACGGAATA 2060

Search completed: June 20, 2002, 12:04:07
Job time: 20962 sec

Fri Jun 21 08:38:25 2002

us-09-509-234c-48.rst

Page 1

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2002, 14:26:50 ; Search time 8551.36 Seconds
(without alignments)
2047.107 Million cell updates/sec

Title: US-09-509-234C-48
Perfect score: 1297
Sequence: 1 acgacgcgcgaattcgtgc.....tatgaattacagagttaa 1297

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : EST:
1: em_estba:*
2: em_esthm:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	77.6	6.0	1135	12	CNS0336Q
2	76.8	5.9	1101	12	CNS0021J
3	75.2	5.8	885	12	AG136199
4	75	5.8	614	12	AG104915
5	74.8	5.8	614	12	CNS0152H
6	73	5.6	652	12	AL514935
7	72	5.6	907	12	AL244551
8	71.8	5.5	894	12	CNS02134
9	71.4	5.5	879	12	CNS0188G
10	71.4	5.5	879	12	CNS00601
11	71.4	5.5	910	12	BM415636
12	71	5.5	834	12	BM415636
13	71	5.5	1101	12	CNS0039G
14	70.8	5.5	966	10	BM415686
15	70.2	5.4	1036	12	CNS00599
16	69.6	5.4	660	12	BM183498
17	69.6	5.4	660	12	CNS070NT

18	69.4	5.4	756	3	BI644558
19	68.2	5.3	974	12	CNS0017T
20	69.2	5.3	1101	12	CNS0017B
21	69	5.3	1101	12	CNS01772
22	68.6	5.3	905	12	AZ550256
23	68	5.2	1147	12	BI3042
24	67.8	5.2	922	12	AZ548363
25	67.8	5.2	1007	12	CNS06X9S
26	67.8	5.2	1101	12	CNS00GPB
27	67.2	5.2	865	12	AQ324474
28	67	5.2	769	12	AQ194503
29	67	5.2	769	12	AG134867
30	67	5.2	1001	12	CNS01400
31	66.8	5.2	802	12	CNS02CV8
32	66.8	5.2	1223	12	BI2981
33	66.6	5.2	833	12	AQ446640
34	66.6	5.1	838	12	A2199419
35	66.6	5.1	1101	12	CNS00KHB
36	66.6	5.1	581	12	CNS01UPZ
37	66.4	5.1	1092	12	CNS020K7
38	66.4	5.1	850	12	A2186328
39	66.2	5.1	1101	12	CNS00H87
40	66.2	5.1	770	12	A2196926
41	66	5.1	1101	12	CNS0153V
42	66	5.1	1139	12	AQ897537
43	66	5.1	1184	12	BI3117
44	65.6	5.1	908	12	AG160668
45					

ALIGNMENTS

RESULT 1
CNS0336Q 1135 bp DNA linear GSS 15-MAY-2000
Tetradon nigroviridis genome survey sequence POC-ori end of clone
208P24 of library G from Tetradon nigroviridis, genomic survey
sequence.

ACCESSION AL226115.1 GI:7885026
VERSION GSS: genome survey sequence.
KEYWORDS Tetradon nigroviridis.
SOURCE Tetradon nigroviridis.
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorphia; Acanthopterygii; Percomorphia; Tetraodontiformes; Tetraodontidae; Tetradon.

REFERENCE 1 (bases 1 to 1135)
Roest-Crollius H., Jallion O., Dasilva C., Fitzames C., Fisher C., Bouneau L., Billault A., Queller F., Saurin W., Bernot A. and Weissenbach J.
Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradon nigroviridis

TITLE Unpublished
JOURNAL 2 (bases 1 to 1135)
AUTHORS Roest-Crollius H., Jallion O., Dasilva C., Bouneau L., Fisher C., Bernot A., Fitzames C., Wincker P., Brottier P., Queller F., Saurin W. and Weissenbach J.
HUMAN GENOME NUMBER ESTIMATE PROVIDED BY GENOME WIDE ANALYSIS USING Tetradon nigroviridis DNA sequence

REFERENCE 3 (bases 1 to 1135)
Genoscope.
Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DBI databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetradon nigroviridis genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetradon.

FEATURES
source location/Qualifiers
1..1135
/organism="Tetradon nigroviridis"

us-09-509-234c-48.rst

Fri Jun 21 08:38:25 2002

Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR05N11 of RPCI-98 library from drosophila melanogaster (fruit fly), genomic survey sequence.

AL061936
AL061936.1 GI:4940214
GSS.
fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

1 (bases 1 to 1101)
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osogawa and Aaron Mammeter in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the p1 and E37 libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
Location/Qualifiers

1..1101
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR05N11"
/note="end : TET3"

BASE COUNT 631 a 7 c 28 g 289 t 146 others
ORIGIN

Query Match 5.9%; Score 76.8; DB 12; Length 1101;
Best Local Similarity 40.3%; Pred. No. 0.0081;
Matches 328; Conservative 43; Mismatches 437; Indels 6; Gaps 2;

QY 484 tcaaaagacatcttaaatggaataatttaagaaagaaagaaatacgaagaaagacag 543
DB 78 TNNAAANAKWKAATNATAATTTTAAATTTAAKAKWDTAAATAAANHAANAAAA 137
QY 544 aaaaatggtgaaagtcgcgtatctaaacgaagatgaaatattccgctcgttt 603
QY 138 AGTGTGTTTCATGAAGTTTAAANAAAAANAAAAANAAAAANAAAAANAAAAAN 197
QY 604 atggaagatcatctgaaacaaagattttgtgagatgagatgagatgatttatcat 663
DB 198 NHAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAA 257
QY 664 cgtatgaataactataaagatcgtgcgcgtaccatgctgatatattgatttaagca 723
DB 258 AAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAA 317
QY 724 tatttagcagagctcaacacgtgaaagcgaagcatttaaaagaaagaaagcagat 783
DB 318 CAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAA 377
QY 784 aaagacatcgacagcgctcctgaaatcagaagccataataaagaaagaaatttagag 843
DB 378 AAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAA 437
QY 844 caacaactagaagcgaatcaagctaaataaagaaagcgaagaaacattgcaactaaacac 903

/db_xref="taxon:99883"
/clone="208P24"
/clone_lib="G"
/note="Genoscope sequence ID : COAG208DH12SP1-end : PUC-ori"

BASE COUNT 863 a 65 c 43 g 124 t 40 others
ORIGIN

Query Match 6.0%; Score 77.6; DB 12; Length 1135;
Best Local Similarity 43.1%; Pred. No. 0.0061;
Matches 341; Conservative 14; Mismatches 435; Indels 2; Gaps 1;

QY 473 aaataaaacatacaagacatcttaaatcaatggataatttaagaaagaaagaaatagca 532
DB 323 AAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAA 382
QY 533 aaaaagtcagaaagatggtgaaagtcgcgtatctaaacgaagatgaattacatttt 592
DB 383 AAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAA 442
QY 593 tcggttcgtttagaagatacatctgaacaaacattttgtagatgagatgacgatt 652
DB 443 AAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAA 502
QY 653 ttattatcatgataaactataaagatggtgcgcgtaccatgagctgatttg 712
DB 503 AAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAA 562
QY 713 attttatgcatatttagcagagctcaacactgagcgcgaagcatttaaaagaaatg 772
DB 563 AAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAA 622
QY 773 caaaagcagataaagacatcgacagcgtcctgaaatcgaaagccataataaaga 832
DB 623 AAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAA 682
QY 833 aaaaattagcaacaaactgaagcgaatcaagctgaaataaagaaagcagacattgc 892
DB 683 AAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAA 742
QY 893 aacttaaacgcgtgacacattacgatttcggtggtgattttattatttaacattg 952
DB 743 ATNTAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAAAN 802
QY 953 aggtgtgtattatgcagcgcgcagcaacagaaatttcgctcattgtggtgagactag 1012
DB 803 A--TWTATAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAA 860
QY 1013 cagtgcaatgggaatgatttaattatgattgatttcaattccagatataactttt 1072
DB 861 AAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAA 920
QY 1073 atggcattagtggtattttcagaagatgcagaagatgcaggtgtagataaaatttaaa 1132
DB 921 AATAAAATAACTTAACCAAAAAANAAAAANAAAAANAAAAANAAAAANAAAAAN 980
QY 1133 aaggctataatgcagaagtaataagatgctcgggtgatttttaagcctataaacaac 1192
DB 981 AAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAA 1040
QY 1193 ctgcctatacagctctacttaataaagcaattaaagacagataaagaaagataagata 1252
DB 1041 AVTCAAAATTAATTCAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAA 1100
QY 1253 tagcaagagaa 1264
DB 1101 AAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAAANAAAA

RESULT 2
CNS0021J 1101 bp DNA linear GSS 03-JUN-1999
LOCUS

Page 3

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 614)	Genoscope.	Direct Submission		
		Submitted (23-JUL-1999)	Genoscope - Centre National de Sequencage	
		BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr)		
		- Web : www.genoscope.cns.fr		
		Determination of this BAC-end sequence was carried out as part of		
		collaboration with the European Drosophila Genome Project (EDGP) -		
		http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC		

Web : www.genoscope.cns.fr.

```

FEATURES
source
Location/Qualifiers
1..619
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CLO8B012ZD08"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/Note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
52 a 8 c 10 g 514 t 35 others

```

BASE COUNT	52 a	8 c	10 g	514 t	35 others
Query Match	5.8%	Score 74.8;	DB 9;	Length 619;	
Best Local Similarity	46.3%	Pred. No. 0.02;			
Matches 199;	Conservative	1;	Mismatches 230;	Indels 0;	Gaps 0;
QY	473	aaataaacaatcaagaagacattcaaatcaaatgataatttaaggaagaagaataacga	532		
DB	472	AA	413		
QY	533	aaaaagcacagaataatggtggaagtcgcgtatctaaacgaagatgaattacatat	592		
DB	412	AAAAAAAAAANNNAAA	353		
QY	593	tcggttcgttatggaagatcacatctgaacaaagatttctgtagagatgcatt	652		
DB	352	AA	293		
QY	653	tttattcatcgtatgaatactataagatcgtctcgcgtaccactagcgtatattg	712		
DB	292	TTTTTTTTTTMMNANNNNNNAAAAAAAAAAAAAAAANNNNNANNTNCCCCCNNGATTTNTNN	233		
QY	713	atttaagcatatttagcagctcaacactgagcgaagactttaaaagaagaattg	772		
DB	232	TTTTTTTAA	173		
QY	773	caaaagcagataagacatcgacaagcgtccttgaaatcgaaagccataataaaga	832		
DB	172	AA	113		
QY	833	aaatttagagcaacaactagagcgaaatcaagctaaataaagaagcaaacattgc	892		
DB	112	AA	53		
QY	893	aacttaaca	902		
DB	52	AAAAAAAAAA	43		

RESULT	6
CNS03HOU	
LOCUS	652 bp DNA linear GSS 17-MAY-2000
DEFINITION	Tetradon nigroviridis genome survey sequence T7 end of clone O27K10 of library G from Tetradon nigroviridis, genomic survey sequence.
ACCESSION	AL244551
VERSION	AL244551.1 GI:7965563
KEYWORDS	GSS; genome survey sequence.
SOURCE	Tetradon nigroviridis.
ORGANISM	Tetradon nigroviridis. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Library (Dros BAC) was made by Alain Billaut at CAPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelOBAC11.

FEATURES	source	Location/Qualifiers
pberoBAC11	1. 614	/organism="Drosophila melanogaster" /plasmid="pBeloBAC11" /db_xref="taxon:7227" /clone_lib="DrosBAC" /clone="BAC12N03" /note="end : SP6"

BASE COUNT	553 a	0 c	0 g	41 t	20 others
ORIGIN					
Query Match	5.8%;	Score 75;	DB 12;	Length 614;	
Best Local Similarity	46.7%;	Pred. No. 0.019;			
Matches 201;	Conservative	7;	Mismatches 222;	Indels 0;	Gaps 0;
473	aaataaacaatcaaaagcacctttaataacaaatggataatttaaggaagaagaatacga	532			
QY					
DB	39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATNAAAAAAAAATTAATAAAAAAAAAATAAA 98				
533	aaaaatcacagaataatggtgaaagtcgcgtctctctaaacgaagatgaattacatat	592			
QY	:				
DB	99 AATTAAANWAAAAAAAAAAAAAAAAATTAATAATTTTTTATTAATAATAAAAAAAAAATAA 158				
593	tcgcgttcgttatggaagatcacatctggaacaaagaattgtgtagatgaagatgcagatt	652			
QY	:				
DB	159 AAAAAAAAAAAAAAAAAATAAAAAAAAAATTTAAAAAAAAAAAAAAAAATAAAAAAAAAATA 218				
653	tttattatcatcgtatgaatactataagatcgtgcgcgtagccactagcgtatattg	712			
QY	: :				
DB	219 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATAAAAAAAAAATAWAAAAAAAAATWNAWTAATAA 278				
713	atttaatgcattatttagcagctcacactgaagcgaagactttcaaaagaagaattg	772			
QY	:				
DB	279 WATAAAAAAAAAWATAAAAAAAAAAAAAAAAAWATWNAWAAAAAAAAAAAAAAAAAAAAAAAAAWAA 338				
773	caaaagcagataaagacatcgacaagcgtccctgaaatcagaaagccataataaaaaaga	832			
QY					
DB	339 AAAAAAAAAATAA 398				
833	aaatttagagcacaactagagcgaatccaagctaaataaacaagcagaacattgc	892			
QY					
DB	399 AAAAAATAA 458				
893	aacttaaca	902			
QY					
DB	459 AAAAAAAAAAAAAA	468			

RESULT	5
AL514935/c	
LOCUS	619 bp mRNA linear EST 13-FEB-2001
DEFINITION	AL514935 LTI_NFL006.PL2 Homo sapiens cDNA clone CLOBB012ZD08.3
PRIMER	prime, mRNA sequence.
AL514935	
ACCESSION	AL514935.1 GI:12778428
VERSION	
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1 (bases 1 to 619)
AUTHORS	Li.W.B., Gruber,C., Jesseee,J. and Polayes,D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage Genoscope, Bld006 Evry cedex - France

RESULT 7
CNS021J4/C

D0 404 AAAAAAAAAAAAAAAAAA
QY 548 atggtgtgaagtcgcgcctacctaacaagatgaattacatatattccggtcgttatgg 607

us-09-509-234c-48.rst

Fri Jun 21 08:38:25 2002

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Db 404 AKGAAAAA... 345
QY 608 agatacatctgaaacaaagatttttagatagatgacgatttttattatcatcgta 667
Db 344 CAATDA... 285
QY 668 tgaatactataaagatcggtccgcgtaccactagctgtatattgatttttaagtcatt 727
Db 284 NAAAAA... 225
QY 728 tagcagagctcaactgagcgcaagactttaaaagaaatgcaaaagcagataag 787
Db 224 AAAAAA... 165
QY 788 acatgacagcgctcctgaaatcgaaagccataataaaagaataatttagagcaac 847
Db 164 AAAAAA... 105
QY 848 aactagagcgcaatcaagctaaataaagagcagaaacattgcaacttaacaa 902
Db 104 AAAAAA... 50

RESULT 8
CNS018BG 894 bp DNA linear GSS 26-JUL-1999
LOCUS CNS018BG
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC
BACN13B16 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL109126
VERSION AL109126.1 GI:5629430
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 894)
AUTHORS Direct Submission
TITLE Submitted (23-JUL-1999) Genoscope - Centre National de Sequenage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (BDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelOBAC11.
FEATURES
Location/Qualifiers
1..894
/organism="Drosophila melanogaster"
/plasmid="pBelOBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN13B16"
/note="end : 77"
BASE COUNT 452 a 101 c 85 g 138 t 118 others
ORIGIN
Query Match 5.5%; Score 71.8; DB 12; Length 894;
Best Local Similarity 38.4%; Pred. No. 0.051;
Matches 170; Conservative 55; Mismatches 218; Indels 0; Gaps 0;
QY 470 ttgaaataaacaacaaagacatttcaatgataatttaagaaagaaata 529
Db 27 TTATWAT... 86
QY 530 ogaataagctacgaataagtgtaagtcgctatctaaacgaagatgaattacata 589

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Db 87 AAAAAA... 146
QY 590 ttttcggttcgtttatgaagatacatctgaaacaaagatttttagatagatgacg 649
Db 147 TTGGCA... 206
QY 650 atttttatcatcgctagaaataactataaagatcggtccgcgtaccactagctata 709
Db 207 WACRTM... 266
QY 710 ttgattttaatgcataatttagcagctgcaactgaagcgcaagcacttttaaaagaaa 769
Db 267 AAAAAA... 326
QY 770 ttgcaaaagcagataaagacatcgacaagcgctcctgaaatcagaagccataataaa 829
Db 327 AAAAAA... 385
QY 830 agaaaatttagcgaacaactagcgaagcgaatcaagctaaataaaagcagaacat 889
Db 387 WAGAAA... 446
QY 890 tgcaacttaaacacacggtgacaca 912
Db 447 AAAAAA... 469

RESULT 9
CNS0060I 990 bp DNA linear GSS 03-JUN-1999
LOCUS CNS0060I/c
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR14J23 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL065624
VERSION AL065624.1 GI:4944693
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 990)
AUTHORS Direct Submission
TITLE Submitted (02-JUN-1999) Genoscope - Centre National de Sequenage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osogawa and
Aaron Mammeter in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES
Location/Qualifiers
1..990
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR14J23"
/note="end : TET3"
BASE COUNT 158 a 51 c 40 g 592 t 149 others
ORIGIN

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Query Match	5.5%;	Score 71.8;	DB 12;	Length 990;
Best Local Similarity	37.8%;	Prod. No. 0.049;		
Matches 297;	Conservative	56;	Mismatches 452;	Indels 0;
				Gaps 0

Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
Culicoidae; Anopheles.
1 (bases 1 to 879)

TITLE Direct Submission
Submitted (16-FEB-2000) Genoscope - Centre National de Sequençage
JOURNAL pp 191 91006 EMBY cedex - FRANCE (E-mail : secref@genoscope.cns.fr)

REFERENCE
2 (bases 1 to 879)
Bath C.W., Brev. P.T., Ke, Z., Collins, F.H., and Weissenbach, J.

TITLE Direct Submission
SUBMITTED (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr
Pour Paris 75015, France

COMMENT
This clone is from an *A. gambiae* B cell library provided by F. H. Collins and sequenced by genoscope in collaboration with the laboratory of Biochem. and Biol. Molec. of insects, Institut Pasteur.

FEATURES	Location/Qualifiers
source	1. .879
	/organisms="Anopheles gambiae"

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Query Match	5.5%	Score 71.4;	DB 12;	Length 879;
Best Local Similarity	43.0%	Prod. No. 0.059;		
Matches 185;	Conservative 37;	Mismatches 207;	Indels 1;	Caps. 1;

OY		538	gtacagaaaatcgtgctgaagtcgcgtatctaagaagatgatcatcatctccgt	597
Dd		553	AATATAAAMAAAAATDKTAAMAAAVATAASBTAAAAATTATGACAAAATTWADXTTAAK	494
OY		558	tcgattatggagaataactctcgaaaacaagaatttgytagatagagtgcacattttat	657
Dd		493	AAWMAAN	434
OY		658	tatcatcgtatgaatactataaagatcgtgctcgcgtacacctgacgtatatgtattt	717
Dd		433	AAA	374
OY		718	aatgcataattagcagagctcaaacgcggaagcgacagacttaaaaaagaattcgaaa	777
Dd		373	AAA	314
OY		778	gcagataaagaca tcgacaagctcctcgaanaatcgaagaagcataataaagaanaat	837
Dd		313	AAA	255
OY		838	ttagsgcaacactagaagcggatcaagcttaaatataaagaagcagaacatgcacatt	897
Dd		253	AAAAAAAAAAGAAARAAAAAAGAAAAAANPRAFRGAHAHAHGAAGAHAHAHAHAAGR	194
OY		898	aaaca	902
Dd		193	AAAA	189

RESULT 10			
CNS01JRG/c			
LOCUS	879 bp	DNA	linear GSS 12-JUN-2001
DEFINITION	CNS01JRG		
	Anopheles gambiae GSS T7 end of clone 14D07 of NotreDame1 library		
	Anopheles gambiae GSS T7 end of clone 14D07 of NotreDame1 library		
	Anopheles gambiae (African malaria mosquito),		
	strain: Anopheles gambiae (African malaria mosquito),		

ACCESSION	AL147405	genomic survey sequence.
VERSION	AL147405.1	GI:7005551
KEYWORDS	GSS.	
SOURCE	african malaria mosquito.	
ORGANISM	Anopheles gambiae	
	taxonomy: Arthropoda; Tracheata; Hexapoda; Insecta;	

RESULT	11				
LOCUS	BM415636/c	910 bp	mRNA	linear	EST-28-JAN-2002
DEFINITION	OP07174 Mixed EST's from <i>Globochloa pallida</i> , the potato cyst nematode <i>Globochloa pallida</i> cDNA, mRNA sequence.				
ACCESSION	BM415636				
VERSION	BM415636.1	GI:18382435			

[illegible]

NC State University; IACR-Rothamsted
Campus Box 7616; Raleigh, NC 27695, USA
Tel: 919.515.5699
Fax: 919.515.9500
Email: warthog@unity.ncsu.edu
GT11-6PCN_F_Hil_FCN_6_F_092.ab1.
Location/Qualifiers

FEATURES

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source
1. .966
/organism="Globodera pallida"
/db_xref="taxon:36090"
/clone_lib="Mixed Stage EST's from Globodera pallida, the
potato cyst nematode"
/notes="Vector: lambda GT11; This is a collaborative effort
between IACR-Rothamsted and North Carolina State
University. The library was constructed from mixed stage
G. pallida in lambda GT11 by Paul Burroughs,
IACR-Rothamsted."
BASE COUNT      18 a  50 c  9 g  811 t  78 others
ORIGIN

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Best Local Similarity 39.4%; Pred. No. 0.071;
Matches 312; Conservative 0; Mismatches 479; Indels 0; Gaps 0;

QY 474 aaataaacatcaaaagacatcttaatacaatggataatttaagaaagaaatacgaa 533
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DB 872 AAAAAAANAAAAAAGAAAAAGAGAGAGGGGGAAGAAAAAAGAAAAAAN 813
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QY 534 aaagtagcagaaatgtgtgaatccgctatcaacgaagatgaattacatttt 593
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DB 812 AAGAAAAAAGAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 753
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QY 594 cggctgtttatggaagacatctgaacaaagattttgtgtgtagagagcattt 653
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DB 752 AAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 693
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QY 654 ttattatcgtatgaataactataaagatggtcgctaccactagctatgta 713
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DB 692 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG 633
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QY 714 tttaatgcatatttagcagagctcaacactgaagcgaagcattttaaagaagaatgc 773
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QY 774 aaagcagataaagacatcgacagcgtcctgaaatcagaagccataaataaagaa 833
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DB 572 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG 513
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QY 834 aaatttagcacaactagcagcgaatcaagctaaataaagaagcagcaaatgca 893
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DB 512 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG 453
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QY 894 acttaaacacggtgacacattccgatttcggtggtattttatttaaccattga 953
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QY 1014 agtgcattgggaatgattatgcgattgattatcaaatcccaagataacttta 1073
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DB 332 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 273
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QY 1134 aggcataatgcagagcaatagatgatttcggtggtattttatttaaccctataaacaacc 1193
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DB 212 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG 153
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QY 1194 tgcctatacagcttacttaaaattaaagcaattaaagcaagataaaagataat 1253
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DB 152 TCGGAAGACTATAGGNAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG 93
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QY 1254 agcaaaagagaa 1264
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RESULT 15
CNS00599/c 1036 bp DNA linear GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #
DEFINITION BACKL116 of RCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL057797
VERSION AL057797.1 GI:4932579
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1036)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osogawa and
Aaron Mammoss in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES
1. .1036
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RCI-98"
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ORIGIN

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Best Local Similarity 40.2%; Pred. No. 0.086;
Matches 173; Conservative 43; Mismatches 214; Indels 0; Gaps 0;

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DB 599 AATKCGAAMAGAAAAAGAGTAATAAAYAGYAATGAKAWAATAAWAKAAGTSTRAATA 540
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DB 539 TWAFAAGAAAGANAKAGRTDGAKAAAAAAGAAAKAATRTADAAAAAAGAAAAA 480
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QY 653 ttattatcatcgtatgaaataactataaagatcgttcgcgcgtaccactagcgtattg 712
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Fri Jun 21 08:38:25 2002

us-09-509-234c-48.rst

Page 11

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Db 419 ATKKKARRGAKKAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 360
QY 773 caaagcagataaagacatcgacagcgctctgaaatcaggaagccataataaaga 832
Db 359 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 300
QY 833 aaaattagagcaaacactagaagcgatcaagctaaataaagaagcagaacattgc 892
Db 299 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 240
QY 893 aacttaaca 902
Db 239 AAAAAAAAA 230
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Search completed: June 20, 2002, 14:26:57
Job time: 17727 sec

SUMMARIES

ALIGNMENTS

Sequence 52 from Patent W09916780.

VERSION A97496.1 GI:6780842

SOURCE	Staphylococcus	nominis
Staphylococcus	nominis	nominis

Bacillus/Staphylococcus group; Staphylococcus.

REFERENCE 1 (bases 1 to 1343)

ADHOC: GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND
TITLE

DEVICES FOR THE IDENTIFICATION OF SIMILAR OCCASION DATA

GALA JEAN LUC (BE); UNIV LOUVAIN (BE)

Source

1. .1343 "Cheshbry oooooo hoin n's"

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Matches 1343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 ataataagatttacaataattcaacagctacagaaatttggcgtatttactgaaaaatgcc 120
DB 61 ATATGAGCTTTACAAATTTAACAGCTACAGAAATTTGGCGATTTTACTGAAAAATGCCA 120
QY 121 tatagccatttacaagagtagctgactgaaattatgatgtttaaagtctgagaaactgaa 180
DB 121 TATAGCCATTTTACACAGATGACTGAAATTTATGAGTTTAAAGTTGCTGAGAAAACTGAA 180
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QY 241 gctgaccgttatgaaattttaaattttaaatttcttcaaatctgctcagcattgat 300
DB 241 GCTGTACCCGTTATGAAATTTTAAATATATTTTATCAATTCGTCGTCAGTCATGAT 300
QY 301 tatgaaacaaagaactcgtctcattttttttaaagaaattaaattttaaatacaaa 360
DB 301 TATGAAACAAAGAACTCGTCTCACTTTTCTTTTAAACGAATTAAGTAATATTTAAACAA 360
QY 361 caacattgtttatagcagtagacacctatttgccttatcaataatcgaatacatgat 420
DB 361 CAACATTTGTTTATGTAGTACGATAGACCCCTATTTGCCCTTATCAATATCGTAATCATGAT 420
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DB 421 GGTGATATTACAGGAATGCTGGGAATGATGTTCTTCGATTAATAATGAACAAATTAGGA 480
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QY 721 agagagagatgtttttactataatcgattgacatttttaaagatagagatttagtaact 780
DB 721 AGAGAGGATAGTTTTTACTATAATCGATTGATCATTTTAAAGATAGAGATTAGTACCT 780
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DB 1021 ATTAATCACTTTGAGTTGATATTATGAGGTGGAACGTCAAATAAATATAGACACTTC 1080
QY 1081 gctggaagttagcagttcaatggactatgatttaattgcaattgacatgcattgac 1140
DB 1081 GCTGGAAGTTTACAGTTCAATGGACTATGATTAATTAATGCAATTGATGCGCATTCAC 1140
QY 1141 cgtataatttttgggattgtagtgcattttacagatgatgctgaagatgcagggttt 1200
DB 1141 CGTTATAAATTTTATGGGATTAGTGTCTATTTCAGATGATGCTGAAGATGCGAGGTGT 1200
QY 1201 gtaaaatttaaaagatttaattgacagatgtaattgtaattgattggtgatttcgttaa 1260
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RESULT 2
SHY12874
LOCUS      SHY12874               1343 bp      DNA      linear      BCT 30-SEP-1997
DEFINITION Staphylococcus hominis fema gene.
ACCESSION  Y12874
VERSION    Y12874.1 GI:2462667
KEYWORDS   fema gene.
SOURCE     Staphylococcus hominis.
ORGANISM   Staphylococcus hominis
            Bacteria; Firmicutes; Bacillus/Clostridium group;
            Bacillus/Staphylococcus group; Staphylococcus.
REFERENCE  1 (bases 1 to 1343)
            Vannuffel,P.
            JOURNAL      Unpublished
            REFERENCE    2 (bases 1 to 1343)
            Vannuffel,P.
            TITLE        Direct Submission
            JOURNAL      Submitted (30-APR-1997) P. Vannuffel, University of Louvain Medical
            School, Laboratoire de Genetique Moleculaire, UCL-GEMO-5225, Avenue
            E. Mounier 52, Brussels, 1200, BELGIUM
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Matches 1342;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

Db 901 GCTAAAAATTACAAGCCGAACATGGTAATGAATTACCAATTTCAGCAGGTTTCTCTT 960

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BASE COUNT 492 a 162 c 214 g 395 t
ORIGIN

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Best Local Similarity 80.6%; Pred. No. 7e-108;
Matches 1018; Conservative 0; Mismatches 245; Indels 0; Gaps 0;

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QY 124 agccattttacacagatgactgaaattatgagtttaaaattgctgagaacactgaact 183
DB 61 AGTCATTTCACACAAATGACTGAAACTATGAGATGAAGAGTGGCAATAAAGACAGAACT 120
QY 184 catttagtaggaattaaaaataaagataagtaagtcattgctgttctgctgaactgct 243
DB 121 CACTTAGTTGGTATTAATAAATAAAGATTAATGAGGTTATTCAGCTGCATGTTGCAGCA 180
QY 244 gtaccggttatgaaaatttttaaatatttttatttcaaatcgtgtccagtcattgattat 303
DB 181 GTACCACTCATGAATTTTAAAGTACTTTTATCTAACCCGAGGACCTGTAATTGATTAT 240
QY 304 gaaacaaagaactogtctcaacttttttcttaacgaatttaagtaaatatttaaacacaa 363
DB 241 GATAATAGAGAGCTGTTTCACCTTTTCTTTAATGAGTTAACAAAGTATTTAAACACGAT 300
QY 364 cattgtttatatagctatagacccttatttgccttatcaaatatcgtatcatcgtatgct 423
DB 301 AATTGCTATATGTTGCGAGTTGACCCCTTATTTACCATATCAATATTTAAATCATGATGT 360
QY 424 gatattacaggaatgctgggaatgattgttcttcgataaaatgaacaaattagatgat 483
DB 361 GAAATTAACAGGTANTGCTGGTANTGANTGTTCTTTGATAGATGAGCATCTCGATTT 420
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DB 481 TTAGATTAAAAATAAATCAATCTAAAGATATATTAATGGAATGGAATGATGATGATGAT 540
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QY 664 ttacctatttcagatcatttatggaagatacatcagagactaaagaattttctgtagaga 723
DB 601 CTTCCATCTTCGTTTCATTTATGGAAGATACACACCGAAACGAAGAAATTCAGATAGA 660
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DB 661 GATGATAGTTCTTATTATAATCGCTATAGACATTTCAAGATCGGCTGTTGTACCACTA 720
QY 784 gcataataaaatttatgaataattctgaaagacttcacgcagaaactcagacattaaat 843
DB 721 GCTTATTAAGTTTGTAGTACATCGAAGATTAACAATGACCGGTAACCTTTAAAT 780
QY 844 aaagacttaacaaagctctaaagattgaaacacgacagatacaacaaaagacaa 903
DB 781 AAGATGTTTAAAGCTTTTAAAGATATTGAAACGACGACGACAAATAAAGGCATTT 840
QY 904 aataaaaaataaatttagaacgcaattaaagcgaattgagcaaaaaattgtagaagca 963
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QY 1024 aatccatttgaaagttgtatatattatgcagggtggaacgtcaaaataatatagacacttcgct 1083

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QY 1144 tataattttatggattagtgctcatttcacagatgctggaagatgcagggtgttga 1203
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DB 1201 ATTAACAAACCTTTGATTTCAGTGTATAAGACACTCAAAAAGATTAAAAAAGATTTAAT 1260
QY 1324 taa 1326
DB 1261 TAA 1263

RESULT 6
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LOCUS X17688 M23918
ACCESSION X17688.1 GI:46579
VERSION X17688.1
KEYWORDS fema protein.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus.
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus.
REFERENCE 1 (bases 1 to 3446)
Berger-Baechi, B., Barberis-Maino, L., Straessle, A. and Kayser, F. H.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3446)
Berger-Baechi, B., Barberis-Maino, L., Straessle, A. and Kayser, F. H.
Fema, a host-mediated factor essential for methicillin resistance in Staphylococcus aureus: molecular cloning and characterization
Mol. Gen. Genet. 219 (1-2), 263-269 (1989)
JOURNAL 90136516
MEDLINE
COMMENT Draft entry and computer-readable sequence for [1] kindly provided by B. Berger-Baechi, 11-APR-1989.
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repeat_region 416..423
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repeat_region 430..437
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BASE COUNT 1281 a 448 c 617 g 1100 t
 ORIGIN

Query Match 62.8% Score 843.4; DB 1; Length 3446;
 Best Local Similarity 77.3%; Pred. No. 2.6e-104;
 Matches 1037; Conservative 0; Mismatches 301; Indels 3; Gaps 1;

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 DB 615 AATGAGTTTACAAATTTTAAAGCTAAAGATTGGCTTTTACAGATACATGCATA 674

QY 123 tagccatttaccagatgacggaatattagtttaaaagttgcgagaaactggaac 182
 DB 675 CAGTCATTTACGCAAACTGTTGCCACTATGAGTTTAAAGCTTGTGCAAGCTTATGAAAC 734

QY 183 tcatttagtaggaattaaataaagaatgaagtcagtcgctgtaagtcagtcg 242
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QY 243 tgcaccggttaaaaaattttaaatttttaaatcgtggtccagtcattgatta 302
 DB 795 TGTACGCTGTATGAAGTGTCAAGATTTTATTCAAATCGCGGTCCAGTATGATTA 854

QY 303 tgaataaagaactcgttactctttttttaaagaaattagaataatttaaacaca 362
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QY 843 taaagacttaaaacaaagctcctaaagaatctgaaaaacgacgaataacaaaaagcaca 902
 DB 1395 TAAAGATTTTAAATTAAGCTTAAGATTAATGAAAACGCTGTAATAAAGCA 1454

QY 903 aaataaaaaataaatttagaagcagcaattaaagaactgacaaaaattgataagc 962
 DB 1455 TAAACACGAGTAATCACTTAACAACAACTTGATGCAAAATGCAAAAGATTAAGAAAG 1514

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QY 1323 ttaagagggatagtgagaa 1343
 DB 1875 TTAGGAAGGAAATTAATCAAAA 1895

RESULT 7
 AP003133 303750 bp DNA linear BCT 07-FEB-2002.
 LOCUS
 DEFINITION
 Staphylococcus aureus subsp. aureus N315 genomic DNA, complete
 genome, section 5/10.
 ACCESSION
 AP003133 BA000018
 VERSION
 AP003133.2 GI:14349175
 KEYWORDS
 SOURCE
 Staphylococcus aureus subsp. aureus N315 (sub-species:aureus N315,
 strain:N315) DNA.
 ORGANISM
 Staphylococcus aureus subsp. aureus N315
 Bacteria; Firmicutes; Bacillus/Clostridium group;
 Bacillus/Staphylococcus group; Staphylococcus.
 REFERENCE
 AUTHORS
 Kuroda,M., Ohta,T., Uchiyama,I., Baba,T., Yuzawa,H., Kobayashi,T.,
 Cui,L., Oguchi,A., Aoki,K., Nagai,Y., Lian,J., Ito,T., Kanamori,M.,
 Matsunaru,H., Maruyama,A., Murakami,H., Hoshiyama,A.,
 Sekimizu,O., Y., Takahashi,N.K., Sawano,T., Inoue,R., Kaito,C.,
 Mizutani,K., Hirakawa,H., Kubara,S., Goto,S., Yabuzaki,J.,
 Kanehisa,M., Yamashita,A., Oshima,K., Furuya,K., Yoshino,C.,

Fri Jun 21 08:38:28 2002

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Staphylococcus aureus subsp. aureus Mu50
Bacteria; Firmicutes; Bacillus/Clostridium group;

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Bacillus/Staphylococcus group; Staphylococcus.
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AUTHORS Vanuif, P., Heusterspreute, M., Bouyer, M., Philippe, M. and Gala, J.-L.
TITLE Molecular characterization of fema from Staphylococcus hominis, Staphylococcus saprophyticus and Staphylococcus haemolyticus and fema-based discrimination of staphylococcal species
JOURNALS Res. Microbiol. (1998) In press
REFERENCE 2 (bases 1 to 1254)
AUTHORS Vanuif, P., Heusterspreute, M. and Gala, J.-L.
TITLE Direct Submision
JOURNALS Submitted (21-Oct-1998) LBCM, UCL, Clos Chapelle-aux Champs 30/3046, Bruxelles 1200, Belgium
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Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
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AUTHORS Vannuffel, P.
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1350)
 AUTHORS Vannuffel, P.
 TITLE Direct Submission
 JOURNAL Submitted (30-APR-1997) P. Vannuffel, University of Louvain Medical School, Laboratoire de Genetique Moleculaire, UCL-GEMO-5225, Avenue E. Mounier 52, Brussels, 1200, BELGIUM
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 Best Local Similarity 76.3%; Pred. No. 4.3e-101;
 Matches 1008; Conservative 0; Mismatches 313; Indels 0; Gaps 0;
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 DB 127 TCATTTTACGCAATGGTTGGAAATATGTAATTCGAAATTCGAGAAATGACGAAACACA 186
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 DB 367 TGCCTTATATTACAGTAGATGCTTATCTGCTTATCAATATCGTATCATGATGTGA 426
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RESULT 12

LOCUS A97497 1371 bp DNA linear PAT 26-JAN-2000
 DEFINITION Sequence 53 from Patent WO9916780.
 ACCESSION A97497
 VERSION A97497.1 GI:6780844
 KEYWORDS
 SOURCE Staphylococcus saprophyticus.
 ORGANISM Staphylococcus saprophyticus
 Bacteria; Firmicutes; Bacillus/Clostridium group;
 Bacillus/Staphylococcus group; Staphylococcus.

REFERENCE 1 (bases 1 to 1371)
 AUTHORS Gala, J. and Vannuffel, P.
 TITLE GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS
 JOURNAL Patent: NO 9916780-A 53 08-APR-1999;
 GALA JEAN LUC (BE); UNIV LOUVAIN (BE)
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 ORIGIN
 Query Match 61.1%; Score 820.2; DB 6; Length 1371;
 Best Local Similarity 76.3%; Pred. No. 4.3e-101;
 Matches 1008; Conservative 0; Mismatches 313; Indels 0; Gaps 0;

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 Db 1326 A 1326

RESULT 13

A97490 1283 bp DNA linear PAT 26-JAN-2000
 LOCUS A97490
 DEFINITION Sequence 46 from Patent WO9916780.
 A97490
 ACCESSION A97490
 VERSION A97490.1 GI:6780836
 KEYWORDS

SOURCE Staphylococcus capitis.
 ORGANISM Staphylococcus capitis
 Bacteria; Firmicutes; Bacillus/Clostridium group; Staphylococcus.

REFERENCE 1 (bases 1 to 1283)
 AUTHORS Gala, J. and Vannuffel, P.
 TITLE GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS
 JOURNAL Patent: NO 9916780-A 46 08-APR-1999;
 GALA JEAN LUC (BE); UNIV LOUVAIN (BE)
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Best Local Similarity 78.6%; Pred. No. 1.1e-99;
Matches 968; Conservative 0; Mismatches 264; Indels 0; Gaps 0;
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QY 142 actgaaattatgattgataaactgctgagaaactgaaactcatttagtaggaataaa 201
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Db 121 AATATGACACCAAGTGTGACAGATGTTTAACTGCTGCTACCTGTTGTAAGAAAT 180
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QY 322 caattttcttcaagtaataagtaataatttaaaacaacacattgttttatgtacgt 381
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Db 481 ACGGCTAAGATGCTACTCAAGGAATGGATAGTTTAAAGAAAGCGCTAATAGTAAGTA 540
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QY 742 aatcgatttgatcattttaaagatagatttagtaccctcgtcattataataattgat 801
Db 661 AATCGATTAAATACTTTAAGATAGATGATTAGTACCATTTAGCATAGTTGATCTCGAT 720
QY 802 gaatatctggaacttctcagacgctcagacattataaataagaacttaaaacaaagct 861
Db 721 GAGTATATTGAAGAACTTAAATGAAAGAGATGCTTCTTAAATAAGATTTTAAATAAGCGC 780

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QY 862 ctaaaagatatggaaaacgacagatacaaaaaaagcacaaaaataaaattta 921
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QY 922 gaacagcaataaaagcaaaatgacaaaaaattgatgaagcaacacaaacttcaattaga 981
Db 841 CAACAACAATTAGATGCAATCAACAACAAAAAATTTGATGAAGCTTAACAACTTACAACA 900
QY 982 catgtaacaaattaccatattctgtggattcttttatttaataccattgaagtga 1041
Db 901 CATGGTAATGAATTAATTTACCTATTTACCTGGATATTTCTTCAATTAATCCGTTTGA 960
QY 1042 tatlatcagtggtgaaactgcaataataatagacacattcgtggaagttatgcagttca 1101
Db 961 TATTACGAGGTGGACATCGAATCGTTATCGTCACTATGCCGGAAGTTATGCNATTC 1020
QY 1102 tggactatgatttaattatgcaattgattgattgattgattgattgattgattgattgatt 1161
Db 1021 TGGAAATATGAATTAATTTAGAACATGGAATTAACCGTTATTAATTTTATGGAGTT 1080
QY 1162 atgtgcaatttaccagatgattgattgattgattgattgattgattgattgattgatt 1221
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QY 1222 aatgcagatgtaattgattgattgattgattgattgattgattgattgattgattgatt 1281
Db 1141 AATGCTGATGTTTATGAATATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
QY 1282 tcaatatcaacacatttaaaataaaataaa 1313
Db 1201 GCAATCTATACGCACTTAAAGTTAAAGAA 1232
RESULT 14
AF144661 1263 bp DNA linear BCT 01-JUN-1999
LOCUS Staphylococcus aureus subsp. anaerobius factor essential for
DEFINITION methicillin resistance (femA) gene, complete cds.
ACCESSION AF144661
VERSION AF144661.1 GI:4929298
KEYWORDS Staphylococcus aureus subsp. anaerobius.
SOURCE Staphylococcus aureus subsp. anaerobius
ORGANISM Bacteria; Firmicutes; Bacillus/Clostridium group;
REFERENCE Bacillus/Staphylococcus group; Staphylococcus.
AUTHORS 1 (bases 1 to 1263)
TITLE Vannuffel, P., Heusterspreute, M. and Gala, J.-L.
JOURNAL Cloning and characterization of femA genes from Staphylococci
AUTHORS Unpublished
TITLE 2 (bases 1 to 1263)
JOURNAL Vannuffel, P., Heusterspreute, M. and Gala, J.-L.
AUTHORS Direct Submission
TITLE Submitted (21-Apr-1999) LBCM, UCL 3046, Clos Chapelle-aux-Champs,
JOURNAL 30, Bruxelles 1200, Belgium
FEATURES Location/Qualifiers
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BASE COUNT      476 a 196 c 215 g 373 t
ORIGIN
Query Match      60.08; Score 805.6; DB 1; Length 1260;
Best Local Similarity 77.7; Pred. No. 3.9e-99;
Matches 973; Conservative 0; Mismatches 279; Indels 0; Gaps 0;
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QY 124 agccattttacagagactgactgaaataattagttaaaaagttgctgaaaaactgaaact 183
D 61 AGTCATTTTACTCAATGACAGGTAACATAATTTAAAGTTGCGGAAATAACAGAAACA 120
QY 184 cattagtaggaattaaaaataaataaataagctcattgctgctgttgatgctaaactgt 243
D 121 CATTTAGTTGGTGTAAATTAATTAATACGAGTAATTCAGCATGTATTATGACAGCT 180
QY 244 gtaccggttatgaaattttttaaattttttattcaaatcgtggtccagtcattgattat 303
D 181 GTACCAGTCNTGAGTTTAAATACATTTTACAGCAATAGAGGCCAGTTATAGATTAT 240
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D 301 AACTGTCTCTATGTCGCCGCTAGATCCATACATTTACCTTATCAATATAGAGACCATGACGGT 360
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D 361 AATAAAGCAAAATGCTGGCAATGATGTTGTTTCAATAAATGGAACAACTCGGATAC 420
QY 484 caacagaaggggttttacacagagatttgatccaattattacaataattcggttccattcagtt 543
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QY 844 aaagacttaaaaaagctctaaagatatattgaaaaacgaccagatacaaaaaaagacaa 903
  
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XX

WPI: 1999-287521/24.
P-PSDB; AAY08221.

XX New Staphylococcus-specific oligonucleotides

PT Claim 27; Fig 12; 48pp; English.

XX This invention describes novel Staphylococcus-specific oligonucleotides based on the consensus femA nucleotide sequence which are used to develop products for the identification, detection and therapy of infections. The oligonucleotides can be used for the genetic amplification, the identification and/or quantification of various femA sequences which are specific to known or unknown Staphylococci species. Since the femA sequence is similar to the femB sequence, the oligonucleotides can also be used for the molecular genotyping of femB genes of different Staphylococci species or other gram-positive bacteria. The femA nucleic acids can also be used in therapeutic applications or They can also be used to identify inhibitors, e.g. antibodies or antisense oligonucleotides, for blocking expression of the femA nucleotide sequences. They can also be used for producing vaccines against Staphylococci infections.

XX Sequence 1342 BP; 544 A; 161 C; 217 G; 420 T; 0 other;

Query Match 99.1%; Score 1331; DB 20; Length 1342;
Best Local Similarity 99.1%; Pred. No. 8e-215;
Matches 1342; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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DB 61 ataataagattttcaaaattacagctacagaatttggcgattttactgaaaaatgccca 120
QY 121 tatagccattttacacagatgactgaaattatgatgttaaaagtgtcgagaaaactgaa 180
DB 121 tatagccattttacacagatgactgaaattatgatgttaaaagtgtcgga-aaactgaa 179
QY 181 actcatttagtaggaataaaataaataaataaataaataaataaataaataaataaataa 240
DB 181 actcatttagtaggaataaaataaataaataaataaataaataaataaataaataaataa 239
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QY 421 ggtgtattacaggaataatgctgggaatgattggtttcttcgtatgaaatgaaacaaattagga 480
DB 421 ggtgtattacaggaataatgctgggaatgattggtttcttcgtatgaaatgaaacaaattagga 479
QY 481 tatcaacagaagggtttacacagatttgatccaaattattacaaattcggttcattca 540
DB 481 tatcaacagaagggtttacacagatttgatccaaattattacaaattcggttcattca 539
QY 541 gtttttaatttaagataaaactgctaaagattgatttaaaatggaatggatgatttaca 600
DB 541 gtttttaatttaagataaaactgctaaagattgatttaaaatggaatggatgatttaca 599
QY 601 aaaaagaaataactaaaaagttccaaaaaaatgggtttaaagtaagatttcttactaaagaa 660
DB 601 aaaaagaaataactaaaaagttccaaaaaaatgggtttaaagtaagatttcttactaaagaa 659

QY 661 gaattacctattttcagatcattttatggaagatacatcagagactaaagaattttctgat 720
DB 661 gaattacctattttcagatcattttatggaagatacatcagagactaaagaattttctgat 719
QY 721 agagagatagtttttactataatcagatttgattcatttttaagatagatgatttagtacct 780
DB 721 agagagatagtttttactataatcagatttgattcatttttaagatagatgatttagtacct 779
QY 781 ctccgatataaaattttgatgaattttgaaacacttcattcagacgacgtacagacatta 840
DB 781 ctccgatataaaattttgatgaattttgaaacacttcattcagacgacgtacagacatta 839
QY 841 aataaagacttaaaacaaagctctaaagatttgaataaagcagacgacgatacaaaaaagca 900
DB 841 aataaagacttaaaacaaagctctaaagatttgaataaagcagacgacgatacaaaaaagca 899
QY 901 caaataaaaaataaattttagaaacgcaataaataaagcaaaatgagcaaaaaattgatgaa 960
DB 901 caaataaaaaataaattttagaaacgcaataaataaagcaaaatgagcaaaaaattgatgaa 959
QY 961 gcaacacacttcatttagaacaatggttaacgaatttaccgaatttctgtgatttctttt 1020
DB 961 gcaacacacttcatttagaacaatggttaacgaatttaccgaatttctgtgatttctttt 1019
QY 1021 attaatccattttgaagttgtattatgaggtggaacgtcaaaataaataatagacacttc 1080
DB 1021 attaatccattttgaagttgtattatgaggtggaacgtcaaaataaataatagacacttc 1079
QY 1081 gctggaagttatgagttcaattgagacgtatgatttgaattgcaattgattgattgattgac 1140
DB 1081 gctggaagttatgagttcaattgagacgtatgatttgaattgcaattgattgattgattgac 1139
QY 1141 cgttataatttttattggttagttggtcattttacagatgattgctgaagatgaggtgttt 1200
DB 1141 cgttataatttttattggttagttggtcattttacagatgattgctgaagatgaggtgttt 1199
QY 1201 gtaaaatttttaaaagaggatttaattgagatgagatgagatgagatgagatgagatgagatg 1260
DB 1201 gtaaaatttttaaaagaggatttaattgagatgagatgagatgagatgagatgagatgagatg 1259
QY 1261 cctataaaataacaaatgatttctacattatatacaacacatttaaaaaataaaaaagattg 1320
DB 1261 cctataaaataacaaatgatttctacattatatacaacacatttaaaaaataaaaaagattg 1319
QY 1321 aattaagagggaatagtgagaa 1343
DB 1321 aattaagagggaatagtgagaa 1342

RESULT 2
AA37798
ID AAX37798 standard; DNA; 1305 BP.

XX AAX37798;
XX 09-JUL-1999 (first entry)
XX Staphylococcus haemolyticus FemA DNA.

XX FemA; identification; detection; therapy; infection; femB;
XX amplification; genotyping; gram-positive bacteria; vaccine; ss.

XX Staphylococcus haemolyticus.

XX Key Location/Qualifiers
XX CDS 4..1305
XX /*tag= a "FemA"
XX /product= "FemA"

XX WO9916780-A2.
XX 08-APR-1999.

XX 28-SEP-1998; 98MO-BE00141.
 XX PF
 XX 26-SEP-1997; 97EP-0870146.
 XX PR
 XX (BENA-) BELGIAN MIN NAT DEFENCE.
 XX PA (OYLO-) UNIV CATHOLIQUE LOUVAIN.
 XX PA
 PI Gala J, Vannuffel P;
 XX WPI: 1999-287521/24.
 XX DR P-PSDB; AAY08215.
 XX PS
 PS New Staphylococcus-specific oligonucleotides
 PS Claim 15; Fig 6a-d; 48pp; English.
 XX This invention describes novel Staphylococcus-specific oligonucleotides
 CC based on the consensus fema nucleotide sequence which are used to
 CC develop products for the identification, detection and therapy of
 CC infections. The oligonucleotides can be used for the genetic
 CC amplification, the identification and/or quantification of various fema
 CC sequences which are specific to known or unknown Staphylococci species.
 CC Since the fema sequence is similar to the femB sequence, the
 CC oligonucleotides can also be used for the molecular genotyping of femB
 CC genes of different Staphylococci species or other gram-positive bacteria.
 CC The fema nucleic acids can also be used in therapeutic applications.
 CC They can also be used to identify inhibitors, e.g. antibodies or
 CC antisense oligonucleotides, for blocking expression of the fema
 CC nucleotide sequences. They can also be used for producing vaccines
 CC against Staphylococci infections.
 CC XX
 SO Sequence 1305 BP; 513 A; 165 C; 222 G; 405 T; 0 other;

Query Match 65.2%; Score 875.6; DB 20; Length 1305;
 Best Local Similarity 80.5%; Pred No. 2e-138;
 Matches 1025; Conservative 0; Mismatches 249; Indels 0; Gaps 0;

QY 61 ataatgaattacaataattacaagctacagaattggcgattttactctgaataatgccca 120
 Db 1 ataatgaattacaataattacaagctacagaattggcgattttactctgaataatgccca 60
 QY 121 tatagccatttaacacagatgactgaaattatgattgaataatgctggaataactgaa 180
 Db 61 tatagccatttaacacagatgactgaaattatgattgaataatgctggaataactgaa 120
 QY 181 accatttagtaggaataataaataagaataatgagtcattgctgctgtatgact 240
 Db 121 accatttagtaggaataataaataagaataatgagtcattgctgctgtatgact 180
 QY 241 gctgtaccggttaaaaaattttaatatattttatccaatcggtgcagtcattgat 300
 Db 181 gctgtaccggttaaaaaattttaatatattttatccaatcggtgcagtcattgat 240
 QY 301 tatgaataacagaagactcggttcacttttttttaacgaataatgaataatgaataaca 360
 Db 241 tatgaataacagaagactcggttcacttttttttaacgaataatgaataatgaataaca 300
 QY 361 caacattgattatgatacgtatagacccttattgaccttaacatcgtatcatgat 420
 Db 301 caacattgattatgatacgtatagacccttattgaccttaacatcgtatcatgat 360
 QY 421 gctgatatcaggaatgctgggaatgattgcttcttcgataaataagaataatgagg 480
 Db 361 gctgatatcaggaatgctgggaatgattgcttcttcgataaataagaataatgagg 420
 QY 481 tatcaacagaaggttttaacacagatttgatccaattcaaatcgttcattca 540
 Db 421 ttgacacatgaaggttttacttaaaagtttgcctcgatcaacaaatccgatcatctc 480
 QY 541 gtttaaatgaaggaataaaactgtaaatgatatgaatggaatgattgattcaga 600

Db 481 gtttaagattcaaaaataaataacatcctaagatatattaaatggaatgattgattcagt 540
 QY 601 aaaaagaataactaaaagaagtcacaaaataatggtgttaagtaagattttcttaagaag 660
 Db 541 aaaaagaataactaaaagaagtcacaaaataatggtgttaagtaagattttcttaagaag 600
 QY 661 gaattccattttcagatgattcattatgaggaatatacatcagaagactaaatcttgat 720
 Db 601 gaattccattttcagatgattcattatgaggaatatacatcagaagactaaatcttgat 660
 QY 721 agagagatgatttttactaataatcagatttgatcattttaagaatagatgattgact 780
 Db 661 agagagatgatttttactaataatcagatttgatcattttaagaatagatgattgact 720
 QY 781 ctgcataataaaaatttgatgatatcttggaagacttcctgagagcgttcagactta 840
 Db 721 ctgcataataaaaatttgatgatatcttggaagacttcctgagagcgttcagactta 780
 QY 841 aataagacttaaaaagaagcttaagaatgaaagacagacagaatacaaaaaga 900
 Db 781 aataagacttaaaaagaagcttaagaatgaaagacagacagaatacaaaaaga 840
 QY 901 caaataaaaataaatttagaacagcaattaaagaacatgagcaaaaattgataa 960
 Db 841 tttaataaaaagaataatcttgaaaacaattagatgccaatcaacaataattagacag 900
 QY 961 gcaacaacttaattagacaatgtaacagaaattacacattcctgctgattccttt 1020
 Db 901 gctaaaataattacaagcgaaatgtaaatgtaattacacattcctgagcaggttctctt 960
 QY 1021 attaatcattgaatttatattatgacaggtgagcgttcacaaataatagacattc 1080
 Db 961 attaatcattgaatttatattatgacaggtgagcgttcacaaataatagacattc 1020
 QY 1081 gctgaagattacgaattcaatgactatgatttaattatgcaattgacatgacattgac 1140
 Db 1021 gcaagcgattgattgatttcaatgacagcaattgatttaattatgcaattgacatgacattgac 1080
 QY 1141 cgttaaatatttgattgattgattgatttcaatttcagagatgagcgaatgagcaggtt 1200
 Db 1081 agatacaatttcattgattgattgattgatttcaatttcagagatgagcgaatgagcaggtt 1140
 QY 1201 gtaaatattaaaagaatttaattgacagatgtaattgaattggttgattcgttaa 1260
 Db 1141 attaaatttaaaaagaatttcaattgacagatgtaattgaattggttgattcgttaa 1200
 QY 1261 cctataataataccaatgattatcactataatacaacttaaaaataaagaagattg 1320
 Db 1201 cctataataataccaatgattatcactataatacaacttaaaaataaagaagattg 1260
 QY 1321 aattaaagaggaa 1334
 Db 1261 aattaaagaggaa 1274

RESULT 3
 AAX37805
 ID AAX37805 standard; DNA; 1371 BP.
 XX
 AC AAX37805;
 XX
 DE 09-JUN-1999 (first entry)
 XX
 DE Staphylococcus saprophyticus Fema DNA.
 XX
 KW FemA; identification; detection; therapy; infection; femB;
 XX amplification; genotyping; gram-positive bacteria; vaccine; ss.
 OS Staphylococcus saprophyticus.
 XX
 XX Key Location/Qualifiers
 XX 64..1326
 FT CDS
 FT /tag= a

Fri Jun 21 08:38:29 2002

/product= "Fema"

FT XX W09916780-A2.
 PN XX
 XX XX
 PD XX
 XX XX
 PF XX 28-SEP-1998; 98WO-BE00141.
 PR XX 26-SEP-1997; 97EP-0870146.
 XX XX
 PA (BENA-) BELGIAN MIN NAT DEFENCE.
 PA (UYILO-) UNIV CATHOLIQUE LOUVAIN.
 XX XX
 PI Gala J, Vannuffel P;
 XX XX
 DR WPI: 1999-287521/24.
 DR P-PSDB; RAY08222.
 XX XX
 PT New Staphylococcus-specific oligonucleotides
 XX XX
 PS Claim 29; Fig 13; 48pp; English.
 XX XX
 CC This invention describes novel Staphylococcus-specific oligonucleotides
 CC based on the consensus femA nucleotide sequence which are used to
 CC develop products for the identification, detection and therapy of
 CC infections. The oligonucleotides can be used for the genetic
 CC amplification, the identification and/or quantification of various femA
 CC sequences which are specific to known or unknown Staphylococci species.
 CC Since the femA sequence is similar to the femB sequence, the
 CC oligonucleotides can also be used for the molecular genotyping of femB
 CC genes of different Staphylococci species or other gram-positive bacteria.
 CC The femA nucleic acids can also be used in therapeutic applications.
 CC They can also be used to identify inhibitors, e.g. antibodies or
 CC antisense oligonucleotides, for blocking expression of the femA
 CC nucleotide sequences. They can also be used for producing vaccines
 CC against Staphylococci infections.
 XX XX
 SQ Sequence 1371 BP; 545 A; 155 C; 248 G; 423 T; 0 other;
 Query Match 61.1%; Score 820.2; DB 20; Length 1371;
 Best Local Similarity 76.3%; Pred. No. 4e-129;
 Matches 1008; Conservative 0; Mismatches 313; Indels 0; Gaps 0;
 QY 6 tttaaataagtcgaactcaataataaagattcttaattagagattatagagataat 65
 DB 6 tttagattagaattaaactcgaaatagaaactatagataaaatggggtatataaaaaaat 65
 QY 66 gaagtttaaaatttaacagctacagaatttgcgattttactgaaataatgccatataag 125
 DB 66 gaatttgaatttaacagctacagaatttgcgattttactgaaataatgccatataag 125
 QY 126 ccatittacacagatgactgaaattatgatttgaatttgaatttgcgaaactgaactca 185
 DB 126 tcaatttgcgaatttgaatttgaatttgaatttgaatttgcgaaactgaactca 185
 QY 186 tttagtgaatttaaaataaagaattgaatttgaatttgaatttgcgaaactgctgt 245
 DB 186 cctagtaggttataagaattgaatttgaatttgaatttgaatttgcgaaactgctgt 245
 QY 246 accggttatgaatttgaatttgaatttgaatttgaatttgcgaaactgctgtatgata 305
 DB 246 tccgttatgaatttgaatttgaatttgaatttgaatttgcgaaactgctgtatgata 305
 QY 306 aaacaagaactgctgtatgataatttgaatttgaatttgaatttgcgaaactgaactca 365
 DB 306 aaataagaactgctgtatgataatttgaatttgaatttgaatttgcgaaactgaactca 365
 QY 366 ttgtttatagctatgatacccttatttgccttatcaattatgaattatgattggtga 425
 DB 366 tgccttatattagctatgatacccttatttgccttatcaattatgaattatgattggtga 425
 QY 426 tattacaggaaatgctgggaatgattggtttcttcgataaaatgaacaattaggtatca 485

Db 426 agtattagcaaatgcgggtcagcagattggtatttggatataaaatgaacaactcgggtataa 485
 QY 486 acacgaagggtttacacacagagatttgatcccaattattacaaatcgggtccattcagtttt 545
 Db 486 gcatgaagggtttttaaactggcttgacccaatacttcaataaagattccattcgttttt 545
 QY 546 aaatttaagagataaaaactgcctaaagatgtattaaatggaatgagatgtttacgaaag 605
 Db 546 agatttagctggaaaaactgctaaagcgtacttaattggtgaaatgagatttttagtgtaacg 605
 QY 606 aaatactaaaaagtcacaaaaaattggtttaaagtaagattttcttactaaagaagaatt 665
 Db 606 aaatactaaaaagtcacaaaaaattggtttaaagtaagattttcttactaaagaagaatt 665
 QY 666 accattttcagatcattttatggaagatcacatcagagactaaagaattttctgatagaga 725
 Db 666 gccaattatccgcatttcagagatcatttctgaaacaaaggattttgacgatagaga 725
 QY 726 ggatagttttactataatcagatttgatcatttttaagatagatgatttagctctcgcg 785
 Db 726 tgacgattttttattataatggttaagatattataaagatcgtgctgtccattagc 785
 QY 786 atataaaaaatttaataatcttgaagaacttctcagacacgtcagacattataataa 845
 Db 786 ttatatggatttgatgataataacagaataaaggctgaacgcgaagtatttaagtaa 845
 QY 846 agacttaaaaaagctcttaaaagatattgaaaaaacgacagataacaaaaaacacaaa 905
 Db 846 agatataaaaaagcagtgatgataagaaaaagacacagataaataaaaaacgctataa 905
 QY 906 taaaaaaataatttagacagcaataaaaaagcaaatgagcaaaaaattgatgaacaa 965
 Db 906 taaaaaagaaaaatttagacacaaactgattgcaaaccaacaaaaataatagatgaacaa 965
 QY 966 acaacttcaattagacacatggttaacgaattaccaatattcgtggtgattctttattaa 1025
 Db 966 tgcgttacaagaagcagtggttaacgaattaccgatttctgcgacttattattaa 1025
 QY 1026 tccatttggaattgttatattatgcaggtggaacgtcaataataatagacactcgtg 1085
 Db 1026 tccattgaagtcgtttactatgcaggtggttacatctaataatgattagacatttgcgtg 1085
 QY 1086 agttatgcagttcaattgactatgatttaattgcaattgattgcattgacogtta 1145
 Db 1086 tagttatgcatacaatggaagatgatttaattgctatagatcataatagatagata 1145
 QY 1146 taattttatgggattagtggttcattttacagatgagtgctgaagatgcaggtgtgttaa 1205
 Db 1146 taattttatgggattagtggttcattttacagatgagtgctgaagatgcaggtgtgttaa 1205
 QY 1206 atttaaaaaaggatttaacgagatgataattgaaatgattggtgatttcgttaaacctat 1265
 Db 1206 atttaaaaaaggatttaacgagatgataattgaaatgattggtgatttcgttaaacctat 1265
 QY 1266 aaataaaccatgatttactactatatacacacacttaaaaaaatttaaaagagatgaatta 1325
 Db 1266 taataagccaatgacaaaattttacacacatttaccacattgaaataaagaagataa 1325
 QY 1326 a 1326
 Db 1326 a 1326

RESULT 4
 AAX37801
 ID AAX37801 standard; DNA; 1283 BP.
 XX
 AC AAX37801;
 XX 09-JUL-1999 (first entry)
 DT
 DE Staphylococcus capitis FemA DNA.

XX fema: identification; detection; therapy; infection; fema;
 KW amplification; genotyping; gram-positive bacteria; vaccine; ss.
 OS Staphylococcus capitis.
 XX Key Location/Qualifiers
 FT CDS 1..1283
 FT /tag- a
 FT /product- "fema"
 FT /note- "partial sequence, no start or stop codon"
 MO916780-A2.
 XX 08-APR-1999.
 XX 28-SEP-1998: 98MO-BE00141.
 XX 26-SEP-1997: 97EP-0870146.
 XX (BENA-) BELGIAN MIN NAT DEFENCE.
 XX (UYLO-) UNIV CATHOLIQUE LOUVAIN.
 XX Gala J, Vannuffel P;
 XX WPI: 1999-287521/24.
 XX P-PSDB: AAY08218.
 XX New Staphylococcus-specific oligonucleotides
 XX Claim 21; Fig 9a-b; 48pp; English.
 XX This invention describes novel Staphylococcus-specific oligonucleotides
 CC based on the consensus fema nucleotide sequence which are used to
 CC develop products for the identification, detection and therapy of
 CC infections. The oligonucleotides can be used for the genetic
 CC amplification, the identification and/or quantification of various fema
 CC sequences which are specific to known or unknown Staphylococci species.
 CC Since the fema sequence is similar to the femb sequence, the
 CC oligonucleotides can also be used for the molecular genotyping of femb
 CC genes of different Staphylococci species or other gram-positive bacteria.
 CC The fema nucleic acids can also be used in therapeutic applications.
 CC They can also be used to identify inhibitors, e.g. antibodies or
 CC antisense oligonucleotides, for blocking expression of the fema
 CC nucleotide sequences. They can also be used for producing vaccines
 CC against Staphylococci infections.
 XX Sequence 1283 BP; 484 A; 170 C; 224 G; 405 T; 0 other;

Query Match 60.3%; Score 809.6; DB 20; Length 1283;
 Best Local Similarity 78.6%; Pred. No. 2.4e-127;
 Matches 968; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

QY 82 acagctacgaatttgcgatttactgaaataatgcataatgacatttaccagatg 141
 DB 1 acagctacgaatttgcgatttactgaaataatgcataatgacatttaccagatg 60
 QY 142 actgaaatattgattgaaagttgcgaaagaaacgaatacttagtaggaattaa 201
 DB 61 gaagtaattatgaacttaagttgcgaaagaaacgaatacttagtaggaattaa 120
 QY 202 aataaagataatgaatgactgctgctgatactgatactgctgataccgctatgaaatt 261
 DB 121 aataaagataatgaatgactgctgctgatactgatactgctgataccgctatgaaatt 180
 QY 262 tttaaatatttattacaatcggtgcagtcagtcagtcagtcagtcagtcagtcagtc 321
 DB 181 tttaaatatttattacaatcggtgcagtcagtcagtcagtcagtcagtcagtcagtc 240
 QY 322 caatttctttaaagataatgataatgataatgataatgataatgataatgataatgata 381
 DB 241 caatttctttaaagataatgataatgataatgataatgataatgataatgataatgata 300

QY 382 atagacccttattgcttcttacaataatgataatgataatgataatgataatgataatgata 441
 DB 301 gtcgaccttattcttcttacaataatgataatgataatgataatgataatgataatgataatgata 360
 QY 442 gggatgattgcttcttacaataatgataatgataatgataatgataatgataatgataatgata 501
 DB 361 ggcgattgattgcttcttacaataatgataatgataatgataatgataatgataatgataatgata 420
 QY 502 acaggtattgataatgataatgataatgataatgataatgataatgataatgataatgataatgata 561
 DB 421 aaagcttcttcttcttacaataatgataatgataatgataatgataatgataatgataatgata 480
 QY 562 actgtaagataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgata 621
 DB 481 acgctaaagataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgata 540
 QY 622 caaaaaatggttgaagataatgataatgataatgataatgataatgataatgataatgataatgataatgata 681
 DB 541 caaaaaatggttgaagataatgataatgataatgataatgataatgataatgataatgataatgataatgata 600
 QY 682 tttaagaaatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgata 741
 DB 601 tttaagaaatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgata 660
 QY 742 aatgattgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgata 801
 DB 661 aatgattgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgata 720
 QY 802 gaatatctgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgata 861
 DB 721 gaatatctgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgata 780
 QY 862 cttaagataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgata 921
 DB 781 cttaagataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgata 840
 QY 922 gaacagcaatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgata 981
 DB 841 caacacaaatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgata 900
 QY 982 catgtaagataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgata 1041
 DB 901 catgtaagataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgata 960
 QY 1042 tattatcgatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgata 1101
 DB 961 tattatcgatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgata 1020
 QY 1102 tggactatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgata 1161
 DB 1021 tggactatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgata 1080
 QY 1162 atgtgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgata 1221
 DB 1081 atgtgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgata 1140
 QY 1222 aatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgata 1281
 DB 1141 aatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgataatgata 1200
 QY 1282 tcaactataacacttaaaaaaattaaaaa 1313
 DB 1201 gcaattataacgacttaaaaaaattaaaaa 1232

RESULT 5
 AAH54373 standard; DNA: 4434 BP.
 XX AAH54373;
 AC
 XX 03-SEP-2001 (first entry)

XX S. epidermidis genomic polynucleotide sequence SEQ ID NO:3737.
 DE Staphylococcus epidermidis SRI strain; infection; diagnosis;
 KW vaccination; endocarditis; ds.
 KW Staphylococcus epidermidis.
 OS WO200134809-A2.
 PN 17-MAY-2001.
 XX 09-NOV-2000; 2000WO-0530782.
 XX 09-NOV-1999; 99US-0164258.
 XX (GLAX) GLAXO GROUP LTD.
 XX Kimmerly WJ;
 XX WPI; 2001-316495/33.
 XX Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
 PT useful for vaccinating against infections, e.g. endocarditis -
 XX Claim 8; Page 1358-1360; 2188pp; English.
 XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
 CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
 CC (I) and (II) can have antibacterial activity and therefore can be used
 CC in vaccination. The nucleic acids (I) may be used to produce the
 CC S. epidermidis polypeptides (II) via the production of vectors
 CC containing them which are used to produce hosts cells which express the
 CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
 CC used to vaccinate subjects and to raise antibodies against the bacteria.
 CC The polypeptides may also be used to assay for other inhibitors of their
 CC activity and therefore identify compounds that may be used for the
 CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
 CC AAH55090 represent specifically claimed S. epidermidis genomic DNA
 CC polynucleotide sequences from the present invention. AAH55091 to
 CC AAH55098 represent oligonucleotide sequences and primers which are used
 CC in the exemplification of the present invention.
 CC N.B. The present invention specifically claims all the polynucleotide
 CC sequences given in the sequence listing of the present specification,
 CC however the sequence listing only goes up to SEQ ID NO:4454 so even
 CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
 CC no sequences are present for SEQ ID NO:4455 to 4464.
 XX Sequence 4434 BP; 1676 A; 554 C; 819 G; 1385 T; 0 other;
 SQ

Query Match 59.8%; Score 803.2; DB 22; Length 4434;
 Best Local Similarity 77.0%; Pred. NO. 3e-126;
 Matches 992; Conservative 0; Mismatches 293; Indels 3; Gaps 1;
 QY 26 aattaataaagattcttaattaggaggtatagatgaatgaattacaaattacacag 85
 DB 2832 aaatadagataaagataataatggaggtat---gaagatgaattacgaattgacag 2888
 QY 86 ctacagaattggcgtatttactgaataatgccatagcattttacacagatgactg 145
 DB 2889 ctaagaattttagtgacttactatgatgatgacatagcattttacacaaagggaag 2948
 QY 146 aaaattatgattgaatgtgctgagaanaactgaactcatttagtagggaattaaata 205
 DB 2949 gtaattacgaatgaatgttctgactgctgactgctgactgctgactgctgactg 3008
 QY 206 aagataatgaatgcttctgctgctgctgctgctgctgctgctgctgctgctgctg 265
 DB 3009 atgataacgaagtgtgctgctgctgctgctgctgctgctgctgctgctgctgctg 3068
 QY 266 aatattttatcaatgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 325

DB 3069 aatatattttatcccaatcgcggtccagtaataatagattataataataaagagctgtacatt 3128
 QY 326 tttcttttaacgaataaagtaataattataaacaacaacattgtttatgtatgcgtatag 385
 DB 3129 tttcttttaagtaattgagtaataattgtaaaaaataataattgtttatcatttaaggttg 3188
 QY 386 accctattgtccctatcaatcgtaattcgatcatcatgtgtatattacaggaatgcgggga 445
 DB 3189 accataacctccatatacaatttaataatcatgagggagaaataaactggaatgcagggtc 3248
 QY 446 atgattgtttctcgataaaaaataaacaatttaggatatacaacacgaagggtttacaacag 505
 DB 3249 atgattgagattttgatgaattagagagtttaggataataacacgaaggattccacaag 3308
 QY 506 gattgatccaatattacaataatcggttccattcagtttttaatttaaaagataaaaactg 565
 DB 3309 gattgatccgtattacaataatcgatcatcatctgttcttaaattagcaacaagaagt 3368
 QY 566 ctaaaagtattataaaggaatgagattttacgaaaaaagaataactaaaaagtcacaa 625
 DB 3369 ctaatgatgttttaaaaaacatggatgggttttaagaagcgtataatactaaaaaagtta 3428
 QY 626 aaaatggtttaagtaagattttctactaaagaagaattacaccttttcagatcattta 685
 DB 3429 aaaatggtttaagtcocgtttttatctcgaagaagattacctatatttaggtcattta 3488
 QY 686 tggaaagtacatcagacgactaaagaattttctgatagagagatagtttttactataatc 745
 DB 3489 tggaggataacctcgaaactaaagattttgcagtagagagaagatagtttttattacaaca 3548
 QY 746 gatttgatcttttaagaatagattagtagtaccctctcgcataataaaaatttgataat 805
 DB 3549 gattcaaacattataaagaccgtgttttagtaccactagcctataataactttgatagt 3608
 QY 806 atcttgaagaacttcctcagacgcctcagacattataaataaagacttaaacaaagctctaa 865
 DB 3609 atatagaggaaactaaataatgaagaatgtcgttaataaagattataataaagctttaa 3668
 QY 866 aagatattgaaaaacgacagataacaaaaaagcacaataaaaaataaatttagaac 925
 DB 3669 aagacattgaaaactccagagaataaaaaaagcacataaaaaaggaaatttagaac 3728
 QY 926 agcaattataaagaactgagcaaaaaaattgtatgaagcaacacacacttcaattagaacatg 985
 DB 3729 acaactcgatgcgaatccagcaaaaaaataatgaagctaaaaacttaaaacaagaacatg 3788
 QY 986 gtaacgaattacaaatactcgtggtgattcttctttatataatccatttgaggtgtatatt 1045
 DB 3789 gcaatgaattacccatctcgtggtctctttataatccggttcgaggtgattact 3848
 QY 1046 atcgagggtgaacgcgaataataatagacacttcgctggaagttaatgcagttcaatgga 1105
 DB 3849 agcgtgggggaactcaaatcgattatccatttcgagggagctatcggttcaatgga 3908
 QY 1106 ctatgatttaattatgcaattgatcatggaattgacccgttataatattttatgggattagt 1165
 DB 3909 agatgattaaactatgcaattgaacatggtatttaacggtataatattctctgtgtattgt 3968
 QY 1166 gtcattttacagatgagtcgaagaatgcaggtgtgttaaaatttaaaagagatttaagt 1225
 DB 3969 gtgacttttagtgaagaatgcgaagaatgcgtggtggttagttaggtttcaaaagggtctatg 4028
 QY 1226 cagatgtaattgaatgattgtgtggtgatttcgtttaaacctataaaataaaccaatgtattcac 1285
 DB 4029 ccgattttatagaatacgttgggtgactttattaaactattataaaccaatgtataaca 4088
 QY 1286 tatatacaacacttaaaataataaaaa 1313
 DB 4089 tttatagaacacttaaaataataaaaa 4116

RESULT	8
AAAX37799	
ID	AAAX37799 standard; DNA; 1280 bp.
XX	
XX	AAAX37799;
XX	
XX	
DT	09-JUL-1999 (first entry)
XX	

DE Staphylococcus lugdunensis FemA DNA.
 XX FemA: identification; detection; therapy; infection; femB;
 KM amplification; genotyping; gram-positive bacteria; vaccine; ss.
 XX Staphylococcus lugdunensis.
 OS
 FH Key Location/Qualifiers
 FT 1..1280
 FT CDS /*tag- a
 FT /product= "FemA"
 FT /note= "partial sequence, no start or stop codon"
 XX
 PD MO9916780-A2.
 XX 08-APR-1999.
 XX 28-SEP-1998; 98MO-BE00141.
 XX 26-SEP-1997; 97EP-0870146.
 XX (BENA-) BELGIAN MIN NAT DEFENCE.
 PA (UYLO-) UNIV CATHOLIQUE LOUVAIN.
 XX Gala J, Vannuffel P;
 XX WPI: 1999-287521/24.
 DR P-PSDB; AAY08216.
 XX
 PT New Staphylococcus-specific oligonucleotides
 XX
 PS Claim 17; Fig 7a-b; 48pp; English.
 XX
 CC This invention describes novel Staphylococcus-specific oligonucleotides
 CC based on the consensus femA nucleotide sequence which are used to
 CC develop products for the identification, detection and therapy of
 CC infections. The oligonucleotides can be used for the genetic
 CC amplification, the identification and/or quantification of various femA
 CC sequences which are specific to known or unknown Staphylococci species.
 CC Since the femA sequence is similar to the molecular genotyping of femA
 CC oligonucleotides can also be used for the molecular genotyping of femA
 CC genes of different Staphylococci species or other gram-positive bacteria.
 CC The femA nucleic acids can also be used in therapeutic applications.
 CC They can also be used to identify inhibitors, e.g. antibodies or
 CC antisense oligonucleotides, for blocking expression of the femA
 CC nucleotide sequences. They can also be used for producing vaccines
 CC against Staphylococci infections.
 CC
 SQ Sequence 1280 BP; 484 A; 197 C; 221 G; 378 T; 0 other;

Query Match 58.6%; Score 787.6; DB 20; Length 1280;
 Best Local Similarity 77.4%; Pred. NO. 1.2e-123;
 Matches 955; Conservative 0; Mismatches 279; Indels 0; Gaps 0;

Db 241 cacttttcttaagtgaactaataattttaaaagaataaactgtctctatgcgcg 300
 QY 382 atagacccttatttgcccttacaatacgtatcatatgtgtatgacaggaatgct 441
 Db 301 atagacccttatttgcccttacaatacgtatcatatgtgtatgacaggaatgct 360
 QY 442 gggaaatgattgtgtcttcgaataaagcaaatatgatatcaacgaagggttaca 501
 Db 361 gggaaatgattgtgtcttcgaataaagcaaatatgatatcaacgaagggttaca 420
 QY 502 acagatttgatccaataattacaatcggtccatccatgatttaattaaagattaa 561
 Db 421 acagatttgatccaataattacaatcggtccatccatgatttaattaaagattaa 480
 QY 562 actgttaagatgtatcaatgaatggaatgattttagcgaagaagaataactaaagtc 621
 Db 481 acagctaaagatgtttaaataatgatatgagcgtttagcgaagaagaataactaaagtc 540
 QY 622 caaaaaatggtgttaagaatgatttcttacttaagaagaataacttaactatccatga 681
 Db 541 tcaaaaaatggtgttaagaatgatttcttacttaagaagaataacttaactatccatga 600
 QY 682 ttatgtgaagatcatatcagagactaaagaatttctgtatagagaggtatttactat 741
 Db 601 ttatgtgaagatcatatcagagactaaagaatttctgtatagagaggtatttactat 660
 QY 742 aatgatttcatctttaaagaatgattttagtactctctgcacataataaattgat 801
 Db 661 aatgatttcatctttaaagaatgattttagtactctctgcacataataaattgat 720
 QY 802 gaattcttgaagaacttcatgacagcgttcagacatttaataaagacttaaacagat 861
 Db 721 gaattcttgaagaacttcatgacagcgttcagacatttaataaagacttaaacagat 780
 QY 862 ctaaaagatgtgaagaacagacagatacaaaaaagcacaataaataaataatta 921
 Db 781 ctaaaagatgtgaagaacagacagatacaaaaaagcacaataaataaataatta 840
 QY 922 gaacgcatatgaagaagaatgacgaagaatgtatgaaagacacaaactcaattaga 981
 Db 841 caacgaacatgacagatgcacatacaaaaagttaaggtcattcaagcggaa 900
 QY 982 catggaacgaattacacaaatctggtgattctcttttaacatccattgaagttga 1041
 Db 901 catggaacgaattacacaaatctggtgattctcttttaacatccattgaagttga 960
 QY 1042 tattatgcaggtggaagcgttaataatataagacacttcgtgaagttatgcagtt 1101
 Db 961 tattatgcaggtggaagcgttaataatataagacacttcgtgaagttatgcagtt 1020
 QY 1102 tggactatgatttaattgaattgcaattgcatgcatgcatgcatgcatgcatgcatg 1161
 Db 1021 tggactatgatttaattgaattgcaattgcatgcatgcatgcatgcatgcatgcatg 1080
 QY 1162 agtgcatttcaatgaatgattgctgaatgctgaatgctgaatgctgaatgctgaatg 1221
 Db 1081 agtgcatttcaatgaatgattgctgaatgctgaatgctgaatgctgaatgctgaatg 1140
 QY 1222 aatgcagatgattgaatgattgctgaatgctgaatgctgaatgctgaatgctgaatg 1281
 Db 1141 ggtgcagatgattgaatgattgctgaatgctgaatgctgaatgctgaatgctgaatg 1200
 QY 1282 tcaactatatacaacttaaaaaataaaga 1315
 Db 1201 aaacttattcaggtgttaaaagcaattcaaaata 1234

RESULT 9
 AAH52400
 ID AAH52400 standard; DNA; 1179 BP.
 XX
 AC AAH52400;

Staphylococcus sp. Fema consensus DNA sequence.

DE Fema: Identification; detection; therapy; infection; fema;
 KW amplification; genotyping; gram-positive bacteria; vaccine; ss.
 OS Synthetic.
 OS Staphylococcus sp.
 XX MO9916780-A2.
 XX
 XX 08-APR-1999.
 XX
 XX 28-SEP-1998; 98MO-BE00141.
 XX
 XX 26-SEP-1997; 97EP-0870146.
 XX
 XX (BENA-) BELGIAN MIN NAT DEFENCE.
 XX (UYLO-) UNIV CATHOLIQUE LOUVAIN.
 XX
 XX Gala J, Vannuffel P;
 XX
 XX MPI; 1999-287521/24.
 XX
 XX New Staphylococcus-specific oligonucleotides
 XX
 XX Claim 1; Fig 3; 48pp; English.

This invention describes novel Staphylococcus-specific oligonucleotides based on the consensus fema nucleotide sequence which are used to develop products for the identification, detection and therapy of infections. The oligonucleotides can be used for the genetic amplification, the identification and/or quantification of various fema sequences which are specific to known or unknown Staphylococci species. Since the fema sequence is similar to the molecular genotyping of fema oligonucleotides can also be used for the molecular genotyping of fema genes of different Staphylococci species or other gram-positive bacteria. The fema nucleic acids can also be used in therapeutic applications. They can also be used to identify inhibitors, e.g. antibodies or antisense oligonucleotides, for blocking expression of the fema nucleotide sequences. They can also be used for producing vaccines against Staphylococci infections. This sequence represents a Fema consensus DNA sequence composed from Staphylococcus sp. sequences.

Sequence 1328 BP; 304 A; 78 C; 146 G; 227 T; 573 other;

Query Match 54.6%, Score 733; DB 20; Length 1328;
 Best Local Similarity 57.9%, Pred. No. 1.7e-114;
 Matches 733; Conservative 0; Mismatches 532; Indels 0; Gaps 0;

QY 61 ataatagaattcaattcaacagctacagaattggcatttactgtaaaaaatgcca 120
 DB 14 aanaagaattcaacattcaacgcnanagantgmnnttcaacgannnatgcn 73
 QY 121 tataacatttcaacagatgactgaaatataagtttaaaagtgcgagaaactgaa 180
 DB 74 nanagactttacnancanannnnnnnnantangannttgcannnnnnngan 133
 QY 181 actcaattagtaggaatataaaaaataagaatagaactgctgctgtatgtaact 240
 DB 134 nccanantagngnatnaanaanaanaanaangantttgctgcngtntntna 193
 QY 241 gctgaccgctatgaataatttataatatttatacaaatgctgtgctcagtcatt 300
 DB 194 gcngtcncngnatgaanctntnaantatttatacnaangngcngtntatgat 253
 QY 301 tatgaataacaaagaactgcgtcatttcttcaacgaattagaataattataaaca 360
 DB 254 tntnaaannnagantgntcancantttcttcaangantttnnaantatntnaaan 313
 QY 361 caacattgtttatagtagcagatgaaccttattgacctatacatatgtaataat 420
 DB 314 nannntnnntatannntnnngancntannnnntatcataannnaatcatgan 373

QY 421 ggtgatatacagaagaatgctggaatgattgcttcttcgataaaatgaacaattagga 480
 DB 374 gngnannntnnnnngnatgcnngnangantgntnttngantnnnnnnnnngn 433
 QY 481 tatcaacagaagggtttacacagaatttgatccaatatacaaatccgttccatca 540
 DB 434 tntnancannnnngntttnnnnangntttgancntnnnnnnnnnnngntnncan 493
 QY 541 gtttaaatataagaataaaactgctaaagtatttataaagtgaatgattagta 600
 DB 494 gntnataatttann 553
 QY 601 aaaaagaatacctaaaaaagtccaaaaatggtttaaagtaagatttccataagaa 660
 DB 554 aanngaanaacnaaaaaagctnnnaanaaatgngtlnaaagtntnnntnnnnnaagan 613
 QY 661 gaattaccatttcaagatcattatggaagatacaccagagactaagaatttctgat 720
 DB 614 gannntcnaatnttngtcatatnagangatacncngnannnnnnnnnnnnngat 673
 QY 721 agagagagatttcttactatgaatcattggaacttcacagaaagtcagacatta 780
 DB 674 nngnangannnttntntananaangntnnnnnnnnnnnnnnnnnnnnnnnnnnnn 733
 QY 781 ctgcataataaaatttgatgaatcttggaacttcacagaaagtcagacatta 840
 DB 734 nngnntatntnn 793
 QY 841 aataagacttaacaaagctcctaagaatattgaaagaacagacagatacaaaaagca 900
 DB 794 antaagannnnnaaagcnnlnaanganainganaaangncngnanaaaaaangcn 853
 QY 901 caaataaaaaaataaatttgagacagcaataaagcaaaatgagcaaaatgagaa 960
 DB 854 nnnnaann 913
 QY 961 gcaacacactcaattagacatgtaacgaattcccaattcctgcgtgattccttt 1020
 DB 914 gnnann 973
 QY 1021 acttaacattggaagtgtatattatgacagtggaagcgaataaataatagacactc 1080
 DB 974 atnaatccnttgaagtcnntanangcngtggnacntcnaatnnnnnnnnnnnnnn 1033
 QY 1081 gctggaagttagcagttcaatggaactatgaatattatgcaattgacatgagattgac 1140
 DB 1034 gcnngnagntatgcnntncaatgcnmatgcttaantatgcnntnancatnnnnnnnn 1093
 QY 1141 cgttaaatattttaggattagtgatgcttcaatttcaagatgctggaagtcagtgct 1200
 DB 1094 ngntanaattttatggnntagngnttannnttannngangangcgaagagngngntn 1153
 QY 1201 gtaaatttaaaaaaggaattatgcaagatgaaatgaaatggttggatgctgtaaa 1260
 DB 1154 ntnaantttaaaagngntnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 1213
 QY 1261 cctataataacaaacagttatcactatatacacaacttaaaaaaattaaaaagattg 1320
 DB 1214 ccaataaanaaann 1273
 QY 1321 aatta 1325
 DB 1274 nntta 1278

RESULT 11
 AAX37802
 ID AAX37802 standard; DNA; 1297 BP.
 XX
 AC AAX37802;
 XX
 DT 09-JUL-1999 (first entry)

Fri Jun 21 08:38:29 2002

XX	Staphylococcus schleiferi FEMa DNA.	
DE		
XX	FEMa; identification; detection; therapy; infection; femB;	
KW	amplification; genotyping; gram-positive bacteria; vaccine; ss.	
OS	Staphylococcus schleiferi.	
XX		
XX	Key	Location/Qualifiers
FT	CDS	1..1297
FT		/tag- a "FEMa"
FT		/product-
FT		/note- "partial sequence, no start or stop codon"
XX	W09916780-A2.	
XX		
XX	08-APR-1999.	
XX	28-SEP-1998; 98WO-BE00141.	
XX	26-SEP-1997; 97EP-0870146.	
XX	(BENA-) BELGIAN MIN NAT DEFENCE.	
PA	(UYLO-) UNIV CATHOLIQUE LOUVAIN.	
XX		
PI	Gala J, Vannuffel P;	
DR	WPI; 1999-287521/24.	
DR	P-PSDB; AAY08219.	
XX		
XX	New Staphylococcus-specific oligonucleotides	
PS	Claim 23; Fig 10a-b; 48pp; English.	
XX	This invention describes novel staphylococcus-specific oligonucleotides	
CC	based on the consensus fema nucleotide sequence which are used to	
CC	develop products for the identification, detection and therapy of	
CC	infections. The oligonucleotides can be used for the genetic	
CC	amplification, the identification and/or quantification of various fema	
CC	sequences which are specific to known or unknown staphylococci species.	
CC	Since the fema sequence is similar to the femB sequence, the	
CC	oligonucleotides can also be used for the molecular genotyping of femB	
CC	genes of different staphylococci species or other gram-positive bacteria.	
CC	The fema nucleic acids can also be used in therapeutic applications.	
CC	They can also be used to identify inhibitors, e.g. antibodies or	
CC	antisense oligonucleotides, for blocking expression of the fema	
CC	nucleotide sequences. They can also be used for producing vaccines	
CC	against staphylococci infections.	
XX		
SQ	Sequence 1297 BP; 495 A; 184 C; 249 G; 369 T; 0 other;	
XX		
XX	Query Match	50.7%; Score 681; DB 20; Length 1297;
XX	Best Local Similarity	71.6%; Pred. No. 8.9e-106;
XX	Matches 894; Conservative	0; Mismatches 355; Indels 0; Gaps 0;
Qy	82 acagtcacgaatttggtgatttactgaaataatgcccataatgacatttaccacagatg 141	
Db	1 acgagcgtgatttggtgctttacagatacaatgcccataatgacatttaccacagatg 60	
Qy	142 actgaaataatgattgatttgaagtgtgtagaaactgaacacttattagtaggaattaa 201	
Db	61 gtgggaactatgaattaaagtgtgtagaaactgaacacttattagtaggaattaa 120	
Qy	202 aataagataatgaatgattgattgattgattgattgattgattgattgattgattgatt 261	
Db	121 gataac 180	
Qy	262 tttaaatatttttttcaaatcgtggtccagtcattgattgattgattgattgattgattgatt 321	
Db	181 tttaaatatttttttcaaatcgtggtccagtcattgattgattgattgattgattgattgatt 240	
Qy	322 cacttttttttaacgaattaaatattttaaataattttaaataattttaaataattttaaata 381	

RESULT 12
AAAX37803
ID AAAX37803 standard; DNA; 1284 BP.
XX
XX AAAX37803;
AC

XX 09-JUL-1999 (first entry)
 XX Staphylococcus sciuri FemA DNA.
 DE FemA, identification; detection; therapy; infection; femB;
 KM amplification; genotyping; gram positive bacteria; vaccine; ss.
 XX Staphylococcus sciuri.
 OS
 XX
 FH Key Location/Qualifiers
 FT 1.1284
 FT /tag= a
 FT /product= "FemA"
 FT /note= "partial sequence, no start or stop codon"
 XX
 PN MO9916780-A2.
 XX
 PD 08-APR-1999.
 XX
 PF 28-SEP-1998; 98WO-BE00141.
 XX
 PR 26-SEP-1997; 97EP-0870146.
 XX
 PA (BENA-) BELGIAN MTN NAT DEFENCE.
 PA (UYLO-) UNIV CATHOLIQUE LOUVAIN.
 XX
 PI Gala J, Vannuffel P;
 XX
 XX WPI; 1999-287521/24.
 DR P-PSDB; AAI08220.
 XX
 PT New Staphylococcus-specific oligonucleotides
 XX
 PS Claim 25; Fig 11a-b; 48pp; English.
 XX
 CC This invention describes novel Staphylococcus-specific oligonucleotides
 CC based on the consensus femA nucleotide sequence which are used to
 CC develop products for the identification, detection and therapy of
 CC infections. The oligonucleotides can be used for the genetic
 CC amplification, the identification and/or quantification of various femA
 CC sequences which are specific to known or unknown Staphylococci species.
 CC Since the femA sequence is similar to the femB sequence, the
 CC oligonucleotides can also be used for the molecular genotyping of femB
 CC genes of different Staphylococci species or other gram-positive bacteria.
 CC The femA nucleic acids can also be used in therapeutic applications.
 CC They can also be used to identify inhibitors, e.g. antibodies or
 CC antisense oligonucleotides, for blocking expression of the femA
 CC nucleotide sequences. They can also be used for producing vaccines
 CC against Staphylococci infections.
 XX
 XX Sequence 1284 BP; 518 A; 181 C; 215 G; 370 T; 0 other;
 SQ
 Query Match 46.6%; Score 626.4; DB 20; Length 1284;
 Best Local Similarity 70.0%; Pred. No. 1.3e-96;
 Matches 859; Conservative 0; Mismatches 366; Indels 3; Gaps 1;

QY 331 ttaaagaaatgaataattttaaaacaaacacattgtttatgtacgtatagacccct 390
 DB 247 tttaagaataatcgtagcatttaaaagaatttaaaagatttattttagaacgtaccct 306
 QY 391 tattgccttaataatcgttaatacgtatgagtgatatttaacggaatgctgggaatgat 450
 DB 307 tacttgcacatacaactaagaagatcatatgagcaattatataaaacattcaacgttgc 366
 QY 451 tggcttcctgaataaatgaacaattagatatacaacgaagggtttacaacagagatt 510
 DB 367 gtttaattaaacaatttgaacattagattatgataaacaacaggttcaacacgtgttc 426
 QY 511 gatccattatacaattcgttccattcagttttaatttaagataaacaacgtctaa 570
 DB 427 caaccaatacatcaattagatgagcttcgttacttatttgaagaattgagcaaaa 486
 QY 571 gatgtataatggaatgtagtagtttaagaaaagaataactaaagttccaaaaaat 630
 DB 487 acgctcatcaagaacacgtgacagtttaagaanaaagaataactaaagttccaaaaaat 546
 QY 631 ggtgttaagtaagatttcttactaagaagaattactaatttcagatcattatgaa 690
 DB 547 ggtttaaagttcgtttccattcaagaatggaatgacgagattccgtaattatgaa 606
 QY 691 gatactcagaagaataaatttctgataagagagtagttttactatatacgtatt 750
 DB 607 gatacacaagaagaagaatttccacagatcgtgagtagcttattacataagata 666
 QY 751 gatcattttaaagatagatattagtagcttcgcataattataaattttagatatt 810
 DB 667 aaatactttgaaat---gtaagattcctttagatataatagacttgaacttaact 723
 QY 811 gaagaacttcagcagaacgctgacacatttaataaagacttaacaagaacttaagaat 870
 DB 724 ccaaatatgaanaaagaacacgtgacacacatacaacaagaatattgtaaaaagat 783
 QY 871 attgaanaagcagacatacaacaanaagcacaanaataaataattagaaacgaa 930
 DB 784 ttgaanaagaacacagatatacaanaaagatttaataatagcaacttaaaacaa 843
 QY 931 ttaaagaacaaatgagcaanaaattgtagaagcaacacattcaatttagaacaatgtaac 990
 DB 844 aagaagaagaatgaagctaatatgaagaagcacttcaactcaacaagaacatggtgat 903
 QY 991 gaattacaatacctcgtgatttcttatttaacacatttgaagtgtatattatgca 1050
 DB 904 acattaccaatagcagcgtgttcttattatcaacatttgaagttgatatattgca 963
 QY 1051 ggtggaagcaataatagacacattcgtggaagtgtatgacgttcaatgagctatg 1110
 DB 964 ggtgtcatcagaatgaatataatcgtcacttgcagtagtattgcaactcagtggaatg 1023
 QY 1111 attaatatgcaattgacatgagcattacacgttatattttagatttagattgagtagtgc 1170
 DB 1024 attaatagcgttagatccacacatttaccgtttataacttcaatgagtagtaacagcgagac 1083
 QY 1171 tttaacagatgctgtgaagatgtaggtgtgtttaaatttaaaagatttaagtcagat 1230
 DB 1084 ttctcagaagaagacgtgaggtgtgtgtatttaatttaaaagatttaacagtcagat 1143
 QY 1231 gtaattgataatgtgtgtatttgcgttaaacctataaataaacaacatgattacattat 1290
 DB 1144 gtttaagataatgtgtgtatttgcgttaaacctataaataaacaacatgattacattat 1203
 QY 1291 acaacacttaaaaaaataaagaagat 1318
 DB 1204 acaacacttaaaaaaataaagaat 1231

Db	583	ATGATAACGAAGTGATTCAGCTTGTGTTTATTAAACAGCTGTTCCTGTAATGAATAATTTTA	524
Qy	266	aatttttttattcaaatcgctgcagtcgattgattgaatacaagaactcgctcaact	325
Db	523	AATATTTTTTATCCAAATCCGGTCCAGTAATAGATTATAATTAAGAGCTTGTACATT	464
Qy	326	ttttctttaacgaataaagtaaatatttaaaacaaacacattgtttatatgtacgtatag	385
Db	463	TTTCTTTTATGAATGGAGTAATATGATGAAAAATAAATGTTTATATTTAAGAGTTG	404
Qy	386	accttatttgccttatcaatatcgtaataatcgatggcgattacacaggaaatgctggga	445
Db	403	ACCATACTCTCCATATCAATATTTAAATCATGAGGGAGAAATACCTGGNAATGCAGTTC	344
Qy	446	atgattggtcttcgataaaatgaacaaataggatatacaacagaagggtttacaacag	505
Db	343	ATGATGTGGATTTTGTGATGAATTAGAGATTTAGGATATAACACGAAGGATCCACAAAG	284
Qy	506	gatttgatccaattattcaaatctgggtccattcagttttaaattaaaggataaaactg	565
Db	283	GATTTGATCCGTGATTACAAATCCGATATCATCTCTTCTAAATTTAGCAACAAGTGT	224
Qy	566	ctaaagatgtattaaatggaatgtagatttacgaaagaataactaaaaagctccaaa	625
Db	223	CTAATGATGTTTAAAAAACATGSGATGTTTGTAGAAAGCGTAACTATAAAAAGTTAGA	164
Qy	626	aaaatggtttaaagtaagattcttactaaagaagaattacctattttcagatcatcta	685
Db	163	AAATGTGGAGTTTAAAGTCCGTTTTTATCTGGAAGAGGTTACCTATATTAGGTCATTTA	104
Qy	686	tgaagatgacatcagagataagaattttctgatagagagatagtttttactataaatc	745
Db	103	TGGAGGATACCTCTGAACCTAAAGATTTTGCGATAGAGAAGATAGTTTTTATTACARCA	44
Qy	746	gatttgatcatttaaatgaagatagattagctacctctcgcata	788
Db	43	GATTCAAACATTATANAAGCCGTTTGTAGTACCACCTAGCCCTA	1
RESULT 14			
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XX	AAV74747 standard; DNA; 3271 BP.		
XX	AAV74747;		
XX	AC		
XX	AC		
DT	16-MAR-1999 (first entry)		
XX	Staphylococcus aureus contig SEQ ID #436.		
DE			
XX			
XX	Computer readable medium; vaccine; S.aureus infection; immunodetection;		
KW	cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;		
KW	skin infection; surgical wound infection; scalded skin syndrome;		
KW	toxic shock syndrome; ds.		
XX			
OS	Staphylococcus aureus.		
XX			
FH	Key	Location/Qualifiers	
FT	misc_feature	1561..1620	
FT		/*tag= a	
FT		/note= "these bases represent a line of missing text in	
FT		the sequence listing in the specification. They	
FT		are included to maintain the nucleotide numbering	
FT		given in the specification for this DNA sequence"	
FT			

[illegible]

Fri Jun 21 08:38:29 2002

us-09-509-234c-52.rng

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 20, 2002, 12:04:14 ; Search time 208.59 Seconds
(without alignments)
1581.503 Million cell updates/sec

Title: US-09-509-234C-52

Perfect score: 1343

Sequence: 1 taataatttaaatgacga.....taagaggggaatagtagaa 1343

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents, NA:
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2: /cgn2_6/prodata/2/ina/5B.COMB.seq:*
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6: /cgn2_6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	802.8	59.8	1257	1	US-08-330-154-1 Sequence 1, Appl 1
2	278.8	20.8	453	3	US-08-714-918-9 Sequence 9, Appl 1
3	278.8	20.8	453	4	US-09-265-315-9 Sequence 9, Appl 1
4	278.8	20.8	453	4	US-09-265-315-9 Sequence 9, Appl 1
5	278.8	20.8	453	4	US-09-265-315-9 Sequence 9, Appl 1
6	251.2	18.7	410	3	US-08-714-918-6 Sequence 6, Appl 1
7	251.2	18.7	410	3	US-09-265-315-6 Sequence 6, Appl 1
8	251.2	18.7	410	4	US-09-265-315-6 Sequence 6, Appl 1
9	251.2	18.7	410	4	US-08-714-918-4 Sequence 4, Appl 1
10	232.4	17.3	400	4	US-09-265-315-4 Sequence 4, Appl 1
11	232.4	17.3	400	4	US-09-265-315-4 Sequence 4, Appl 1
12	232.4	17.3	400	4	US-09-265-315-4 Sequence 4, Appl 1
13	232.4	17.3	400	4	US-09-265-315-4 Sequence 4, Appl 1
14	103	7.7	5253	3	US-08-714-918-19 Sequence 19, Appl 1
15	103	7.7	5253	4	US-09-265-315-19 Sequence 19, Appl 1
16	103	7.7	5253	4	US-09-265-315-19 Sequence 19, Appl 1
17	103	7.7	5253	4	US-09-265-315-19 Sequence 19, Appl 1
18	76.4	5.1	19124	2	US-08-487-8268-13 Sequence 13, Appl 1
19	68.4	5.1	930	4	US-08-936-1658-74 Sequence 74, Appl 1
20	65.2	4.9	19124	2	US-08-446-8558-13 Sequence 13, Appl 1
21	63	4.7	8920	3	US-08-487-8268-13 Sequence 13, Appl 1
22	63	4.7	8920	3	US-08-487-8268-13 Sequence 13, Appl 1
23	62.2	4.6	398	4	US-09-150-741-1 Sequence 1, Appl 1
24	62.2	4.6	398	4	US-08-714-918-5 Sequence 5, Appl 1
25	62.2	4.6	398	4	US-09-265-315-5 Sequence 5, Appl 1
26	62.2	4.6	398	4	US-09-265-315-5 Sequence 5, Appl 1
27	60	4.5	7218	1	US-08-232-463-14 Sequence 14, Appl 1

28	59.4	4.4	240	1	US-08-628-417-6
29	59.4	4.4	2223	1	US-08-257-073-4
30	57.2	4.3	2447	2	US-09-014-969-14
31	56.8	4.2	3095	6	5231168-1
32	56.2	4.2	6243	2	US-09-056-075-1
33	55.8	4.2	658	4	US-08-998-416-595
34	55	4.1	5852	1	US-07-867-106-2
35	54.8	4.1	6124	4	US-08-213-419B-3
36	53.8	4.0	5361	4	US-08-973-462-2
37	53.6	4.0	1482	4	US-08-098-327E-41
38	52.8	3.9	4766	5	US-08-462-625-41
39	52.6	3.9	1493	4	PCT-US93-07261-10
40	52.6	3.9	1493	4	US-08-098-327E-38
41	52.6	3.9	1493	4	US-08-462-625-38
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43	52	3.9	1482	4	US-08-098-327E-45
44	52	3.9	1482	4	US-08-462-625-45
45	51.6	3.8	837	4	US-08-998-416-288

ALIGNMENTS

RESULT 1
US-08-330-154-1 Application US/08330154
; Sequence 1, Patent No. 5587307
; GENERAL INFORMATION:
; APPLICANT: Alborn Jr., William E
; APPLICANT: Hoskins, Joann
; APPLICANT: Skatrud, Paul L
; APPLICANT: Unal, Serhat
; TITLE OF INVENTION: FEMA GENE OF STAPHYLOCOCCUS EPIDERMIDIS,
; TITLE OF INVENTION: FEMA PROTEIN, AND VECTORS AND MICROORGANISMS COMPRISING
; TITLE OF INVENTION: THE FEMA GENE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: Patent Division/AEH
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/330,154
; FILING DATE: 27-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,925
; FILING DATE: 09-MAR-1994
; APPLICATION NUMBER: US/08/057,163
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hamilton, Amy E
; REGISTRATION NUMBER: 33,894
; REFERENCE/DOCKET NUMBER: X-8894
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-1294
; TELEFAX: 317-276-1294
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1257 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS

us-09-509-234c-52.rni

Fri Jun 21 08:38:29 2002

LOCATION: 1..1257

US-08-330-154-1

Query Match 59.8%; Score 802.8; DB 1; Length 1257; Best Local Similarity 77.5%; Pred. No. 3.9e-156; Matches 972; Conservative 0; Mismatches 282; Indels 0; Gaps 0;

QY 60 gataatgaatttcaaatcaacagctacagaaatttgagatttctactgaaataatgcc 119
 DB 3 GAAGATGAAGTTTACGAATTGACACCTPAAGATTAGTACTTACTGATGATGAC 62
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 DB 63 ATATAGTCATTTACACAATGGAAGTAAATTTACGAATTAAGGTTGCTGGAAGGTACCGA 122
 QY 180 aactcatttagtaggaataaaataaataaataaataaataaataaataaataaataa 239
 DB 123 GTCACATTTAGTTGGAATTAATAATTAATGACGAAGTATGACGCTTGTATTAAAC 182
 QY 240 tctgtaccggttatgaaatttttaatttttttttttttttttttttttttttttttt 299
 DB 183 AGCTGTTCCGTGTAAGAAATTAATTAATTTTATTTTCCAAATCGCGTCCAGTAATAGA 242
 QY 300 ttatgaaacaaagaactogttcactttcttttaacgaataaagtaaatatttaaaaca 359
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 QY 360 acaacattgtttatgtacgtatagacccttttcttttaacgaataaataatcgtaacatga 419
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 DB 363 GGGAGAAATTAACGTAAGTGAAGTCAATGATGTTGATGTTTGAATTAAGAGAGTTAGG 422
 QY 480 atatacaacacgaaggttttacacagggatttgatcccaataattcaaaattcggtccattc 539
 DB 423 ATATAACACGAGGATTTCCACAAAGGATTTGATGCTGTATTAACAAATCCGATATCATTC 482
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 DB 663 TAGAGAAGTAGTGTATTTATACACAGATTCACAACTTAAAGACCGTGTATTAGTACC 722
 QY 780 tctgcataataaaatttgatgaattcttgaagaacttcattgacagactgacagacatt 839
 DB 723 ACTAGCTATATTAACTTTGATGATATATAGAGGAACTTAATTAAGAAATTTGCTGCT 782
 QY 840 aataaagacttaaaacaaagctcaaaagatttgaaacagcagacagatacaaaaaaagc 899
 DB 783 TAATAAGATTATATAAAGCTTTAAGACATTTGAGAAACGTTCCAGAGAATAAAAAAGC 842
 QY 900 acaaaataaaaaataaatttagaacagcaataaagaacaaatgcaaaaaaattatga 959
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 QY 960 agcaacaaacttaaatagaacatggttaacgaattaccaaataatctgctgattctctt 1019
 DB 903 AGCTAAAAACTTAAAAACAGCAATGGCAATGAATTAACCCATCTCTGCTGCTCTTTAT 962
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DB 963 AATTATCGGTTGAAGTACTTTACTACGCTGGTGAACATTCAAATCGTTATCGCCATTT 1022
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 QY 1140 ccttataatattttatggatttagtggtcattttacagatgagtcgaagatgcaggtgt 1199
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 QY 1200 tgaataatttaaaagatttaaatgagatgcagatgagatgagatgagatgagatgagat 1259
 DB 1143 AGTTAGTTTAAAGGCTATGATGCGGATGTTATAGAAATACGTTGGTGACTTTATTAA 1202
 QY 1260 acctataataaacaatgatttaccattatatacaacacttaaaaaataaaaaa 1313
 DB 1203 ACCTATTAAATAACCAATGATATAACATTTTATAGAACACTTAAATAAAGAA 1256

RESULT 2

US-08-714-918-9
 : Sequence 9, Application US/08714918
 : Patent No. 6037123
 : GENERAL INFORMATION:
 : APPLICANT: Benton, Bret
 : APPLICANT: Lee, Ving
 : APPLICANT: Malouin, Francois
 : APPLICANT: Martin, Patrick K.
 : APPLICANT: Schmid, Molly B.
 : APPLICANT: Sun, Dongxu
 : TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
 : NUMBER OF SEQUENCES: 111
 : CORRESPONDENCE ADDRESS:
 : ADDRESS: Lyon & Lyon
 : STREET: Suite 4700
 : CITY: Los Angeles
 : STATE: California
 : COUNTRY: U.S.A.
 : ZIP: 90071-2066
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 : MEDIUM TYPE: storage
 : COMPUTER: IBM Compatible
 : OPERATING SYSTEM: IBM P.C. DOS 5.0
 : SOFTWARE: Word Perfect 5.1
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08714,918
 : FILING DATE: September 13, 1996
 : CLASSIFICATION: 424
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 60/009,102
 : FILING DATE: December 22, 1995
 : APPLICATION NUMBER: 60/003,798
 : FILING DATE: September 15, 1995
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Warburg, Richard J.
 : REGISTRATION NUMBER: 32,327
 : REFERENCE/DOCKET NUMBER: 222/005
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (213) 489-1600
 : TELEFAX: (213) 955-0440
 : TELEX: 67-3510
 : INFORMATION FOR SEQ ID NO: 9:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 453 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : US-08-714-918-9

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1168 cattttacagatgatgctgaagtgcagggtg 1199
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422 NAATTCAGNAGGTGCTGAAGATGCTGGTG 453
Ddb

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RESULT      5
US-09-266-417-9
; Sequence 9, Application US/09266417
; Patent NO. 6228588
; GENERAL INFORMATION:
; APPLICANT: Benton, Bret
; APPLICANT: Lee, Ving J.
; APPLICANT: Malouin, Francois
; APPLICANT: Martin, Patrick K.
; APPLICANT: Schmid, Molly B.
; APPLICANT: Sun, Dongxu
; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
; TITLE OF INVENTION: TARGET GENES

```

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1 TITLE OF INVENTION: ANAL. CEN.
2
3 NUMBER OF SEQUENCES: 111
4
5 CORRESPONDENCE ADDRESS:
6 ADDRESSEE: Lyon & Lyon
7 STREET: 633 West Fifth Street
8
9 STREET: Suite 4700
10
11 CITY: Los Angeles
12
13 STATE: California
14
15 COUNTRY: U.S.A.
16
17 ZIP: 90071-2066
18
19 COMPUTER READABLE FORM:
20
21 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
22
23 MEDIUM TYPE: storage
24
25 COMPUTER: IBM Compatible
26
27 OPERATING SYSTEM: IBM P.C. DOS 5.0
28
29 SOFTWARE: Word Perfect 5.1
30
31 CURRENT APPLICATION DATA:
32
33 APPLICATION NUMBER: US/09/366,417
34
35 FILING DATE: March 9, 1999
36
37 CLASSIFICATION: 435
38
39 PRIOR APPLICATION DATA:
40
41 APPLICATION NUMBER: 08/714,918
42
43 FILING DATE: September 13, 1996

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Query Match	20.8%;	Score 278.8;	DB 4;	Length 433;	
Best Local Similarity	74.6%;	Pred. No. 5.6e-49;			
0: Mismatches	115;	Indels	0;	Gaps	0;

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QY	808	cttgaagaactcatcagaacgctcagacattaaataaagacttaaacaaagcgtctaaaa	867
Db	62	ATTAAAGACATAACGAGAGCGGTGATTTTAAATAAAGATTAAATTAAGCGTTAAG	121
QY	868	gatattgaataaacgaccagataacaaaaagcacaataaaaaataaatttagaacag	927
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Db	182	CAACTTGATGCAAATAGCAAAAGATTGANGACGGTTAAGCTCTACAGANGANCATGGT	241
QY	988	aacgaattaccaatctcggtatctcttatttaataccatttgtaagtgtgatatatt	1047
Db	242	AATGNTTTTACCTATCTCTCGTGTTCCTCTTATCAATCCNTTGGANGTGTGTTATTAT	301
QY	1048	gcaggttgaacgccaataataatagacacttcgctggaggtatgcaggttcattgaact	1107
Db	302	GCTGCTGGTACATCAAAATGCNTCCGTCATTTTNCGGANGTATGCTNGTCAATGGGAA	361
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Length 453; PB 4: 270 g.

Query Match	20.8%;	Score 276.6;	25.47
Best Local Similarity	74.6%;	Pred. No. 5.6e-49;	
Matches 337; Conservative	0;	Mismatches 115;	Indels 0;
Gaps	0;		

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867

APPLICATION NUMBER: 05/03/

RESULT 7
 US-09-265-315-6
 Sequence 6, Application US/09265315
 Patent No. 6187541
 GENERAL INFORMATION:
 APPLICANT: Benton, Bret
 APPLICANT: Lee, Vang J.
 APPLICANT: Malouin, Francois
 APPLICANT: Martin, Patrick K.
 APPLICANT: Schmidt, Molly B.
 APPLICANT: Sun, Dongxun
 TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
 TITLE OF INVENTION: ACTIVE ON STRAPHYLOCOCCUS AUREUS
 TITLE OF INVENTION: TARGET GENES
 NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/265.315

us-09-509-234c-52.ini

Fri Jun 21 08:38:29 2002

; FILING DATE: March 9, 1999
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/714,918
 ; FILING DATE: September 13, 1996
 ; APPLICATION NUMBER: 60/009,102
 ; FILING DATE: December 22, 1995
 ; APPLICATION NUMBER: 60/003,798
 ; FILING DATE: September 15, 1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 240/247
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 410 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-09-265-315-6

Query Match 18.7%; Score 251.2; DB 4; Length 410;
 Best Local Similarity 75.4%; Pred. No. 2.4e-43;
 Matches 307; Conservative 0; Mismatches 100; Indels 0; Gaps 0;
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 QY 785 catatataaaatttgatgaattcttgaagacttcattgacgaagtcagacattataa 844
 Db 64 CGTATATCAACTTTAATGATATATTAAGAACTTAACGAGAGCGTGATATTTTAAATA 123
 QY 845 aagacttaaacaaagctctaaagattgtaaaagacagacatacaaaaaagacacaa 904
 Db 124 AAGATTAAATTAAGGCTTAAAGGATATTGAAACCGCTCTGAAATATAAAAGCACATA 183
 QY 905 ataaaaaaataatttagaacagcaattaaagcaaatgagcaaaattgatgaagcaa 964
 Db 184 ACAAGCGAGATAACTTACAAACAACCTTGATGCAATGAGCAAAAGATTGAAGAGTA 243
 QY 965 cacaacttaagacatggttaacgaattaccacattctgctggattcttcttatta 1024
 Db 244 AAGCTTACAAGANGACATGTTAATGATTAACCTATCTCTGCTGTTCTTCTTATCA 303
 QY 1025 atccattgaagttgattattatgcaggtggaagtcacaaataaatagacattcgctg 1084
 Db 304 ATCCATTGANGTTGTTATTATGCTGGTGATACATCAATGCAATCCGTCATTTCNCG 363
 QY 1085 gaagttatgcagttcaatgagctattgatttaattgcaattgatcat 1131
 Db 364 GAAGTTATGCTAGTGAATGGAATGATTAATATGCAATTAATCAT 410

RESULT 8
 US-09-265-315-6
 ; Sequence 6, Application US/09265315
 ; Patent No. 6187541
 ; GENERAL INFORMATION:
 ; APPLICANT: Benton, Bret
 ; APPLICANT: Lee, Ying J.
 ; APPLICANT: Malouin, Francois
 ; APPLICANT: Martin, Patrick K.
 ; APPLICANT: Schmid, Molly B.
 ; APPLICANT: Sun, Dongxu
 ; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
 ; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
 ; TITLE OF INVENTION: TARGET GENES

; NUMBER OF SEQUENCES: 111
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; SUITE: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/265,315
 ; FILING DATE: March 9, 1999
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/714,918
 ; FILING DATE: September 13, 1996
 ; APPLICATION NUMBER: 60/009,102
 ; FILING DATE: December 22, 1995
 ; APPLICATION NUMBER: 60/003,798
 ; FILING DATE: September 15, 1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 240/247
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 410 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-09-265-315-6

Query Match 18.7%; Score 251.2; DB 4; Length 410;
 Best Local Similarity 75.4%; Pred. No. 2.4e-43;
 Matches 307; Conservative 0; Mismatches 100; Indels 0; Gaps 0;
 QY 725 aggatagttttactataatcagttgatttataaagatagattagtagtacctctg 784
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 QY 785 catatataaaatttgatgaattcttgaagacttcattgacgaagtcagacattataa 844
 Db 64 CGTATATCAACTTTAATGATATATTAAGAACTTAACGAGAGCGTGATATTTTAAATA 123
 QY 845 aagacttaaacaaagctctaaagattgtaaaagacagacatacaaaaaagacacaa 904
 Db 124 AAGATTAAATTAAGGCTTAAAGGATATTGAAACCGCTCTGAAATATAAAAGCACATA 183
 QY 905 ataaaaaaataatttagaacagcaattaaagcaaatgagcaaaattgatgaagcaa 964
 Db 184 ACAAGCGAGATAACTTACAAACAACCTTGATGCAATGAGCAAAAGATTGAAGAGTA 243
 QY 965 cacaacttaagacatggttaacgaattaccacattctgctggattcttcttatta 1024
 Db 244 AAGCTTACAAGANGACATGTTAATGATTAACCTATCTCTGCTGTTCTTCTTATCA 303
 QY 1025 atccattgaagttgattattatgcaggtggaagtcacaaataaatagacattcgctg 1084
 Db 304 ATCCATTGANGTTGTTATTATGCTGGTGATACATCAATGCAATCCGTCATTTCNCG 363
 QY 1085 gaagttatgcagttcaatgagctattgatttaattgcaattgatcat 1131

us-09-509-234c-52.rni

Fri Jun 21 08:38:29 2002

FILING DATE: September 15, 1995

ATTORNEY/AGENT INFORMATION:

NAME: Wardburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 240/247

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 400 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-265-315-4

Query Match 17.3%; Score 232.4; DB 4; Length 400;

Best Local Similarity 74.5%; Pred. No. 1.7e-39;

Matches 298; Conservative 0; Mismatches 101; Indels 1; Gaps 1;

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Db 340 AAAATATGTTAAAAACATCGTGTGNCATACCTACATACATGATCCATATTTAGCATATCA 281

QY 405 atactgtaactgattgattatgaacacaaagaaactggttcacattttttttaaagaaatta-ag 464

Db 280 ATACTTGAATCATGATGGCGAGATTACAGGTAATGCTGTAATGATGTTGTTTGTATTA 221

QY 465 aatgaacaaattaggatatcaacacaaagaaactggttcacattttttttaaagaaatta-ag 524

Db 220 AATGAGTAACCTAGGATTGAAACATACCTGATTCATTAAGAGATTAACAGCATCATTTNAAA 161

QY 525 aattcggttcattcagtttttaaaatttaaaagataaaactgcttaagatgtatttaaaag 584

Db 160 AATCGGTTATCAGTCAGTGTGTTAAAGATTAAGATTAAGATTAAGATTAAGATTAAG 101

QY 585 aatgtagattttacgaaaaaagaaactaataaaagttccaaagttccaaagttccaaag 644

Db 100 TATGATGAGCTTAGAAAAAGAAACACGGAANNAGTTNAAAAGATGTTTAAAGATTAAG 41

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RESULT 11

US-09-265-315-4/c

; Sequence 4, Application US/09265315

; Patent No. 6187541

; GENERAL INFORMATION:

; APPLICANT: Benton, Bret

; APPLICANT: Lee, Ving J.

; APPLICANT: Malouin, Francois

; APPLICANT: Martin, Patrick K.

; APPLICANT: Schmid, Molly B.

; APPLICANT: Sun, Dongxu

; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS

; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS

; TITLE OF INVENTION: TARGET GENES

; NUMBER OF SEQUENCES: 111

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Suite 4700

; STATE: Los Angeles

; COUNTRY: California

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/265,315

; FILING DATE: March 9, 1999

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/714,918

; FILING DATE: September 13, 1996

; APPLICATION NUMBER: 60/009,102

; FILING DATE: December 22, 1995

; APPLICATION NUMBER: 60/003,798

METHODS OF SCREENING FOR COMPOUNDS

ACTIVE ON STAPHYLOCOCCUS AUREUS

TARGET GENES

NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

Fri Jun 21 08:38:29 2002

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Page 9

ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-265-315-4

Query Match 17.3%; Score 232.4; DB 4; Length 400;
Best Local Similarity 74.5%; Pred. No. 1.7e-39;
Matches 298; Conservative 0; Mismatches 101; Indels 1; Gaps 1;
QY 286 ggtccagtcattgtatgaagaagaagccttccttccttaagaatta-ag 344
DB 400 GGTCCAGTCATTGTATGAAGAAGACGAGACTCGTACCTTTTCTTAAGATTATCC 341
QY 345 taatatttaaacacaacatgittatgtagtagtagacccttattgcttatca 404
DB 340 AAAATGTGTTAAAAACATCGTTGCTGATACCTACATGATGATTCATCA 281
QY 405 atatcgtatcatgtagttagatatacaggaagctgtagtagtagtagtagtag 464
DB 280 ATACTGTAATCATGATGCGGAGATTAAGTATGCTGATGATGCTGCTTTGATTA 221
QY 465 aatgaacaattagatatacacaagaaggtttacaacaggatttgcataatata 524
DB 220 AATGAGTAACCTTAGATTGAACTACTGATTCATTAAGGATTTGATCTGCTACA 161
QY 525 aatcggttcattcagtttaaatattaaagataaactgcttaagaatgattataatg 584
DB 160 AATCGGTATCACTAGCTGATTTAGATTAAAAAGATTAAGATGATCACTTTAAAA 101
QY 585 aatgtagattttagaagaagaataactaaagaagcccaaaaatggttttaagaag 644
DB 100 TATGATGAGACTTAGAAAAAGAACACGGAANNAGTTNAAAGATGTTGTTAAGTAG 41
QY 645 atttcactaaagaagaattaccatttccagtaatt 684
DB 40 ATTTTATCTGAAGAGNACTCAATTTTATGATTATTT 1

RESULT 13
US-09-266-417-4/c
; Sequence 4, Application US/09266417
; Patent No. 6228588
; GENERAL INFORMATION.

APPLICANT: Benton, Bret
APPLICANT: Lee, Ying J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmidt, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 613 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/266,417
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/248
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-266-417-4

Query Match 17.3%; Score 232.4; DB 4; Length 400;
Best Local Similarity 74.5%; Pred. No. 1.7e-39;
Matches 298; Conservative 0; Mismatches 101; Indels 1; Gaps 1;
QY 286 ggtccagtcattgtatgaagaagaagccttccttccttaagaatta-ag 344
DB 400 GGTCCAGTCATTGTATGAAGAAGACGAGACTCGTACCTTTTCTTAAGATTATCC 341
QY 345 taatatttaaacacaacatgittatgtagtagtagtagtagtagtagtagtagtag 404
DB 340 AAAATGTGTTAAAAACATCGTTGCTGATACCTACATGATGATTCATCA 281
QY 405 atatcgtatcatgtagttagatatacaggaagctgtagtagtagtagtagtagtag 464
DB 280 ATACTGTAATCATGATGCGGAGATTAAGTATGCTGATGATGCTGCTTTGATTA 221
QY 465 aatgaacaattagatatacacaagaaggtttacaacaggatttgcataatata 524
DB 220 AATGAGTAACCTTAGATTGAACTACTGATTCATTAAGGATTTGATCTGCTACA 161
QY 525 aatcggttcattcagtttaaatattaaagataaactgcttaagaatgattataatg 584

Fri Jun 21 08:38:29 2002

us-09-509-234c-52.rn1

Page 11

;;
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 633 West Fifth Street
;; STREET: Suite 4700
;; CITY: Los Angeles
;; STATE: California
;; COUNTRY: U.S.A.
;; ZIP: 90071-2066
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; MEDIUM TYPE: storage
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: IBM P.C. DOS 5.0
;; SOFTWARE: Word Perfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/265,315
;; FILING DATE: March 9, 1999
;; CLASSIFICATION: 435
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: 08/714,918
;; FILING DATE: September 13, 1996
;; APPLICATION NUMBER: 60/009,102
;; FILING DATE: December 22, 1995
;; APPLICATION NUMBER: 60/003,798
;; FILING DATE: September 15, 1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard J.
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 240/247
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 19:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5253 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
US-09-265-315-19

Query Match 7.7%; Score 103; DB 4; Length 5253;
Best Local Similarity 46.7%; Pred. No. 9e-13;
Matches 399; Conservative 1; Mismatches 446; Indels 9; Gaps 2;
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QY 517 atattacaattcggttcacatcagttttaaatttaaagataaacctgtaagaatgta 576
DB 2907 gactacatccaacacgactatgactatgatttacacccaattgataaaatgatgatgta 2848
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us-09-509-234c-52.rni

Fri Jun 21 08:38:29 2002

Fri Jun 21 08:38:31 2002

us-09-509-234c-52.rst

Page 1

GenCore version 4.5
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OK nucleic - nucleic search, using sw model

Run on: June 20, 2002, 14:27:04 ; Search time 8551.36 Seconds
(Without alignments)
2119.711 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em.estba:*
2: em.esthum:*
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5: em.estov:*
6: em.estpl:*
7: em.estro:*
8: em.estc:*
9: gb.est1:*
10: gb.est2:*
11: gb.estc:*
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13: em.gss.hum:*
14: em.gss.inu:*
15: em.gss.pln:*
16: em.gss.vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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5	91.4	6.8	1101	12	CNS0021J
6	90.4	6.7	1101	12	CNS0152H
7	90.4	6.7	1885	10	BE420745
8	89.2	6.6	1101	12	CNS00L72
9	88.4	6.6	1135	12	CNS0336Q
10	87.4	6.5	1059	12	CNS0022B
11	87.2	6.5	619	9	AL514935
12	87.2	6.5	1092	12	CNS020K7
13	86.8	6.5	737	12	CNS008B0
14	86.2	6.4	747	12	CNS011R0
15	86.2	6.4	974	12	CNS001T7
16	85.8	6.4	1101	12	CNS00EVL
17	85.8	6.4	1101	12	CNS01219

18	85.2	6.3	1101	12	CNS001B8
19	85.2	6.3	1101	12	CNS01772
20	85	6.3	652	12	CNS03H0U
21	84.6	6.3	1029	12	CNS01ZGM
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
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BACN1111 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

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AL104216
VERSION
AL104216.1 GI:5615827
KEYWORDS
fruit fly.
SOURCE
Drosophila melanogaster
ORGANISM
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
1 (bases 1 to 1025)
Genoscope.
Submitted (23-JUN-1999) Genoscope - Centre National de Sequencage ;
Submitted (23-JUN-1999) Genoscope - FRANCE (E-mail : seqref@genoscope.cns.fr
BP 191 91006 EVRY cedex - FRANCE)

COMMENT
JOURNAL
- Web : www.genoscope.cns.fr
- Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billard at CNRS (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.

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/db_xref="taxon:7227"
/clone-lib="DrosBAC"
/clone="BACN1111"
/note="end : T7"

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Fri Jun 21 08:38:31 2002

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AG134867
AG134867.1 GI:16664545
GSS: GSS (genome survey sequence), clone_lib:PTB Chimpanzee Male
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-147P14.F.

ORGANISM
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

1 (sites)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of library PTB

REFERENCE
2 (bases 1 to 769)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
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LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI
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Location/Qualifiers
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"organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-147P14.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
BASE COUNT 521 a 28 c 24 g 78 t 118 others
ORIGIN

Query Match 7.18; Score 95; DB 12; Length 769;
Best Local Similarity 45.4%; Pred. No. 0.00094;
Matches 244; Conservative 0; Mismatches 293; Indels 1; Gaps 1;

QY 464 aaatgaacaaataggatgacacgaggggtttacacagaggttgatcccaattac 523
D 147 AAATAAATTGNNAAATAAANAAANAAANNAATAGNNAAGNNGAATTNAAATAAANA 206
QY 524 aaatcggttccattcagtttttaatttaagagataaaactgctaaagatgtat 583
D 207 TNAANNANANNNNNAATAATANNATNNAANNAATAATGAAANNAANNAANNA 266
QY 584 gaatggatgttcagaaagaaataactaaagtcacaaagtcgaagaaatggtt 643
D 267 AAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 326
QY 644 gattcttactaagaagattacattacattttcagatcatttgcgaagatacagag- 702
D 327 AATTTTTTATNATNAAANNAANNAANNAANNAANNAANNAANNAANNAANNA 386
QY 703 actaagaattttctgtagagggatagtttttactataatcgtattgattcatt 762
D 387 AANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 446
QY 763 gatagagatttagctcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 822
D 447 AAAAAAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 506
QY 823 gcgaagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 882

RESULT 2
AG134867 769 bp DNA linear GSS 04-NOV-2001
LOCUS AG134867
DEFINITION Pan troglodytes DNA, clone: PTB-147P14.F, genomic survey sequence.

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Db 507 TAAA 566

Qy 883 ccagatacaaaaagcacaaataaataattgagacagcaattaaagcaat 942

Db 567 AATTTAAATNN 626

Qy 943 gaggcaaaaattgctgagcaacacacttaattgacacgctgaactaccac 1000

Db 627 ACAGAAAAAANNN 684

RESULT 3

CNS009DO 781 bp DNA linear GSS 03-JUN-1999

LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #

DEFINITION BACR19009 of RPCI-98 library from Drosophila melanogaster (fruit fly); genomic survey sequence.

ACCESSION AL053444

VERSION AL053444.1 GI:4934889

KEYWORDS GSS.

SOURCE fruit fly.

ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE Genoscope.

AUTHORS Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr)

JOURNAL

COMMENT

- Web : www.genoscope.cns.fr

- Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see [http://www.fruitfly.org/The BDGP Drosophila melanogaster BAC library](http://www.fruitfly.org/The%20BDGP%20Drosophila%20melanogaster%20BAC%20library) was prepared by Kazutoyo Osoegawa and Aaron Mamoser in Pierer de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2: cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source 1..781

location/Qualifiers

1..781

/organism="Drosophila melanogaster"

/db_xref="taxon:7227"

/clone_lib="RPCI-98"

/clone="BACR19009"

/note="end : TET3"

BASE COUNT 440 a 71 c 6 g 189 t 75 others

ORIGIN

Query Match 7.0%; Score 93.4; DB 12; Length 781;

Best Local Similarity 45.7%; Pred. No. 0.0015;

Matches 226; Conservative 22; Mismatches 247; Indels 0; Gaps 0;

Qy 536 attcagtttaatttaagataaactgctaaagtatttaattgaagtagtggtt 595

Db 49 WTAAATTTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTA 108

Qy 596 tacgaaaaagaatacctaaagaagtcacaaaagaatggttaagaatattcttacta 655

Db 109 TAAATATWAAAAATTTATPAAAAATTTATPAAAAATTTATPAAAAATTTATPAAAA 168

Qy 656 aagaagaattaccatttcagatcatttaagagaatatacagagactaaagaattt 715

Db 169 AAAAAAANNN 228

Qy 716 ctgagtagagagatagtttactataatcgattgctattttaagaatagatag 775

Db 229 ATAAATTAANNN 288

Qy 776 taccctcgcatataaatttgatgatalctgaaagacttcgagagactcaga 835

Db 289 AATTTAAATTTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAA 348

Qy 836 catlaataaagaacttaacaaagctcctaaagatattgaaagacagcaatacaaa 895

Db 349 AAAAAAANNN 408

Qy 896 aagcaaaaataaataaatttagaagcaacttaaaagcaaatgagcaaaaattg 955

Db 409 AAAAAAANNN 468

Qy 956 atgagcaacacacacttaacattgatacgttaacgaattcccaatctcgtcgattct 1015

Db 469 ATAAATTTAAATTAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 528

Qy 1016 tcttattatccat 1030

Db 529 AATTAATTAANNN 543

RESULT 4

CNS01JRG 879 bp DNA linear GSS 12-JUN-2001

LOCUS Anopheles gambiae GSS T7 end of clone 14D07 of NotreDame1 library

DEFINITION from strain PST of Anopheles gambiae (African malaria mosquito); genomic survey sequence.

ACCESSION AL147405

VERSION AL147405.1 GI:7005551

KEYWORDS GSS.

SOURCE African malaria mosquito.

ORGANISM Anopheles gambiae

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.

REFERENCE Genoscope.

AUTHORS Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr)

JOURNAL

COMMENT

- Web : www.genoscope.cns.fr

- 2 (bases 1 to 879)

- Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J. Direct Submission

- Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France

- This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut Pasteur.

FEATURES

source 1..879

location/Qualifiers

1..879

/organism="Anopheles gambiae"

/strain="PST"

/db_xref="taxon:7165"

/clone="14D07"

/clone_lib="NotreDame1"

/note="end : T7"

BASE COUNT 66 a 38 c 1 g 670 t 104 others

ORIGIN

Query Match 6.9%; Score 93.2; DB 12; Length 879;

Best Local Similarity 41.3%; Pred. No. 0.0016;

Matches 278; Conservative 53; Mismatches 341; Indels 1; Gaps 1;

Qy 331 tttaagatttaagtaattatttaaacacacacattgttatatgacgtatagacct 390

Db 855 TATATTAANNN 796

QY 1250 attcgttaaa 1260
 Db 728 TKKKKKKAAA 738
 RESULT 9
 CDS033GQ 1135 bp DNA linear GSS 15-MAY-2000
 LOCUS Tetradon nigroviridis genome survey sequence PUC-Or1 end of clone
 DEFINITION 208P24 of library G from Tetradon nigroviridis, genomic survey
 sequence.
 ACCESSION AL226115.1 GI:7885026
 VERSION GSS: genome survey sequence.
 KEYWORDS Tetradon nigroviridis.
 SOURCE Tetradon nigroviridis
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 Tetraodontidae; Tetradon.
 REFERENCE 1 (bases 1 to 1135)
 AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C.,
 Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
 Weissenbach,J.
 TITLE Characterization and repeat analysis of the compact genome of the
 freshwater pufferfish Tetradon nigroviridis
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1135)
 AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C.,
 Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
 Saurin,W. and Weissenbach,J.
 TITLE Human gene number estimate provided by genome wide analysis using
 Tetradon nigroviridis DNA sequence
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 1135)
 AUTHORS Direct Submission
 TITLE Submitted (12-ARR-2000) to the EMBL/GenBank/DBJ databases
 JOURNAL This sequence is a single read and was generated as part of a large
 scale clone-end sequencing project of the Tetradon nigroviridis
 genome. For more information, please take a look at
 http://www.genoscope.cns.fr/Tetradon.
 FEATURES
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 1. 1135
 /organism="Tetradon nigroviridis"
 /db_xref="taxon:99883"
 /clone_1db="208P24"
 /clone_1lb="G"
 /note="Genoscope sequence ID : C0AG208DH12SP1-end :
 PUC-Or1"
 BASE COUNT 863 a 65 c 43 g 124 t 40 others
 ORIGIN
 Query Match 6.6%; Score 88.4; DB 12; Length 1135;
 Best Local Similarity 46.3%; Pred. No. 0.0061;
 Matches 251; Conservative 9; Mismatches 282; Indels 0; Gaps 0;
 QY 461 ataaatgaacattggtatcaacaggaaggttacaacaggaattgacccat 520
 Db 369 AA 428
 QY 521 tacaattcggttcattcagtttaatttaaggaataaactgtcaagatgataa 580
 Db 429 AA 488
 QY 581 atggaatgattgattacgaagaagaataactcaaaagtccaaaagtgttaag 640
 Db 489 AA 548
 QY 641 taagattcttactaagaagaattccatttcagatcattatgaagaatatacag 700
 Db 549 AAAAAAAAAATATTAATAAAAAAAAAAAAAAAAAAAAAAAAAATTAATAA 608

QY 701 agactaagaatttcgtatagagagatagttttctataatcattgacattta 760
 Db 609 AAAAAAAAAATTAATAAAAAAAAAAAAAAAAAAAAAAAAAATTAATAA 668
 QY 761 aagatagattatgtaacctcgcacatatataaattgataatctctgaagacttc 820
 Db 669 AATATTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATTAATAA 728
 QY 821 atcgagaagtcagacattaaataagacttaacaaagctctaaagaattgaaac 880
 Db 729 AAAAAAAAAATTAATCAATNTAAAAAAAAAAAAAAAAAAAAAAAAA 788
 QY 881 gaccagatacaaaaagcacaaaataaataattagacagcaattaaagca 940
 Db 789 AATATTAATTAATAATTAATAATAATAATAATAATAATAATAATA 848
 QY 941 atgagcaaaaattgtagaagcaacacacttaattgaaatgtagaagattacaa 1000
 Db 849 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATTAATAATCAATTA 908
 QY 1001 ta 1002
 Db 909 AA 910
 RESULT 10
 CDS0022B/C 1059 bp DNA linear GSS 26-JUL-1999
 LOCUS Drosophila melanogaster genome survey sequence 17 end of BAC
 DEFINITION BACN01115 of DrosBAC library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 ACCESSION AL097133 GI:5608744
 VERSION AL097133.1
 KEYWORDS GSS.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 1059)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
 COMMENT - Web : www.genoscope.cns.fr
 - Determination of this BAC-end sequence was carried out as part of a
 collaboration of this BAC-end sequence was carried out as part of a
 library (Dros BAC) was made by Alain Billaut at CRPH (Centre
 d'Etude du Polymorphisme Humain) with funding provided by a MRC
 project grant. The DNA was prepared from embryos by Alain Bucheton
 and Genevieve Payan. It has been constructed in the vector
 pBelobAC11.
 FEATURES
 source
 1. 1059
 /organism="Drosophila melanogaster"
 /plasmid="pBelobAC11"
 /db_xref="taxon:7227"
 /clone_1lb="DrosBAC"
 /clone="BACN01115"
 /note="end : 17"
 BASE COUNT 14 a 21 c 66 g 760 t 198 others
 ORIGIN
 Query Match 6.5%; Score 87.4; DB 12; Length 1059;
 Best Local Similarity 40.0%; Pred. No. 0.0084;
 Matches 286; Conservative 44; Mismatches 385; Indels 0; Gaps 0;
 QY 288 tccagcatgattatgaaacaagaactcgcttcactttctttaaagaattagtaa 347
 Db 757 KCAKSCMKRBRBCKRCWACAYAAACKSCBAACKCAAAKMANAAAAAAAA 698

[illegible]

EcocRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source

1. 974

/organism="Drosophila melanogaster"

/db_xref="taxon:7227"

/clone_lib="RPCI-98"

/clone="BACR37D06"

/note="end : TEP3"

Location/Qualifiers

BASE COUNT

77 a 59 c 13 g 605 t 220 others

ORIGIN

Query Match 6.4% Score 86.2; DB 12; Length 974;

Best Local Similarity 38.4%; Pred. No. 0.012;

Matches 208; Conservative 65; Mismatches 269; Indels 0; Gaps 0;

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QY 461 ataaatgaacaattagatatacaacgaagggttacacagagattgacccaatat 520
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DB 644 AAAAAAAAAAAAAAAAAATGKTAKKADAMTMTKKTAWATGKTGKASFSARADA 585
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QY 521 tacaattcggttcattcagtttaatttaagagataaactgctaagatgataa 580
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 584. RAAAAAAAAAAAAAAAAAKTGKRTAKAKGAKAKAKKDDAAAAAAAAATAYGYK 525
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QY 581 atggaatgagatagttacgaagaagaatcctaagaagtcacaaatggttaag 640
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DB 524 NTACCAAYKABAGAAAGVAAAAAANAGTAKTINKNTATATAAASAAATAT 465
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 641 taagttctactaagaagaattaccatttcagatcatttaagagatcacacag 700
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 464 TMAATKMAADAAAAAAAAASATAKAATAAAATATKAWTKAATAATAKABASBNKTT 405
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 701 agactaagaatttcgtatagagagatagtttactataatcgattgatttita 760
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 404 AATYGMMAAABBNBSSCAAAADAAABBRABWAKBSBBYCKSKBTSTTTTDYAA 345
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 761 aagatagagatttagtaccctcgcataataaattgataatacttgaagaacttc 820
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DB 344 AAAAAAAAAKMAAABMACWATTGTRTANAAAAAAAAAAAAAAAAAAAAAAAAAAAA 285
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QY 821 atgcagaacgtcagacatttaataaagacttaacaagctctaagaatattgaac 880
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 284 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 225
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 881 gaccagatacaaaaagcacaaataaataaatttagaacgacgcaattaaagcaa 940
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DB 224 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 165
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QY 941 atgagcaaaaattgataagcacacacacttaattagaacatgtaacgaattacca 1000
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DB 164 AAAAAAAAAAAATATRAAAAAAAAAAAAAAAAAAAAAAAAAANANAAAAAAAAAACACAAAAA 105
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QY 1001 ta 1002
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DB 104 NA 103
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Search completed: June 20, 2002, 14:27:12
Job time: 17742 sec

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C 367	11.2	22.4	34	6	164563	164563 Sequence 11	440	11	22.0	21	6	AR008503	Sequence
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C 369	11.2	22.4	35	6	A59049	A59049 Sequence 37	442	11	22.0	21	6	AR099639	Sequence
C 370	11.2	22.4	35	6	115403	115403 Sequence 3	443	11	22.0	21	6	I13737	Sequence 13
C 371	11.2	22.4	35	6	115410	115410 Sequence 10	444	11	22.0	21	6	I34533	Sequence 27
C 372	11.2	22.4	37	6	A16619	A16619 Nucleotide	445	11	22.0	21	6	I39803	Sequence 46
C 373	11.2	22.4	37	6	A28283	A28283 Hybridplasm	446	11	22.0	22	6	A82572	Sequence
C 374	11.2	22.4	37	6	AR080929	AR080929 Sequence	447	11	22.0	22	6	AR152843	Sequence
C 375	11.2	22.4	37	6	AR080971	AR080971 Sequence	448	11	22.0	23	6	AR139931	Sequence
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C 377	11.2	22.4	37	6	AR080973	AR080973 Sequence	450	11	22.0	23	6	AR140528	Sequence
C 378	11.2	22.4	37	6	AR107927	AR107927 Sequence	451	11	22.0	24	6	AX036505	Sequence
C 379	11.2	22.4	37	6	AR167902	AR167902 Sequence	452	11	22.0	24	12	AB068825	Synthetic
C 380	11.2	22.4	37	6	I15415	I15415 Sequence 15	453	11	22.0	27	6	A57176	Sequence 17
C 381	11.2	22.4	37	6	I60278	I60278 Sequence 12	454	11	22.0	27	6	A57179	Sequence 20
C 382	11.2	22.4	37	6	I60320	I60320 Sequence 54	455	11	22.0	27	6	AR096112	Sequence
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C 384	11.2	22.4	37	6	AX220443	AX220443 Sequence	457	11	22.0	27	6	AX133905	Sequence
C 385	11.2	22.4	38	6	AX220458	AX220458 Sequence	458	11	22.0	28	6	AR069342	Sequence
C 386	11.2	22.4	38	6	AX320492	AX320492 Sequence	459	11	22.0	28	6	AR070480	Sequence
C 387	11.2	22.4	38	6	AX320560	AX320560 Sequence	460	11	22.0	28	6	AR090804	Sequence
C 388	11.2	22.4	39	6	A16618	A16618 Nucleotide	461	11	22.0	28	6	AX000859	Sequence
C 389	11.2	22.4	39	6	A28282	A28282 Hybridplasm	462	11	22.0	28	6	I64559	Sequence 7
C 390	11.2	22.4	39	6	AR165967	AR165967 Sequence	463	11	22.0	29	6	AR058926	Sequence
C 391	11.2	22.4	39	6	E60079	E60079 Endonuclease	464	11	22.0	29	6	AR112797	Sequence
C 392	11.2	22.4	40	6	AR176016	AR176016 Sequence	465	11	22.0	29	6	AR170336	Sequence
C 393	11.2	22.4	40	6	AR098688	AR098688 Sequence	466	11	22.0	29	6	E47141	Protein fro
C 394	11.2	22.4	40	6	E35055	E35055 Novel nucle	467	11	22.0	31	6	AR148841	Sequence
C 395	11.2	22.4	40	6	I63345	I63345 Sequence 32	468	11	22.0	31	6	AX248295	Sequence
C 396	11.2	22.4	41	6	I63345	I63345 Sequence 32	469	11	22.0	32	6	AR038821	Sequence
C 397	11.2	22.4	41	6	A11519	A11519 Oligonucleo	470	11	22.0	32	6	E47143	Sequence 10
C 398	11.2	22.4	41	6	A11540	A11540 Oligonucleo	471	11	22.0	32	6	I60423	Sequence
C 399	11.2												


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CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH key Location/Qualifiers
FT source 1..40 /organism='Artificial sequences'
FEATURES
source 1..40 Location/Qualifiers
/organism='unidentified'
/db_xref='taxon:32644'
BASE COUNT 18 a 6 c 7 g 9 t
ORIGIN
Query Match 32.8%; Score 16.4; DB 6; Length 40;
Best Local Similarity 77.3%; Pred. No. 1.9e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 14 aaatgaattacnaatttca 35
17 AAATGAAGTTAACTAATTCA 38

RESULT 4
AX162446/c 50 bp DNA linear PAT 22-JUN-2001
LOCUS AX162446
DEFINITION Sequence 5774 from Patent WO0140521.
ACCESSION AX162446
VERSION AX162446.1 GI:14543777
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Shinkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 5774 07-JUN-2001;
Curagen Corporation (US)
LOCATION/Qualifiers
FEATURES
source 1..50 Location/Qualifiers
/organism='Homo sapiens'
/db_xref='taxon:9606'
misc_feature 25..26
/organism='Homo sapiens'
/Note="Nucleotide deleted between bases 25 and 26"
Accession number cg44032208"
misc_feature 26
/Note="2 of 2 allelic variants (5773 is other entry)"
Accession number cg44032208"
BASE COUNT 16 a 7 c 7 g 20 t
ORIGIN
Query Match 30.8%; Score 15.4; DB 6; Length 50;
Best Local Similarity 59.4%; Pred. No. 3.7e+05;
Matches 19; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 16 aatgaattacnaatttcaacgnaagant 47
43 AATGAACCTAAAGACTTTCACAGCAGATGAGT 12

RESULT 5
AX162448/c 50 bp DNA linear PAT 22-JUN-2001
LOCUS AX162448
DEFINITION Sequence 5776 from Patent WO0140521.
ACCESSION AX162448
VERSION AX162448.1 GI:14543779
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Shinkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 5776 07-JUN-2001;
Curagen Corporation (US)
LOCATION/Qualifiers
FEATURES
source 1..50 Location/Qualifiers
/organism='Homo sapiens'
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misc_feature 25..26
/organism='Homo sapiens'
/Note="Nucleotide deleted between bases 25 and 26"
Accession number cg44032208"
misc_feature 26
/Note="2 of 2 allelic variants (5777 is other entry)"
Accession number cg44032208"
BASE COUNT 16 a 7 c 8 g 19 t
ORIGIN
Query Match 30.8%; Score 15.4; DB 6; Length 50;
Best Local Similarity 59.4%; Pred. No. 3.7e+05;
Matches 19; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 16 aatgaattacnaatttcaacgnaagant 47
40 AATGAACCTAAAGACTTTCACAGCAGATGAGT 9

RESULT 7
E13173/c 37 bp DNA linear PAT 24-JUN-1998
LOCUS E13173
DEFINITION PCR primer.

```


TITLE GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS

JOURNAL Patent: WO 9916780-A 4 08-APR-1999;
GALA JEAN LUC (BE); UNIV LOUVAIN (BE)

FEATURES
source 1..20
Location/Qualifiers
/db_xref="taxon:32644"

BASE COUNT 8 a 1 c 2 g 8 t 1 others
ORIGIN

Query Match 28.8%; Score 14.4; DB 6; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+06;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 16 aatgaattacnaattt 33
Db 2 AATGAAGTTACNAATT 19

RESULT 12 AX000930/c 36 bp DNA linear PAT 10-MAR-2000
LOCUS Sequence 3 from Patent WO9902989.
DEFINITION AX000930
ACCESSION AX000930
VERSION AX000930.1 GI:7241174
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 36)
AUTHORS Fersht, A. and Chatellier, J.
TITLE CHAPERONE FRAGMENTS
JOURNAL Patent: WO 9902989-A 3 21-JAN-1999;
MEDICAL RES COUNCIL (GB); FERSHT ALAN (GB)

FEATURES
source 1..36
Location/Qualifiers
/db_xref="taxon:32644"

BASE COUNT 12 a 7 c 9 g 8 t
ORIGIN

Query Match 28.4%; Score 14.2; DB 6; Length 36;
Best Local Similarity 64.0%; Pred. No. 9.8e+05;
Matches 16; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 19 gaattacnaattacnagcnaa 43
Db 34 GAATTTACGCTTACGTCACATA 10

RESULT 13 AX048695/c 36 bp DNA linear PAT 12-JAN-2001
LOCUS Sequence 9 from Patent WO0069907.
DEFINITION AX048695
ACCESSION AX048695
VERSION AX048695.1 GI:12225850
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.

REFERENCE 1 (bases 1 to 36)
AUTHORS Hill, F.C., Chatellier, J. and Fersht, A.M.
TITLE Protein scaffold and its use to multimerise monomeric polypeptides
JOURNAL Patent: WO 0069907-A 9 23-NOV-2000;
MEDICAL RESEARCH COUNCIL (GB)

FEATURES
source 1..36
Location/Qualifiers
/db_xref="taxon:32630"
/note="PCR Primer for GroEL"

BASE COUNT 12 a 7 c 9 g 8 t
ORIGIN

Query Match 28.4%; Score 14.2; DB 6; Length 36;
Best Local Similarity 64.0%; Pred. No. 9.8e+05;
Matches 16; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 19 gaattacnaattacnagcnaa 43
Db 34 GAATTTACGCTTACGTCACATA 10

RESULT 14 AX048724/c 36 bp DNA linear PAT 12-JAN-2001
LOCUS Sequence 9 from Patent WO0069886.
DEFINITION AX048724
ACCESSION AX048724
VERSION AX048724.1 GI:12225869
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.

REFERENCE 1 (bases 1 to 36)
AUTHORS Hill, F.C., Chatellier, J. and Fersht, A.M.
TITLE Oligomeric chaperone proteins
JOURNAL Patent: WO 0069886-A 9 23-NOV-2000;
MEDICAL RESEARCH COUNCIL (GB)

FEATURES
source 1..36
Location/Qualifiers
/db_xref="taxon:32630"
/note="PCR Primer for GroEL"

BASE COUNT 12 a 7 c 9 g 8 t
ORIGIN

Query Match 28.4%; Score 14.2; DB 6; Length 36;
Best Local Similarity 64.0%; Pred. No. 9.8e+05;
Matches 16; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 19 gaattacnaattacnagcnaa 43
Db 34 GAATTTACGCTTACGTCACATA 10

RESULT 15 AX248640 31 bp DNA linear PAT 28-SEP-2001
LOCUS Sequence 719 from Patent WO0166800.
DEFINITION AX248640
ACCESSION AX248640
VERSION AX248640.1 GI:15863263
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 31)
AUTHORS Cargill, M., Ireland, J.S. and Lander, E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0166800-A 719 13-SEP-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)

FEATURES
source 1..31
Location/Qualifiers
/db_xref="taxon:9606"
/db_xref="taxon:9606"

Query Match 28.0%; Score 14; DB 6; Length 31;
Best Local Similarity 82.4%; Pred. No. 1.2e+06;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

us-09-509-234c-1_copy_1_50.primer.rge

Fri Jun 21 08:38:15 2002

Qy 19 gaattttacnaatttna 35
||| ||||| ||||| |
Db 31 GAATTTTACCAATTIYA 15

Search completed: June 20, 2002, 23:42:07
Job time: 17352 sec

C 229	12	24.0	21	19	AAV67373	Nucleotide fragment
230	12	24.0	25	19	AAV58842	Primer 568R for G.
231	12	24.0	25	19	AAV58843	Primer 568R for G.
232	12	24.0	25	19	AAV58845	Glycosylation cons
233	12	24.0	22	22	AAH37410	SNP specific lower
234	12	24.0	30	17	AAH41679	Endo-xyloglucan tr
235	12	24.0	30	22	AAH41219	PCR primer ADJ027.
236	12	24.0	30	22	AAH41220	PCR primer ADJ028.
237	12	24.0	31	18	AAH62394	Granule bound stat
238	12	24.0	32	17	AAH62394	Human immunodefici
239	12	24.0	33	16	AAH62394	HIV ampliflier prob
240	12	24.0	33	16	AAH62394	Human immunodefici
241	12	24.0	33	16	AAH62394	PDL promoter 140 f
242	12	24.0	33	16	AAH62394	Human pax protein
243	12	24.0	35	21	AAH62394	Nesleria species
244	12	24.0	35	21	AAH62394	3' PCR primer OT-1
245	12	24.0	36	19	AAH62394	Nucleotide sequenc
246	12	24.0	38	19	AAH62394	Probe based on B.b
247	12	24.0	40	12	AAH62394	B. burgdorferi PC-
248	12	24.0	40	12	AAH62394	CI0475 Synthetic c
249	12	24.0	40	20	AAH62394	A. thaliana ribofl
250	12	24.0	41	20	AAH62394	(-)-limonene-6-hyd
251	12	24.0	41	22	AAH62394	A. thaliana ribofl
252	12	24.0	41	22	AAH62394	Spearmint (-)-limo
253	12	24.0	42	18	AAH62394	Left side ampliflc
254	12	24.0	42	18	AAH62394	Nucleotide sequenc
255	12	24.0	42	20	AAH62394	HIV gag ampliflc
256	12	24.0	43	16	AAH62394	S.pombe pho4 gene
257	12	24.0	43	17	AAH62394	Escherichia coli D
258	12	24.0	44	22	AAH62394	Staphylococcus aur
259	12	24.0	45	24	AAH62394	Human map-related
260	12	24.0	47	21	AAH62394	Human map-related
261	12	24.0	47	21	AAH62394	Human map-related
262	12	24.0	47	21	AAH62394	CNS disorder-relat
263	12	24.0	47	21	AAH62394	Staphylococcus aur
264	12	24.0	50	18	AAH62394	Yeast tGFI gene re
265	12	24.0	50	19	AAH62394	Neuroserpin antise
266	12	24.0	50	20	AAH62394	Synthetic plasmid
267	12	24.0	50	20	AAH62394	Murine neuroserpin
268	12	24.0	50	21	AAH62394	Human SNP oligonuc
269	12	24.0	50	22	AAH62394	Human SNP oligonuc
270	12	24.0	50	22	AAH62394	Human cervical can
271	12	24.0	50	22	AAH62394	Probe A for retino
272	12	24.0	50	22	AAH62394	Burkholderia casid
273	11.8	23.6	20	19	AAH62394	Oligonucleotide 68
274	11.8	23.6	20	21	AAH62394	Primer hybridising
275	11.8	23.6	20	21	AAH62394	PCR primer for L.
276	11.8	23.6	20	21	AAH62394	Primer used for sp
277	11.8	23.6	20	22	AAH62394	Corynebacterium sp
278	11.8	23.6	22	17	AAH62394	Ataxia telangiecta
279	11.8	23.6	22	19	AAH62394	Human BRCA2 gene P
280	11.8	23.6	23	20	AAH62394	Mouse EGR-1 transc
281	11.8	23.6	23	22	AAH62394	Primer F for E.coli
282	11.8	23.6	24	20	AAH62394	Primer STS s1272 l
283	11.8	23.6	24	21	AAH62394	E. coli Pyrg PCR P
284	11.8	23.6	24	21	AAH62394	Human Y-specific S
285	11.8	23.6	24	21	AAH62394	Human RNA gyrase 1
286	11.8	23.6	24	24	AAH62394	Aequorea victoria
287	11.8	23.6	26	21	AAH62394	PCR primer #5 to a
288	11.8	23.6	26	21	AAH62394	Helicobacter pylori
289	11.8	23.6	28	18	AAH62394	Reverse PCR primer
290	11.8	23.6	28	20	AAH62394	Neurofibromatosis
291	11.8	23.6	28	22	AAH62394	E. coli mcrA gene f
292	11.8	23.6	30	22	AAH62394	E. coli mcrA gene f
293	11.8	23.6	30	22	AAH62394	E. coli mcrA gene f
294	11.8	23.6	30	22	AAH62394	E. coli mcrA gene f
295	11.8	23.6	30	22	AAH62394	Primer Y175R. Sy
296	11.8	23.6	31	20	AAH62394	Human BRAC1 PCR pr
297	11.8	23.6	31	22	AAH62394	Potato starch bran
298	11.8	23.6	32	18	AAH62394	Potato starch bran
299	11.8	23.6	32	18	AAH62394	PCR primer used to
300	11.8	23.6	32	19	AAH62394	Potato class B sta
301	11.8	23.6	32	19	AAH62394	

Fri Jun 21 08:38:16 2002

959 10.8 21.6 27 20 AAX87837 Phosphatidylglycer
c 960 10.8 21.6 27 22 AAX39954 SNP specific lower
c 961 10.8 21.6 28 16 AAX92590 Thermus thermophil
c 962 10.8 21.6 28 18 AAT94764 Human progesterone
c 963 10.8 21.6 28 18 AAT84755 Primer for human P
c 964 10.8 21.6 29 15 AAT84755 LO-CD2a Vb RACE-PC
c 965 10.8 21.6 29 19 AAV57436 Staphylococcus aur
c 966 10.8 21.6 29 19 AAV57436 LO-CD2a chimeric a
c 967 10.8 21.6 29 19 AAV62616 PCR primer used to
c 968 10.8 21.6 29 19 AAV38779 PCR-CD2a VL specifi
c 969 10.8 21.6 29 19 AAV22872 PCR primer for Gre
c 970 10.8 21.6 29 20 AAZ31639 PCR primer used to
c 971 10.8 21.6 29 20 AAZ31640 PCR primer used to
c 972 10.8 21.6 29 21 AAF05852 Hammerhead ribozym
c 973 10.8 21.6 29 21 AAF05852 E. coli heterologo
c 974 10.8 21.6 30 17 AAT04479 5' primer for 56RB
c 975 10.8 21.6 30 18 AAT48103 E.coli chloramphen
c 976 10.8 21.6 30 19 AAV44906 Petunia flower bud
c 977 10.8 21.6 30 20 AAZ30432 Arabidopsis Mlo fu
c 978 10.8 21.6 30 21 AAA99149 Plasmid pGRXhNP P
c 979 10.8 21.6 30 21 AAA07497 HI loop region PCR
c 980 10.8 21.6 30 22 RAD21278 Bacteriophage Mu R
c 981 10.8 21.6 30 22 AAF24606 PCR primer H76041-
c 982 10.8 21.6 30 24 RAD26324 Human L-TM-alpha
c 983 10.8 21.6 31 15 AAV67530 Nucleotide fragmen
c 984 10.8 21.6 31 19 AAV06381 Human biallelic po
c 985 10.8 21.6 31 20 AAC64041 Green fluorescent
c 986 10.8 21.6 31 21 AAG97428 pea praz gene prom
c 987 10.8 21.6 31 21 AAG97428 Plasmid pGRShNP P
c 988 10.8 21.6 31 21 AAG9145 Vector pIGS:GTP PC
c 989 10.8 21.6 31 21 AAX39636 Human single nucle
c 990 10.8 21.6 31 22 AAI30107 Human single nucle
c 991 10.8 21.6 31 22 AAI30762 Staphylococcus aur
c 992 10.8 21.6 32 20 AAZ21084 Oligonucleotide RB
c 993 10.8 21.6 32 20 AAX55481 CGRP receptor gene
c 994 10.8 21.6 33 17 AAT08717 Human vesicular tr
c 995 10.8 21.6 33 22 AAT69841 Mitotic kinase ASK
c 996 10.8 21.6 33 24 ABA03721 Human Cdk5 related
c 997 10.8 21.6 33 24 ABA04099 Human Cdk5 related
c 998 10.8 21.6 33 24 ABA04100 Nucleotide sequenc
c 999 10.8 21.6 34 19 AAV36566 PCR primer used in
c1000 10.8 21.6 34 22 AAF30966

ALIGNMENTS

RESULT 1
AAX37751
ID AAX37751 standard; DNA; 35 BP.
XX
AC AAX37751;
XX
DT 09-JUL-1999 (first entry)
XX
DE Staphylococcus sp. detecting oligonucleotide 1.
XX
KW femA; primer; identification; detection; therapy; infection; femB;
KW amplification; genotyping; gram-positive bacteria; vaccine; ss.
XX
OS Synthetic.
OS Staphylococcus sp.
PN WO9916780-A2.
XX
PD 08-APR-1999.
XX
PF 28-SEP-1998; 98WO-BE00141.
XX
PR 26-SEP-1997; 97EP-0870146.
XX
PA (BENA-) BELGIAN MIN NAT DEFENCE.
PA (UYLO-) UNIV CATHOLIQUE LOUVAIN.

XX Gala J, Vannuffel P;
PI WPI; 1999-287521/24.
XX
DR New Staphylococcus-specific oligonucleotides
XX
PT Claim 5; Page 8; 48pp; English.
XX
PS This invention describes novel Staphylococcus-specific oligonucleotides
XX based on the consensus femA nucleotide sequence which are used to
CC develop products for the identification, detection and therapy of
CC infections. The oligonucleotides can be used for the genetic
CC amplification, the identification and/or quantification of various femA
CC sequences which are specific to known or unknown Staphylococci species.
CC Since the femA sequence is similar to the femB sequence, the
CC oligonucleotides can also be used for the molecular genotyping of femB
CC genes of different Staphylococci species or other gram-positive bacteria.
CC The femA nucleic acids can also be used as inhibitors, e.g. antibodies or
CC They can also be used to identify inhibitors, e.g. antibodies or
CC antisense oligonucleotides, for blocking expression of the femA
CC nucleotide sequences. They can also be used for producing vaccines
CC against Staphylococci infections.
XX
SQ Sequence 35 BP; 12 A; 3 C; 3 G; 9 T; 8 other:

Query Match 54.0%; Score 27; DB 20; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 anaatgaatttcaaattnacngcnanagatt 48
|||||
Db 1 anaatgaatttcaaattnacngcnanagatt 35

RESULT 2
AAX37792/C
ID AAX37792 standard; DNA; 29 BP.
XX
AC AAX37792;
XX
DT 09-JUL-1999 (first entry)
XX
DE Staphylococcus sp. detecting oligonucleotide 27.
XX
KW femA; primer; identification; detection; therapy; infection; femB;
KW amplification; genotyping; gram-positive bacteria; vaccine; ss.
XX
OS Synthetic.
OS Staphylococcus sp.
PN WO9916780-A2.
XX
PD 08-APR-1999.
XX
PF 28-SEP-1998; 98WO-BE00141.
XX
PR 26-SEP-1997; 97EP-0870146.
XX
PA (BENA-) BELGIAN MIN NAT DEFENCE.
PA (UYLO-) UNIV CATHOLIQUE LOUVAIN.
XX
PI Gala J, Vannuffel P;
XX WPI; 1999-287521/24.
XX
DR New Staphylococcus-specific oligonucleotides
XX
PT Example 1; Fig 1; 48pp; English.
XX
PS This invention describes novel Staphylococcus-specific oligonucleotides
XX based on the consensus femA nucleotide sequence which are used to
CC

develop products for the identification, detection and therapy of infections. The oligonucleotides can be used for the genetic amplification, the identification and/or quantification of various fenn sequences which are specific to known or unknown staphylococci species. Since the fenn sequence is similar to the fenn sequence, the oligonucleotides can also be used for the molecular genotyping of fenn genes of different staphylococci species or other gram-positive bacteria. The fenn nucleic acids can also be used in therapeutic applications. They can also be used to identify inhibitors, e.g. antibodies or antisense oligonucleotides, for blocking expression of the fenn nucleotide sequences. They can also be used for producing vaccines against staphylococci infections.

Sequence 29 BP; 8 A; 5 C; 2 G; 14 T; 0 other;

Query Match 34.4%; Score 17.2; DB 20; Length 29;
Best Local Similarity 67.9%; Pred. No. 5.7e+02;
Matches 19; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 18 tgaattacnaattacnaganaaga 45
|||||
DB 29 TGAATTACAGATTACAGTTAAGCA 2

RESULT 3
AAV22803
ID AAV22803 standard; DNA; 40 BP.

XX AAV22803;
XX 24-JUN-1998 (first entry)

DE PCR primer used to amplify the PDI of *Candida boidinii*.

XX Protein disulphide isomerase; PDI; methyloctrophic yeast;
XX *Candida boidinii* strain S2; endoplasmic reticulum; stable conformation;

KW recombinant; disulphide bond; secretory protein; gene therapy;
KW endoplasmic reticulum retention signal sequence; genetic

KW engineering; PCR primer; ss.

XX Synthetic.
OS *Candida boidinii*.

XX EP828004-A2.

PN 11-MAR-1998.

XX 04-SEP-1997; 97EP-0306871.

XX 04-SEP-1996; 96JP-0234287.

XX (SUNR) SUNTORY LTD.

XX Kato N, Sakai Y, Shihano Y;

XX WPI; 1998-161102/15.

XX Methyloctrophic yeast protein di:disulphide isomerase - and
PT corresponding gene useful for increasing yields of secreted
PT heterologous proteins in *Candida boidinii*

XX Example 2; Page 6; 30pp; English.

XX PCR primers AAV22803-04 were used to amplify the protein disulphide
CC isomerase (PDI) derived from *Candida boidinii* and to create NotI
CC sites at both ends of the DNA sequence. PDI is a major protein
CC present in the lumen of the endoplasmic reticulum. PDI is believed
CC to be an enzyme which catalyses formation of stable conformation by
CC recombinant disulphide bonds of secretory proteins. As the protein
CC must stay in the endoplasmic reticulum, it has a sequence known as
CC the endoplasmic reticulum retention signal sequence at the carboxy
CC terminus (AAW5317) The PDI protein is useful in gene therapy and

CC genetic engineering. The PDI gene may be coexpressed with a gene of
CC interest to ensure the production of a correctly folded biologically
CC active protein.

Sequence 40 BP; 18 A; 6 C; 7 G; 9 T; 0 other;

Query Match 32.8%; Score 16.4; DB 19; Length 40;
Best Local Similarity 77.3%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 14 aaatgaanttaatttana 35
|||||
DB 17 aaatgaagttaatttca 38

RESULT 4
AAI78833/C
ID AAI78833 standard; DNA; 50 BP.

XX AAI78833;

XX 09-NOV-2001 (first entry)

DE Human silent SNP containing nucleic acid SEQ:5774.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
XX protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.

OS Homo sapiens.

PN WO200140521-A2.

PD 07-JUN-2001.

XX 30-NOV-2000; 2000MO-US32758.

XX 30-NOV-1999; 99US-0168138.

PR 29-NOV-2000; 2000US-0726173.

XX (CURA-) CURAGEN CORP.

XX Shimketa RA, Leach M;

XX WPI; 2001-356160/37.

XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy -

PS Claim 1; Page 2277; 2653pp; English.

XX AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC AAW53114 to AAW53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides.

CC For example, (I) may be used to treat disorders by rectifying mutations
CC or deletions in a patient's genome that affect the activity of
CC polypeptides by expressing inactive proteins or to supplement the
CC patients own production of polypeptide. Additionally, (I) and its
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acids
CC in samples, and therefore which patients may be in need of restorative
CC therapy. The polypeptides encoded by (I) may be used as antigens in the
CC production of antibodies specific for polymorphic polypeptides. The
CC antibodies may also be used to down regulate expression and activity
CC of the antibodies may also be used as diagnostic agents for detecting the
CC presence of polymorphic polypeptides in samples.

XX Sequence 50 BP; 16 A; 7 C; 7 G; 20 T; 0 other;


```

RESULT 7
AAAT79137/C
ID AAAT79137 standard; DNA; 37 BP.
XX
XX AAAT79137;
AC
XX 08-OCT-1997 (first entry)
XX
XX Primer for luciferase luxAB reporter gene.
DE
XX Primer: polymerase chain reaction; PCR; amplification; luxAB;
KW luciferase; reporter gene; Synechococcus; plasmid vector; ss.
XX
XX Synthetic.
OS
XX JP09140385-A.
PN
XX 03-JUN-1997.
PD
XX 20-NOV-1995; 95JP-0326586.
PF
XX 20-NOV-1995; 95JP-0326586.
PR
XX (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
PA
XX WPI; 1997-344898/32.
DR
XX Thermally inducible Cyanobacterium Synechococcus vector - useful in
PT high degree, recombinant gene, expression systems
XX
XX Example 1; Page 4; 6pp; Japanese.
XX
XX The present sequence is a primer for the PCR amplification of the
CC luciferase luxAB reporter gene, which was used in the preparation
CC of a novel Synechococcus plasmid vector, comprising a partial
CC replication origin sequence in an intrinsic Synechococcus plasmid
CC and a lambda phage C1857 P1 promoter and repressor gene. The vector
CC can be used in high degree, inducible, the multiplication of a
CC As the vector is thermally inducible, the multiplication of a
CC microorganism and the high level expression of a gene can be
CC carried out in different steps by controlling culture temperature.
CC The product of an arbitrary gene, whether intrinsic or extraneous,
CC can be produced in large amounts by Cyanobacterium Synechococcus.
CC Culture costs can be reduced as the Cyanobacterium can be cultured
CC in an inorganic medium, a pond or the ocean, making large scale
CC culture feasible as compared to E. coli and yeasts.
XX
XX Sequence 37 BP; 13 A; 7 C; 5 G; 12 T; 0 other;
SQ
Query Match 29.6%; Score 14.8; DB 18; Length 37;
Best Local Similarity 72.7%; Pred. No. 5.3e+03;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
OY 14 anaatgaattacnaattna 35
DB 33 AGAAGAACTTCCAAATTTCA 12

```

```

XX
XX Synthetic.
OS
XX Homo sapiens.
XX
XX US5798208-A.
XX
XX 25-AUG-1998.
XX
XX 02-NOV-1992; 92US-0930600.
PF
XX 02-NOV-1992; 92US-0930600.
PR
XX 05-APR-1990; 90US-0505314.
XX
XX (CREM/) CREM R.
XX
XX Crea R;
XX
XX WPI; 1998-480376/41.
DR
XX
XX Multigenesis of pre-determined gene sequences - useful for systematic
PT changes of pre-determined amino acids to see their effect on protein
PF activity, and to create gene expression libraries
XX
XX Example 1; Column 21-22; 33pp; English.
XX
XX The invention relates to a method of generating mutations in proteins by
CC synthesizing a mixture of oligonucleotides in order to alter the codons
CC for specific amino acids within a defined region of the protein. Using
CC a range of oligonucleotides for the mutations, expression libraries of
CC the mutant protein can be constructed. As an example of the method, the
CC antigen-binding region of the monoclonal antibody (MAB) MCP603 (which
CC binds phosphocholine) is altered to contain the catalytic triad residues
CC for a serine protease. Specifically the amino acids to be altered are
CC selected from the Asp of the complementarity determining region (CDR) 1
CC region of the variable heavy chain (Vh) of the antibody, the His of Vh
CC CDR3 and the Ser of the CDR2 from the light chain variable region (Vl).
CC The mutagenesis is by a "walk-through" method. Oligonucleotides
CC AAAT6081-V60900 are used to assemble the Vh gene for monoclonal antibody
CC MCP603 for the construction of variants (see AAAT60860-V60880).
XX
XX Sequence 39 BP; 11 A; 12 C; 4 G; 12 T; 0 other;
SQ
Query Match 29.2%; Score 14.6; DB 19; Length 39;
Best Local Similarity 60.7%; Pred. No. 6.4e+03;
Matches 17; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
OY 21 anttacnaattnacgmanagant 48
DB 9 acttaccagttactcattcaggaatt 36

```

```

RESULT 9
AAAT7691/C
ID AAAT7691 standard; DNA; 41 BP.
XX
XX AAAT7691;
AC
XX 19-FEB-2002 (first entry)
XX
XX Human GAPa protein 9 PCR oligonucleotide probe #1.
DE
XX Human; ss; GAPa protein 9; cancer; HIV; probe;
KW human immunodeficiency virus infection.
XX
XX Homo sapiens.
OS
XX CN1313309-A.
PN
XX 19-SEP-2001.
PD
XX 10-MAR-2000; 2000CN-0111977.
PF
XX
XX

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us-09-509-234c-1_copy_1_50.primers.ng

Fri Jun 21 08:38:16 2002

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PR 10-MAR-2000; 2000CN-0111977.
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX MAO Y, Xie Y;
XX WPI; 2002-042189/06.
XX Polypeptide-human GAPa protein 9 and polynucleotide for coding it -
XX Example 6; Page 19; 29pp; Chinese.
XX The invention relates to a human GAPa protein 9, the polynucleotide
XX encoding it, the process for preparing the polypeptide by DNA
XX recombination, the application of the polypeptide in treating diseases
XX e.g. cancer and HIV (human immunodeficiency virus) infection, the
XX antagonist of the polypeptide and its medical function, and the
XX application of the polynucleotide are disclosed. The present sequence
XX is an oligonucleotide probe used to detect the cDNA encoding human GAPa
XX protein 9.
XX Sequence 41 BP; 8 A; 4 C; 10 G; 19 T; 0 other;
SQ

```

Query Match 29.2%; Score 14.6; DB 24; Length 41;
 Best Local Similarity 65.4%; Pred. No. 6.4e+03;
 Matches 17; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```

QY 14 anaatgaattacnaatttnacnc 39
   ||||| ||||| ||||| |||||
DB 31 AATGAAGTTACAACTTACCCTC 6

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RESULT 10
 AAQ30478/C
 ID AAQ30478 standard; DNA; 47 BP.
 XX
 XX AAQ30478;
 XX
 XX 19-MAR-1993 (first entry)
 DT Phosphothioate hairpin oligonucleotide.
 DE
 XX Transcriptional control recognition element; decoy; cellular RNA;
 XX promoter; hormone receptor element; viral; liver; tissue; viral;
 KW proliferation; Bielinska; interleukin-2; IL-2; ss.
 XX
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH stem_loop 1..47
 FT /*Cag- a
 FT
 XX WO9218522-A.
 PN
 XX 29-OCT-1992.
 PD
 XX 17-APR-1992; 92WO-US03205.
 PF
 XX 18-APR-1991; 91US-0687337.
 PR
 XX (SALK) SALK INST BIOLOGICAL STUDIES.
 PA
 XX Chu BC, Orgel L;
 PI WPI; 1992-382035/46.
 DR
 XX New oligo-nucleotide(s) contg. transcription control recognition
 PT element - stabilised by covalent bonding of two DNA strands, act
 PT as decoys for regulatory protein to modulate specific RNA
 XX
 XX Example 2; Page 16; 41pp; English.
 XX

The double stranded oligonucleotide is a Bielinska phosphothioate probe which is capable of combining with the interleukin-2 octamer transcription factor, thereby inhibiting the expression of proteins under the control of the octamer sequence enhanced in Jurkat cells. The sequence was made into a hairpin structure by addition of a 5 base loop structure, to make the oligomer more resistant to the effects of enzyme mediated degradation, denaturation etc.
 See also AAQ30472-518.

Sequence 47 BP; 18 A; 5 C; 3 G; 21 T; 0 other;

Query Match 29.2%; Score 14.6; DB 13; Length 47;
 Best Local Similarity 60.7%; Pred. No. 6.5e+03;
 Matches 17; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

```

QY 20 aatttaccnaatttnacncnagant 47
   ||||| ||||| ||||| |||||
DB 47 AAATTTACATATTACACATATAGAGAA 20

```

RESULT 11
 AAX37752
 ID AAX37752 standard; DNA; 20 BP.
 XX
 XX AAX37752;
 XX
 XX 09-JUL-1999 (first entry)
 DT
 XX Staphylococcus sp. detecting oligonucleotide FemS1.
 DE
 XX FemA; primer; identification; detection; therapy; infection; femB;
 KW amplification; genotyping; gram-positive bacteria; vaccine; ss.
 KW
 XX Synthetic.
 OS
 XX Staphylococcus sp.
 OS
 XX WO9916780-A2.
 PN
 XX 08-APR-1999.
 PD
 XX 28-SEP-1998; 98WO-BE00141.
 PF
 XX 26-SEP-1997; 97EP-0870146.
 PR
 XX (BENA-) BELGIAN MIN NAT DEFENCE.
 PA (UVLO-) UNIV CATHOLIQUE LOUVAIN.
 XX
 XX Gala J, Vannuffel P;
 PI
 XX WPI; 1999-287521/24.
 DR
 XX New Staphylococcus-specific oligonucleotides
 PS Claim 5; Page 8; 48pp; English.

This invention describes novel Staphylococcus-specific oligonucleotides based on the consensus femA nucleotide sequence which are used to develop products for the identification, detection and therapy of infections. The oligonucleotides can be used for the genetic amplification, the identification and/or quantification of various femA sequences which are specific to known or unknown Staphylococci species. Since the femA sequence is similar to the femB sequence, the oligonucleotides can also be used for the molecular genotyping of femB genes of different Staphylococci species or other gram-positive bacteria. The femA nucleic acids can also be used in therapeutic applications. They can also be used to identify inhibitors, e.g. antibodies or antisense oligonucleotides, for blocking expression of the femA nucleotide sequences. They can also be used for producing vaccines against Staphylococci infections.

Sequence 20 BP; 9 A; 1 C; 2 G; 8 T; 0 other;

Query Match 28.8%; Score 14.4; DB 20; Length 20;
Best Local Similarity 83.3%; Pred. No. 7.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 16 aatgaantttacnaatt 33
||||| ||||| ||||| |||||
DB 2 aatgaagttacaact 19

RESULT 12

AA37753 standard; DNA; 20 BP.

AA37753;

09-JUL-1999 (first entry)

DE Staphylococcus sp. detecting oligonucleotide Fem2.

KM Fem2: primer; identification; detection; therapy; infection; fem2;
amplification; genotyping; gram-positive bacteria; vaccine; ss.

OS Synthetic

OS Staphylococcus sp.

PN W09916780-A2.

PD 08-APR-1999.

PF 28-SEP-1998; 98WO-BE00141.

PR 26-SEP-1997; 97EP-0870146.

PA (BENA-) BELGIAN MIN NAT DEFENCE.

PA (UYLO-) UNIV CATHOLIQUE LOUVAIN.

PI Gala J, Yannuffel P;

DR WPI; 1999-287521/24.

PS New Staphylococcus-specific oligonucleotides

Claim 5; Page 8; 48pp; English.

This invention describes novel staphylococcus-specific oligonucleotides based on the consensus fema nucleotide sequence which are used to develop products for the identification, detection and therapy of infections. The oligonucleotides can be used for the genetic amplification, the identification and/or quantification of various fema sequences which are specific to known or unknown Staphylococci species. Since the fema sequence is similar to the fema sequence, the oligonucleotides can also be used for the molecular genotyping of fema genes of different Staphylococci species or other gram-positive bacteria. The fema nucleic acids can also be used in therapeutic applications. CC They can also be used to identify inhibitors, e.g. antibodies or CC antisense oligonucleotides, for blocking expression of the fema CC nucleotide sequences. They can also be used for producing vaccines CC against Staphylococci infections.

Sequence 20 BP; 8 A; 1 C; 2 G; 8 T; 1 other;

Query Match 28.8%; Score 14.4; DB 20; Length 20;
Best Local Similarity 88.9%; Pred. No. 7.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 16 aatgaantttacnaatt 33
||||| ||||| ||||| |||||
DB 2 aatgaagttacaact 19

RESULT 13

AA267280
ID AA267280 standard; DNA; 47 BP.
XX
XX AA267280;

10-SEP-2001 (first entry)

DE Human map-related biallelic marker SEQ ID NO:1627.

Human genome; biallelic marker; high density disequilibrium map;
genomic map; haplotype; phenotype; polymorphic base; genotyping;
haplotyping; hybridisation; identification; characterisation;
diagnosis; single nucleotide polymorphism; SNP; ds.

OS Homo sapiens.

PH Key location/Qualifiers
FT variation replace(24,6)
FT /tag-a
FT /standard_name="single nucleotide polymorphism"

PN W09954500-A2.

PD 28-OCT-1999.

PF 21-APR-1999; 99WO-IB00822.

PR 21-APR-1998; 98US-0082614.

PR 23-NOV-1998; 98US-0109732.

XX (GEST) GENSET.

XX Cohen D, Blumenfeld M, Chumakov I;

PI WPI; 2000-013267/01.

DR Novel biallelic markers used to construct a high density disequilibrium

PT map of the human genome

PS Claim 1; Page 577; 2745pp; English.

AA265654 to AA269578 represent human biallelic markers from the present CC invention, which contain a polymorphic base at position 24 of their CC nucleotide sequences. AA269579 to AA277440 represent amplification CC primers for the biallelic markers. The biallelic markers of the CC invention have a variety of uses: they can be used for high density CC mapping of the human genome, and in complex association studies and CC haplotyping studies which are useful in determining the genetic basis CC for disease states. Compositions and methods of the invention can also CC be useful for the identification of the targets for the development of CC pharmaceutical agents and diagnostic methods, as well as the CC characterisation of the differential efficacious responses to and side CC effects from pharmaceutical agents acting on a disease as well as other CC treatment. CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 CC and 3367, are not actually given a sequence in the Sequence Listing CC from the present invention.

Sequence 47 BP; 17 A; 9 C; 10 G; 11 T; 0 other;

Query Match 28.8%; Score 14.4; DB 21; Length 47;
Best Local Similarity 58.1%; Pred. No. 7.8e+03;
Matches 18; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 14 anaatgaantttacnaattacnaganaag 44
||||| ||||| ||||| |||||
DB 8 accatgaagtcacacaaattgaatgacagag 38

RESULT 14

AA268033 standard; DNA; 33 BP.

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XX AAN80833;
 XX 30-NOV-1990 (first entry)
 XX Probe no.2 for 16S rRNA of a broad phylogenetic range of bacteria.
 XX Bacteria; probe; 16S ribosomal RNA; ss.
 XX Synthetic.
 XX W08803957-A.
 XX 02-JUN-1988.
 XX 24-NOV-1987; 87WO-US03009.
 XX 24-NOV-1986; 86US-0934244.
 XX 07-AUG-1987; 87US-0083542.
 XX (GENP-) GENPROBE INC.
 XX Hogan JJ, Smith RD, Kop JA, McDonough SH;
 XX WPI; 1988-161626/23.
 XX Probes for non-viral organisms - comprising an oligonucleotide
 XX complementary to a unique variable region rRNA sequence.
 XX Claim 220; Page 161; 21lpp; English.
 XX The probe is designed to hybridise with 16S rRNA in a broad range
 XX of bacteria commonly found in urine, except Ureaplasma urealyticum
 XX but not to yeast or human rRNA. It corresponds to bases 675-715
 XX of the E. coli 16S rRNA and has a Tm of 69 deg.C.
 XX See also AAN80785-N80851.
 XX Sequence 33 BP; 7 A; 12 C; 6 G; 8 T; 0 other;
 XX
 XX Query Match 28.4%; Score 14.2; DB 9; Length 33;
 XX Best Local Similarity 64.0%; Pred. No. 9.1e+03;
 XX Matches 16; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 XX
 XX Qy 19 gaantttacnaatttncngcnana 43
 XX || ||| |||| |||| ||||
 XX Db 4 gatctctacgcatttcacgcgtaca 28

Search completed: June 20, 2002, 23:09:28
 Job time: 30133 sec

XX AC AAN80833;
 XX 30-NOV-1990 (first entry)
 XX Probe no.2 for 16S rRNA of a broad phylogenetic range of bacteria.
 XX Bacteria; probe; 16S ribosomal RNA; ss.
 XX Synthetic.
 XX W08803957-A.
 XX 02-JUN-1988.
 XX 24-NOV-1987; 87WO-US03009.
 XX 24-NOV-1986; 86US-0934244.
 XX 07-AUG-1987; 87US-0083542.
 XX (GENP-) GENPROBE INC.
 XX Hogan JJ, Smith RD, Kop JA, McDonough SH;
 XX WPI; 1988-161626/23.
 XX Probes for non-viral organisms - comprising an oligonucleotide
 XX complementary to a unique variable region rRNA sequence.
 XX Claim 220; Page 161; 21lpp; English.
 XX The probe is designed to hybridise with 16S rRNA in a broad range
 XX of bacteria commonly found in urine, except Ureaplasma urealyticum
 XX but not to yeast or human rRNA. It corresponds to bases 675-715
 XX of the E. coli 16S rRNA and has a Tm of 69 deg.C.
 XX See also AAN80785-N80851.
 XX Sequence 33 BP; 7 A; 12 C; 6 G; 8 T; 0 other;
 XX
 XX Query Match 28.4%; Score 14.2; DB 9; Length 33;
 XX Best Local Similarity 64.0%; Pred. No. 9.1e+03;
 XX Matches 16; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 XX
 XX Qy 19 gaantttacnaatttncngcnana 43
 XX || ||| |||| |||| ||||
 XX Db 4 gatctctacgcatttcacgcgtaca 28

RESULT 15
 AAF23101
 ID AAF23101 standard; DNA; 33 BP.
 XX AAF23101;
 XX 20-MAR-2001 (first entry)
 XX Bacterial rRNA specific sequence #2.
 XX Probe; PCR primer; 5S rRNA; 16S rRNA; 23S rRNA; 28S rRNA; 18S rRNA;
 XX Mycobacterium; Enterococcus; Chlamydia; Mycoplasma; E. coli; Legionella;
 XX Salmonella; Pseudomonas; Campylobacter; Neisseria gonorrhoeae; fungus;
 XX bacterium; ss.
 XX Bacteria.
 XX US6150517-A.
 XX 21-NOV-2000.
 XX 30-MAY-1995; 95US-0454063.
 XX 22-FEB-1994; 94US-0200866.

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us-09-509-234c-1_copy_1_50.primer.rn1

OM nucleic - nucleic search, using sw model

Run on: June 20, 2002, 22:17:00 ; Search time 66.94 Seconds
(without alignments)
183.473 Million cell updates/sec

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Scoring table:

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Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 506208

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Minimum DB seq length: 15
Maximum DB seq length: 50

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries
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6 : /cgn2_6/prodata/2/ina/backfiles1.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB	ID	Description
1	16.4	32.8	40	2	US-08-923-536A-10
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4	13.8	27.6	45	4	US-09-315-793-4
5	13.6	27.2	30	2	US-08-452-722A-4
6	13.4	26.8	33	4	US-08-874-102-24
7	13.4	26.8	50	1	US-08-171-389-483
8	13.4	26.8	50	2	US-08-122-936-483
9	13.4	26.8	50	1	US-08-473-228A-43
10	13.4	26.8	50	3	US-08-482-080A-43
11	13.4	26.8	50	5	PCR-US93-12388-463
12	13.2	26.4	30	4	US-09-237-712-94
13	13.2	26.4	30	4	US-09-177-268-4
14	13.2	26.4	50	3	US-08-388-029A-62
15	13	26.0	22	1	US-08-124-657-82
16	13	26.0	22	3	US-08-675-566-58
17	13	26.0	22	4	US-09-354-118-82
18	13	26.0	30	1	US-08-480-481-5
19	13	26.0	35	1	US-08-368-395-5
20	13	26.0	41	4	US-08-162-836-6
21	12.8	25.6	21	4	US-09-397-168-68
22	12.8	25.6	22	1	US-08-773-776-5
23	12.8	25.6	22	2	US-08-598-607-1
24	12.8	25.6	31	1	US-08-276-853-39
25	12.8	25.6	31	1	US-08-133-011-125
26	12.8	25.6	31	1	US-08-387-874-83
27	12.8	25.6	31	1	US-08-899-575-39

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c	34	12.8	25.6	37	1	US-08-387-315A-9
c	35	12.8	25.6	37	2	US-08-754-555-9
c	36	12.8	25.6	38	4	US-09-366-920-2
c	37	12.8	25.6	39	1	US-08-105-483-165
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c	43	12.8	25.6	50	2	US-08-821-855A-10
c	44	12.6	25.2	33	4	US-09-121-852A-10
c	45	12.6	25.2	33	5	PCT-US99-13376-10
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c	54	12.6	25.2	43	2	US-08-389-564B-11
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c	57	12.6	25.2	45	4	US-09-342-577-24
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c	66	12.6	25.2	47	1	US-08-455-101-401
c	67	12.4	24.8	20	4	US-09-021-701-634
c	68	12.4	24.8	20	4	US-09-021-701-635
c	69	12.4	24.8	20	4	US-09-021-701-636
c	70	12.4	24.8	20	4	US-09-021-701-637
c	71	12.4	24.8	26	2	US-08-557-533A-6
c	72	12.4	24.8	26	2	US-08-459-009-6
c	73	12.4	24.8	26	3	US-08-459-951-6
c	74	12.4	24.8	37	3	US-08-600-656-13
c	75	12.4	24.8	37	4	US-09-354-191A-13
c	76	12.4	24.8	47	6	5202239-8
c	77	12.4	24.8	49	4	US-09-365-121-8
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c	82	12.2	24.4	33	3	US-08-884-324-23
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247	11.2	22.4	37	1	US-08-297-299B-12	Sequence 12, Appl	C 320	11	22.0	28	4	US-09-225-929-924	Sequence 924, App
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249	11.2	22.4	37	1	US-08-297-299B-55	Sequence 55, Appl	C 322	11	22.0	29	2	US-08-818-514-11	Sequence 11, Appl
250	11.2	22.4	37	1	US-08-297-299B-56	Sequence 56, Appl	C 323	11	22.0	29	3	US-08-816-693A-27	Sequence 27, Appl
251	11.2	22.4	37	1	US-08-297-299B-56	Sequence 12, Appl	C 324	11	22.0	29	3	US-08-885-291-27	Sequence 27, Appl
252	11.2	22.4	37	2	US-08-858-083-12	Sequence 54, Appl	C 325	11	22.0	29	3	US-09-115-934A-11	Sequence 11, Appl
253	11.2	22.4	37	2	US-08-858-083-54	Sequence 55, Appl	C 326	11	22.0	29	4	US-09-496-67-27	Sequence 27, Appl
254	11.2	22.4	37	2	US-08-858-083-55	Sequence 56, Appl	C 327	11	22.0	31	4	US-09-262-773-198	Sequence 198, App
255	11.2	22.4	37	3	US-08-963-472-13	Sequence 13, Appl	C 328	11	22.0	31	6	US-08-118-469A-10	Sequence 10, Appl
256	11.2	22.4	37	3	US-09-302-238-1	Sequence 1, Appl	C 329	11	22.0	32	1	US-08-909-119-10	Sequence 10, Appl
257	11.2	22.4	37	5	PCT-US95-11029-12	Sequence 12, Appl	C 330	11	22.0	34	6	5319127-7	Sequence 44, Appl
258	11.2	22.4	37	5	PCT-US95-11029-54	Sequence 54, Appl	C 331	11	22.0	35	1	PCT-US94-09143-44	Sequence 44, Appl
259	11.2	22.4	37	5	PCT-US95-11029-55	Sequence 55, Appl	C 332	11	22.0	35	5	PCT-US94-09143-44	Sequence 44, Appl
260	11.2	22.4	37	5	PCT-US95-11029-56	Sequence 56, Appl	C 333	11	22.0	36	3	US-08-820-970-4	Sequence 4, Appl
261	11.2	22.4	37	6	PCT-US95-11029-56	Sequence 56, Appl	C 334	11	22.0	36	3	US-08-820-970-6	Sequence 6, Appl
262	11.2	22.4	37	6	US-08-185-949B-102	Sequence 102, App	C 335	11	22.0	37	3	US-08-820-970-8	Sequence 8, Appl
263	11.2	22.4	39	4	US-09-316-083-20	Sequence 20, Appl	C 336	11	22.0	37	3	US-08-428-616A-7	Sequence 7, Appl
264	11.2	22.4	40	1	US-08-032-846-32	Sequence 32, Appl	C 337	11	22.0	37	3	US-08-332-420-62	Sequence 62, Appl
265	11.2	22.4	40	4	US-08-474-636-32	Sequence 32, Appl	C 338	11	22.0	39	1	US-08-376-157B-8	Sequence 8, Appl
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268	11.2	22.4	42	3	US-08-258-287B-27	Sequence 27, Appl	C 341	11	22.0	40	1	US-07-938-084-7	Sequence 8, Appl
269	11.2	22.4	42	3	US-08-368-704C-27	Sequence 27, Appl	C 342	11	22.0	40	1	US-08-399-666-50	Sequence 50, Appl
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271	11.2	22.4	42	3	US-08-675-566-110	Sequence 110, App	C 344	11	22.0	40	3	US-08-732-708C-30	Sequence 30, Appl
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273	11.2	22.4	43	4	US-08-129-151A-4	Sequence 4, Appl	C 346	11	22.0	41	4	US-09-476-259-42	Sequence 42, Appl
274	11.2	22.4	43	2	US-08-715-579-4	Sequence 4, Appl	C 347	11	22.0	41	4	US-09-609-154-82	Sequence 82, Appl
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DESCRIPTION: /desc = "chemical synthetic DNA"
US-08-923-536A-10

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Query Match          32.8%; Score 16.4; DB 2; Length 40;
Best Local Similarity 77.3%; Pred. No. 1.5e+02;
Matches 17: Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy 14 anaatgaantttacnaatttna 35
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Db 17 AAAATGAAGTTAACTAATTCA 38

RESULT 2
US-08-452-724A-5
; Sequence 5, Application US/08452724A
; Patent No. 5830650

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: GENERAL INFORMATION:
:
: APPLICANT: Crea, Roberto
:
: TITLE OF INVENTION: Walk-Through Mutagenesis
:
: NUMBER OF SEQUENCES: 59
:
: CORRESPONDENCE ADDRESS:
:
: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
:
: STREET: 2 Militia Drive
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: CITY: Lexington
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: STATE: MA
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: COUNTRY: USA
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: ZIP: 02173

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FILING DATE: 30-MAY-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/930,600
 FILING DATE: 05-APR-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US91/02362
 FILING DATE: 05-APR-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/505,314
 FILING DATE: 05-APR-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Brook Esq., David E.
 REGISTRATION NUMBER: 22,592
 REFERENCE/DOCKET NUMBER: RC90-019AZ
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 861-6240
 TELEFAX: (617) 861-9540
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 39 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 US-08-452-724A-5

Query Match 29.2%; Score 14.6; DB.2; Length 39;
Best Local Similarity 60.7%; Pred. No. 7.7e+02;
Matches 17; Conservative 0; Mismatches 11; Indels

Qy 21 antttacnaatttnacngcnnanagantt 48
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Db 9 ACTCTACCAAGTTTAAC TCCATGGAA TT 36

RESULT 3
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c 981	10.2	20.4	44	2	US-08-658-655-141	Sequence 141, App
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c 983	10.2	20.4	44	3	US-08-675-566-54	Sequence 54, Appl
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c 986	10.2	20.4	44	4	US-09-085-273-136	Sequence 136, App
c 987	10.2	20.4	44	4	US-09-085-273-141	Sequence 141, App
c 988	10.2	20.4	44	4	US-09-354-138-78	Sequence 78, Appl
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c 994	10.2	20.4	45	4	US-09-460-736-111	Sequence 19, Appl
c 995	10.2	20.4	45	4	US-08-446-114A-6	Sequence 11, App
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c 998	10.2	20.4	46	1	US-08-105-483-82	Sequence 82, Appl
c 999	10.2	20.4	46	1	US-08-766-014-24	Sequence 24, Appl
c 1000	10.2	20.4	46	1	US-08-709-209-82	Sequence 82, Appl

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; Sequence 7, Application US/08122433
; Patent No. 5683985
; GENERAL INFORMATION:
; APPLICANT: Chu, Barbara C.F.
; APPLICANT: Orgel, Leslie
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDES AND
; TITLE OF INVENTION: OLIGONUCLEOTIDES USEFUL AS DECOYS FOR PROTEINS WHICH
; TITLE OF INVENTION: SELECTIVELY BIND TO DEFINED DNA SEQUENCES
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/122,433
; FILING DATE: 22-SEP-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/687,337
; FILING DATE: 18-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 9308
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-1995
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; US-08-122-433-7

; Query Match 29.2%; Score 14.6; DB 1; Length 47;
; Best Local Similarity 60.7%; Pred. No. 7.8e+02;
; Matches 17; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 20 aaattacnaattacngcnagant 47
DB 47 AAATTACATATACATATAGAGAA 20

; RESULT 4
; US-09-315-793-4/C
; Sequence 4, Application US/09315793
; Patent No. 6221597
; GENERAL INFORMATION:
; APPLICANT: Roberts, Christopher J.
; TITLE OF INVENTION: ESSENTIAL GENES OF YEAST AS TARGETS FOR ANTIFUNGAL
; TITLE OF INVENTION: AGENTS, HERBICIDES, INSECTICIDES AND ANTI-PROLIFERATION
; FILE REFERENCE: 9301-048
; CURRENT APPLICATION NUMBER: US/09/315,793
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Description of Artificial Sequence: primer
; US-09-315-793-4

; Query Match 27.6%; Score 13.8; DB 4; Length 45;
; Best Local Similarity 56.2%; Pred. No. 1.6e+03;
; Matches 18; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 17 atgaattacnaattacngcnagant 48
DB 34 ATGAATTTCTTTATTAACCGAAATATAGT 3

; RESULT 5
; US-08-452-724A-4/C
; Sequence 4, Application US/08452724A
; Patent No. 5830650
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; TITLE OF INVENTION: Walk-Through Mutagenesis
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: 2 Millita Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,724A
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,600
; FILING DATE: 05-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02362
; FILING DATE: 05-APR-1991
; APPLICATION NUMBER: US 07/505,314
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; US-08-452-724A-4

; Query Match 27.2%; Score 13.6; DB 2; Length 30;
; Best Local Similarity 61.5%; Pred. No. 1.9e+03;
; Matches 16; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 23 ttacnaattacngcnagant 48
DB 29 TCTACGAGTTACTTCATGGAAT 4

; RESULT 6
; US-08-874-102-24
```

us-09-509-234c-1_copy_1_50.primer.rni

Fri Jun 21 08:38:16 2002

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; Sequence 24, Application US/08874102
; Patent No. 6309644
; GENERAL INFORMATION:
; APPLICANT: Ramaswamy Chandrashekar
; APPLICANT: Kapil Mehta
; TITLE OF INVENTION: PARASITIC NEMATODE TRANSGLUTAMINASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/874,102
; FILING DATE: 12-JUN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: HW-2-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: primer
; US-08-874-102-24

Query Match 26.88; Score 13.4; DB 4; Length 33;
Best Local Similarity 77.88; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 14 anaatgaattacnaat 31
Db 10 AGAATGAATTTACAGAT 27

RESULT 7
US-08-171-389-483/c
; Sequence 483, Application US/08171389
; Patent No. 5578444
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; APPLICANT: Cantor, Charles R.
; APPLICANT: Andrews, Beth M.
; APPLICANT: Turin, Lisa M.
; APPLICANT: Fry, Kirk E.
; TITLE OF INVENTION: Sequence-Directed DNA Binding
; TITLE OF INVENTION: Molecules, Compositions and Methods
; NUMBER OF SEQUENCES: 641
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:

; Sequence 24, Application US/08874102
; Patent No. 6309644
; GENERAL INFORMATION:
; APPLICANT: Ramaswamy Chandrashekar
; APPLICANT: Kapil Mehta
; TITLE OF INVENTION: PARASITIC NEMATODE TRANSGLUTAMINASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/874,102
; FILING DATE: 12-JUN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: HW-2-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: primer
; US-08-874-102-24

Query Match 26.88; Score 13.4; DB 1; Length 50;
Best Local Similarity 56.7%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 19 gaatttaccnaatttaccnaganttt 48
Db 30 GCATTTTATTATTTATTCAGCAGGTGAGGT 1

RESULT 8
US-08-123-936-483/c
; Sequence 483, Application US/08123936
; Patent No. 5726014
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; APPLICANT: Cantor, Charles R.
; APPLICANT: Andrews, Beth M.
; APPLICANT: Turin, Lisa M.
; TITLE OF INVENTION: Screening Assay for the Detection of
; TITLE OF INVENTION: DNA-Binding Molecules
; NUMBER OF SEQUENCES: 640
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,936
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fadian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0075.32/G19P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 483:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Bovine leukemia virus
US-08-123-936-483

Query Match          26.8%; Score 13.4; DB 1; Length 50;
Best Local Similarity 56.7%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 19 gaattacnaattacgcgagtgagct 48
Db 30 GCATTATTAAATTATTCACGACGTGAGCT 1

RESULT 9
US-08-475-228A-483/C
Sequence 483, Application US/08475228A
Patent No. 5869241
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,228A
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 4600-0175.21/G19P3D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 483:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Bovine leukemia virus
US-08-475-228A-483

Query Match          26.8%; Score 13.4; DB 2; Length 50;
Best Local Similarity 56.7%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 19 gaattacnaattacgcgagtgagct 48
Db 30 GCATTATTAAATTATTCACGACGTGAGCT 1

RESULT 10
US-08-482-080A-483/C
Sequence 483, Application US/08482080A
Patent No. 6010849
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,080A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/171,389
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
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; APPLICATION NUMBER: US 07/723,618
; FILING DATE: 27-JUN-1991
; PRIORITY INFORMATION:
; APPLICATION NUMBER: US 08/081,070
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Brady, John F.
; REGISTRATION NUMBER: 39,118
; REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
; TELEPHONE: (650) 324-0880
; TELEFAX: (650) 324-0960
; INFORMATION FOR SEQ ID NO: 483:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Bovine leukemia virus
; US-08-482-080A-483

Query Match 26.8%; Score 13.4; DB 3; Length 50;
Best Local Similarity 56.7%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 19 gaatttacaatttgcacgaggtgaggt 48
| | | | | | | | | | | | | | | | | | | | | |
Db 30 GCATTTTATTATTTATCAGCAGGTGAGGT 1

RESULT 11
PCT-US93-12388-483/c
; Sequence 483, Application PC/TUS9312388
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Sequence-Directed DNA Binding
; TITLE OF INVENTION: Molecules, Compositions and Methods
; NUMBER OF SEQUENCES: 641
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12388
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/123,936
; FILING DATE: 17-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/996,783
; FILING DATE: 23-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4600-0175.41/G19PCT2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0960
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 483:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Bovine leukemia virus
; PCT-US93-12388-483

Query Match 26.8%; Score 13.4; DB 5; Length 50;
Best Local Similarity 56.7%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 19 gaatttacaatttgcacgaggtgaggt 48
| | | | | | | | | | | | | | | | | | | | | |
Db 30 GCATTTTATTATTTATCAGCAGGTGAGGT 1

RESULT 12
US-09-237-712-94
; Sequence 94, Application US/09237712
; Patent No. 6180391
; GENERAL INFORMATION:
; APPLICANT: BROWN, WILLIAM C.
; TITLE OF INVENTION: HIGHLY EFFICIENT CONTROLLED EXPRESSION OF EXOGENOUS
; TITLE OF INVENTION: GENES IN E. COLI
; FILE REFERENCE: A-518
; CURRENT APPLICATION NUMBER: US/09/237,712
; CURRENT FILING DATE: 1999-01-26
; EARLIER APPLICATION NUMBER: 60/072,794
; EARLIER FILING DATE: 1998-01-28
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 94
; LENGTH: 30
; TYPE: DNA
; ORGANISM: oligonucleotide
; US-09-237-712-94

Query Match 26.4%; Score 13.2; DB 4; Length 30;
Best Local Similarity 62.5%; Pred. No. 2.7e+03;
Matches 15; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 24 ttacnaatttgcacgaggtgaggt 47
| | | | | | | | | | | | | | | | | | | | | |
Db 2 ttacnaatttgcacgaggtgaggt 25

RESULT 13
US-09-177-268-4/c
; Sequence 4, Application US/09177268
; Patent No. 6203986
; GENERAL INFORMATION:
; APPLICANT: Singer, Robert H.
; APPLICANT: Bertrand, Egonard
; TITLE OF INVENTION: VISUALIZATION OF RNA IN LIVING CELLS
; FILE REFERENCE: 10445/002001
; CURRENT APPLICATION NUMBER: US/09/177,268
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: most probably a yeast
; US-09-177-268-4

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Page 13

Query Match 26.4%; Score 13.2; DB 4; Length 30;
Best Local Similarity 68.2%; Pred. No. 2.7e+03;
Matches 15; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 17 atgaattacnaattacng 38
||||| ||||| ||||| |||||
DB 26 ATGAATTGTACCAAGTCGACAG 5

RESULT 14
US-08-388-029A-62/c
Sequence 62, Application US/08388029A
Patent No. 6110665

GENERAL INFORMATION:

APPLICANT: FENGER, CLARA K.

APPLICANT: GRANSTROM, DAVID R.

APPLICANT: GAJDAR, ALVIN A.

TITLE OF INVENTION: SARCOCYSTITIS NEURONA DIAGNOSTIC PRIMER

NUMBER OF SEQUENCES: 97

CORRESPONDENCE ADDRESS:

ADDRESSEE: LOME, PRICE, LEBLANC & BECKER

STREET: 99 CANAL CENTER PLAZA, SUITE 300

CITY: ALEXANDRIA

STATE: VIRGINIA

COUNTRY: US

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/388,029A

FILING DATE: 14-FEB-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: PRICE, ROBERT L.

REGISTRATION NUMBER: 22,685

REFERENCE/DOCKET NUMBER: 434-046

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-684-1111

TELEFAX: 703-684-1124

TELEX: AMERPAT

INFORMATION FOR SEQ ID NO: 62:

SEQUENCE CHARACTERISTICS:

LENGTH: 50 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-388-029A-62

Query Match 26.4%; Score 13.2; DB 3; Length 50;
Best Local Similarity 64.0%; Pred. No. 2.9e+03;
Matches 16; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 20 aaattacnaattacngcnaag 44
||||| ||||| ||||| |||||
DB 31 AAATCTAGAAATTTCACCTCTNAG 7

RESULT 15
US-08-224-657-82/c
Sequence 82, Application US/08224657
Patent No. 5756102

GENERAL INFORMATION:

APPLICANT: Paoletti, Enzo

APPLICANT: Tartaglia, James

APPLICANT: Taylor, Jill

TITLE OF INVENTION: POXYVIRUS - CANINE DISTEMPER VIRUS (CDV)

TITLE OF INVENTION: RECOMBINANTS AND COMPOSITIONS AND METHODS EMPLOYING THE
TITLE OF INVENTION: RECOMBINANTS
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtis, Morris & Safford, P.C.

STREET: 530 Fifth Avenue

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/224,657

FILING DATE: 06-APR-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Frommer, William S.

REGISTRATION NUMBER: 25,506

REFERENCE/DOCKET NUMBER: 454310-2550

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 840-3333

TELEFAX: (212) 840-0712

TELEX: 425066 CURTMS

INFORMATION FOR SRO ID NO: 82:

SEQUENCE CHARACTERISTICS:

LENGTH: 22 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-224-657-82

Query Match 26.0%; Score 13; DB 1; Length 22;
Best Local Similarity 86.7%; Pred. No. 3.1e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 18 tgaatttactaatt 32
||||| ||||| ||||| |||||
DB 17 TGAATTTTACTAATT 3

Search completed: June 20, 2002, 23:43:09
Job time: 5169 sec

us-09-509-234c-1_copy_1_50.primer.rni

Fri Jun 21 08:38:16 2002

Fri Jun 21 08:38:18 2002

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1. 46
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U00C1M0118G02"
/clone_lib="Mouse 10kb plasmid U00C1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g114732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      12 a      5 c      14 g      15 t
ORIGIN

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Query Match      30.8%; Score 15.4; DB 12; Length 46;
Best Local Similarity 59.4%; Pred. No. 4.1e-04;
Matches 19; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 17 atgaattacnaatttncngcnnanagantt 48
      ||||| ||||| ||||| ||||| ||||| |||||
DB 37 ATGAATTTGCCACCATCCTCCAAAACCTT 6

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RESULT 2
A2626539/c      40 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION
  A2626539 Mouse 10kb plasmid U00C1M library Mus musculus genomic
  clone U00C1M0466A22 R, DNA sequence.
ACCESSION
  A2626539
VERSION
  A2626539.1 GI:11748729
KEYWORDS
  GSS.
SOURCE
  house mouse.
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 40)
AUTHORS
  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
  Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
  M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
  and Wright, D., Weiss, R.
TITLE
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
JOURNAL
  Unpublished (2000)
COMMENT
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0466 row: A column: 22
  Seq primer: CACACGAAACGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 40.

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A2773199 IM0584P04
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A2465655 IM0275A10
A2601632 IM0420C05
A2626864 IM0467A21
AL473134 T. brucei
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AV852744 AV852744
C21198 HUMGS000222
AZ503091 IM0342P12
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D19987 HUMGS00954
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AZ491341 IM0324A24
AZ595854 IM0408C17
AZ596555 IM0409G24

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ALIGNMENTS

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RESULT 1
A2368099/c      46 bp DNA linear GSS 02-OCT-2000
LOCUS
DEFINITION
  A2368099 Mouse 10kb plasmid U00C1M library Mus musculus genomic
  clone U00C1M0118G02 F, DNA sequence.
ACCESSION
  A2368099
VERSION
  A2368099.1 GI:10481799
KEYWORDS
  GSS.
SOURCE
  house mouse.
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 46)
AUTHORS
  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
  Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
  M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
  and Wright, D., Weiss, R.
TITLE
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
JOURNAL
  Unpublished (2000)
COMMENT
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0118 row: G column: 02
  Seq primer: CGTTGTAACGACGCCAGT
  Class: plasmid ends
  High quality sequence stop: 46.
  Location/Qualifiers

```

FEATURES

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT	25 a	3 c	4 g	18 t
ORIGIN				

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Query Match      28.4%; Score 14.2; DB 12; Length 50;
Best Local Similarity 54.3%; Pred. No. 1.2e+05;
Matches 19; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
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RESULT	6
Dl1997/c	
LOCUS	Dl1997 41 bp mRNA linear EST 02-DEC-1992
DEFINITION	HUMOSL3A04 Liver HepG2 cell line. Homo sapiens cDNA clone sl3a04,

DI1997
DI1997.1 GI:2148820
ACCESSION
VERSION
KEYWORDS
EST.
SOURCE
 human.
ORGANISM
 Homo sapiens
 Eukaryota; Metazoa;
 Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates;
 Catarrhini; Hominidae; Homo.
REFERENCE
 1 (bases 1 to 41)
AUTHORS
 Okubo, K., Horii, N., Matoba, R., Niiyama, T., Fukushima, A., Kojima, Y.,
 and Matsubara, K.
TITLE
 Large scale cDNA sequencing for analysis of quantitative and
 tissue-specific aspects of gene expression

JOURNAL
MEDLINE
COMMENT
FEATURES
source
1. .41
Location/Qualifiers
Kousaku Okubo, Naohiro Hori, Ryo Matoba, Toshiyuki Niiyama
94258199
Contact: Atsushi Fukushima, Yuko Kojima & Kenichi Matsubara
Institute for Molecular and Cellular Biology
Osaka University
1-3 Yamada-oka, Suita, Osaka 565, Japan.
/organism="Homo sapiens"
/db_xref="GDB:D088191E"
/db_xref="taxon:9606"
/clone="sl3a04"
/clone_lib="Liver HepG2 cell line."
/lab_host="E.coli"
/cat="31-Directed regional cDNA library. Cleaved by MboI

BASE COUNT	18 a	8 c	3 g	12 t	
ORIGIN					
Query Match	27.6%	Score 13.8	DB 10	Length 41	
Best Local Similarity	75.0%	Pred. No. 1.6e+05			
Matches 15	Conservative	0	Mismatches 5	Indels 0	Gaps 0
Qy	16	aatgaantttacnaatttna 35			
Db	28	AATGAATTTTATTATTAA 9			
RESULT 7					
AU060450/c			42 bp	mRNA	linear
LOCUS	AU060450	Dictyostelium discoideum SL (H. Urushihara)			Dictyostelium
DEFINITION	AU060450	discoideum cDNA clone SLJ765			mRNA sequence.
ACCESSION	AU060450				
VERSION	AU060450.1	GI:4881554			
KEYWORDS	EST				
SOURCE	Dictyostelium discoideum.				

[illegible]

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ORGANISM      Dictyostelium discoideum
REFERENCE      Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
AUTHORS        1 (bases 1 to 42)
                Morio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M.,
                Yoshino,R., Mitra,B.N., Pl.M., Sato,T., Takemoto,K., Yasukawa,H.,
                Williams,U., Maeda,M., Takeuchi,I., Ochial,H. and Tanaka,Y.
TITLE          Developmental cDNA in Dictyostelium discoideum
JOURNAL        Unpublished (1998)
COMMENT        Contact: Hideko Urushihara
                Institute of Biological Sciences
                University of Tsukuba
                3-3-10 Ten-noda, Tsukuba, Ibaraki 305, Japan
                Email: d402huesakura.cc.tsukuba.ac.jp
PROJECT        Dictyostelium discoideum cDNA project in Japan.
FEATURES       Location/Qualifiers
                source          1..42
                                /organism="Dictyostelium discoideum"
                                /strain="AX4"
                                /db_xref="taxon:44689"
                                /clone="SLD765"
                                /clone_1lb="Dictyostelium discoideum SL (H.Urushihara)"
                                /dev_stage="slug"
BASE COUNT     23 a      1 c      3 g      15 t
ORIGIN
Query Match    27.6%; Score 13.8; DB 9; Length 42;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY      16 aatgaattacnaatttna 35
Db      37 AATTGATTTTACAATTAA 18

RESULT      8
LOCUS       A2332059      46 bp      DNA      linear      GSS 29-SEP-2000
DEFINITION  IM0060A16f Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0060A16 F, DNA sequence.
ACCESSION   A2332059
VERSION     A2332059.1  GI:10395348
KEYWORDS    GSS.
SOURCE      house mouse.
ORGANISM    Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1 (bases 1 to 46)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C.,
             Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
             M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
             and Wright,D., Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
             Plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
             University of Utah
             Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
             84112, USA
             Tel: 801 585 5606
             Fax: 801 585 7177
             Email: ddunn@genetics.utah.edu
             Insert Length: 10000 Std Error: 0.00
             Plate: 0060 row: A column: 16
             Seq primer: CGTGTAAACGACGCGCAGT
             Class: Plasmid ends
             High quality sequence stop: 46.
FEATURES     Location/Qualifiers
             source          1..46
                                /organism="Mus musculus"
                                /strain="C57BL/6J"
                                /db_xref="taxon:10090"

RESULT      9
LOCUS       A2445660/c      50 bp      DNA      linear      GSS 04-OCT-2000
DEFINITION  IM0241007R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0241007 R, DNA sequence.
ACCESSION   A2445660
VERSION     A2445660.1  GI:10595702
KEYWORDS    GSS.
SOURCE      house mouse.
ORGANISM    Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1 (bases 1 to 50)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C.,
             Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
             M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
             and Wright,D., Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
             Plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
             University of Utah
             Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
             84112, USA
             Tel: 801 585 5606
             Fax: 801 585 7177
             Email: ddunn@genetics.utah.edu
             Insert Length: 10000 Std Error: 0.00
             Plate: 0241 row: O column: 07
             Seq primer: CACACAGGAACACGTATGAC
             Class: Plasmid ends
             High quality sequence stop: 50.
FEATURES     Location/Qualifiers
             source          1..50
                                /organism="Mus musculus"
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Fri Jun 21 08:38:18 2002

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/db_xref="taxon:10090"
/clone="UUGC1M0241007"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g11473211419b/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      15 a      11 c      8 g      16 t
ORIGIN

Query Match.      27.6%; Score 13.8; DB 12; Length 50;
Best Local Similarity 56.2%; Pred. No. 1.6e+05;
Matches 18; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 16 aatgaattacnaatttaccngcnaagat 47
Db 38 AATGATATTCATTATAGCGTGAGAGAT 7

RESULT 10
AA921415      46 bp      mRNA      linear      EST 20-APR-1998
LOCUS      v237e06.r1 Soares thymus_2NBMT Mus musculus cDNA clone
DEFINITION      IMAGE:1328674 5' similar to TR:004892 004892 CYTOCHROME P450
LIKE_TBP ;, mRNA sequence.
ACCESSION      AA921415
VERSION      AA921415.1 GI:3068194
KEYWORDS      EST.
SOURCE      house mouse.
ORGANISM      Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 46)
AUTHORS      Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilton,R. and Waterston,R.
TITLE      The WashU-HMI Mouse EST Project
JOURNAL      Unpublished (1996)
COMMENT      Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:688218
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers

```

```

1. .46
source
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1328674"
/clone_lib="Soares_thymus_2NBMT"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGGCGGCCGCTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT      11 a      11 c      10 g      14 t
ORIGIN

Query Match      26.8%; Score 13.4; DB 9; Length 46;
Best Local Similarity 58.6%; Pred. No. 2.3e+05;
Matches 17; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 16 aatgaattacnaatttaccngcnaag 44
Db 8 AATGAATTCCTCATTGACATTCAG 36

RESULT 11
AA618672/c      42 bp      DNA      linear      GSS 13-DEC-2000
LOCUS      IM0450G08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION      clone UUGC1M0450G08 R, DNA sequence.
ACCESSION      AA618672
VERSION      AA618672.1 GI:11740958
KEYWORDS      GSS.
SOURCE      house mouse.
ORGANISM      Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 42)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0450 row: G column: 08
Seq primer: CACACAGGAACACGTATGACC
Class: plasmid ends
High quality sequence stop: 42.
Location/Qualifiers
FEATURES
source
1. .42
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0450G08"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

```

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/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PMD29hV; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
ligated DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g147321419b|Af129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT      28 a      2 c      3 g      9 t
ORIGIN

Query Match      26.4%; Score 13.2; DB 12; Length 42;
Best Local Similarity 54.5%; Pred. No. 2.7e+05;
Matches 18; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Oy      16 aatgaattacnaattacnagcnaagantt 48
      1 | | | | | | | | | | | | | | | | | | | |
Db      42 ACTGATTTTATTATTATTCCTCAATTATT 10

RESULT 12
LOCUS      TA108D050      44 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION      T. brucei sheared genomic DNA clone 108d05, reverse sequence.
ACCESSION      AL460900.1 GI:11831988
VERSION
KEYWORDS
SOURCE
ORGANISM      Trypanosoma brucei.
               Trypanosoma brucei
               Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae;
               Trypanosoma.
REFERENCE      1 (bases 1 to 44)
               Hall, N., Bowman, S., Lennard, N. J., Doggett, J., Atkin, R.,
               Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
               Melville, S. E., Rajandream, M. A. and Barrell, B. G.
               Direct Submission
               Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
               project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
               Cambridge CB10 1SA. E-mail: barrell@sanger.ac.uk and
               nilesanger@ac.uk
COMMENT
               Constructed at the Institute for Genomic Research (TIGR),
               Rockville, MD. Genomic DNA isolated from a cloned population of
               Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
               to give a tight size distribution (
               4 kb). The v + i method used for the library construction is
               described in detail in Smith, H. and Venter, J. C. (Making small
               insert libraries for whole genome shotgun sequencing projects. In
               Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
               Barrell, Oxford University Press, 1999).
               Email: nilesayer@tigr.org
               Details of T. brucei sequencing at the Sanger Centre are available
               at http://www.sanger.ac.uk/projects/T_brucei/.
               Location/Qualifiers
               1..44
               /organism="Trypanosoma brucei"
               /strain="TREU927"
               /db_xref="taxon:5691"
               /clone="108d05"

BASE COUNT      28 a      2 c      3 g      9 t
ORIGIN

Query Match      26.4%; Score 13.2; DB 12; Length 42;
Best Local Similarity 54.5%; Pred. No. 2.7e+05;
Matches 18; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Oy      16 aatgaattacnaattacnagcnaagantt 48
      1 | | | | | | | | | | | | | | | | | | | |
Db      42 ACTGATTTTATTATTATTCCTCAATTATT 10

RESULT 14
LOCUS      A2462649      45 bp      DNA      linear      GSS 04-OCT-2000
DEFINITION      1M0269N1R Mouse 10kb plasmid U06C1M library Mus musculus genomic
ACCESSION      A2462649.1 GI:10620690
VERSION
KEYWORDS
SOURCE
ORGANISM      Mus musculus

BASE COUNT      18 a      5 c      8 g      14 t
ORIGIN

Query Match      26.4%; Score 13.2; DB 9; Length 45;
Best Local Similarity 62.5%; Pred. No. 2.7e+05;
Matches 15; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy      20 aanttaccnaattacnagcnaana 43
      1 | | | | | | | | | | | | | | | | | | | |
Db      20 AATTTAATTAATTTATTGCAATTA 43

RESULT 13
LOCUS      AU007387      45 bp      mRNA      linear      EST 31-JUL-1998
DEFINITION      AU007387 Schizosaccharomyces pombe late log phase cDNA
               Schizosaccharomyces pombe cDNA clone spc01884, mRNA sequence.
ACCESSION      AU007387.1 GI:3343845
VERSION
KEYWORDS
SOURCE
ORGANISM      fission yeast.
               Schizosaccharomyces pombe.
               Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
               Schizosaccharomycetales; Schizosaccharomycetaceae;
               Schizosaccharomyces.
               1 (bases 1 to 45)
               Moriyo, M. and Mita, K.
               Identification of expressed sequence tags of Schizosaccharomyces
               pombe
               Unpublished (1998)
               Contact: Mitsuki Moriyo
               Genome Research Group
               National Institute of Radiological Sciences
               9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 265-8555, Japan
               Email: moriyo@nirs.go.jp.
               Location/Qualifiers
               1..45
               /organism="Schizosaccharomyces pombe"
               /strain="972"
               /db_xref="taxon:4896"
               /clone="spc01884"
               /clone_id="Schizosaccharomyces pombe late log phase cDNA"
               /sex="h minus"
               /note="Vector: M13mp19; The cDNA library of
               Schizosaccharomyces pombe was prepared by cloning cDNA
               into the SmaI site of M13mp19 DNA and the direction of DNA
               sequences was not always from 5' to 3'. The cDNA data of
               Schizosaccharomyces pombe are available for searching on
               the World Wide Web. (URL, http://www.nirs.go.jp)"
               Location/Qualifiers

```

Fri Jun 21 08:38:18 2002

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 45)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0269 row: N column: 11
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 45.
Location/Qualifiers
1. .45
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0269N11"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (g14732114[gb|AF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES

source

BASE COUNT 15 a 5 c 2 g 23 t
ORIGIN
Query Match 26.4%; Score 13.2; DB 12; Length 45;
Best Local Similarity 68.2%; Pred. No. 2.7e+05;
Matches 15; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 14 anaatgaatttcaaattna 35
|||||
DB 24 AAAATTAAATTTATGAATTTGA 3

RESULT 15

AZ798012/c 48 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0054002R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0054002 R, DNA sequence.
ACCESSION AZ798012
VERSION AZ798012.1 GI:12947682
KEYWORDS GSS.
SOURCE house mouse.

REFERENCE 1 (bases 1 to 48)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0054 row: O column: 02
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 48.
Location/Qualifiers
1. .48
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0054O02"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (g14732114[gb|AF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES

source

BASE COUNT 12 a 4 c 11 g 21 t
ORIGIN
Query Match 26.4%; Score 13.2; DB 12; Length 48;
Best Local Similarity 68.2%; Pred. No. 2.7e+05;
Matches 15; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 14 anaatgaatttcaaattna 35
|||||
DB 28 AAAATTATCATGTACAAATTTAA 7

Search completed: June 20, 2002, 23:05:02
Job time: 31067 sec

Fri Jun 21 08:38:18 2002

us-09-509-234c-1_copy_1_50.primer.rst

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 20, 2002, 23:42:07 ; Search time 1932.32 Seconds
(Without alignments)
498.168 Million cell updates/sec

Title: US-09-509-234c-1_COPY_1000_1045
Perfect score: 46
Sequence: 1 ngcngtggnacncaatn.....gncantngcngnagntat 46

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 663590

Minimum DB seq length: 15
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : GenBankl:
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlgc_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Query	Score	Match	Length	DB	ID	Description
SUMMARIES							

1	14	30.4	38	6	AX218691	AX218691 Sequence
2	13.6	29.6	50	6	AR148155	AR148155 Sequence
3	13.2	28.7	49	6	AR050507	AR050507 Sequence
4	13.2	28.7	49	6	AR124635	AR124635 Sequence
5	13.2	28.7	49	6	AX279805	AX279805 Sequence
6	13	28.3	33	6	AR003749	AR003749 Sequence
7	13	28.3	33	6	AR010085	AR010085 Sequence
8	13	28.3	33	6	AR055291	AR055291 Sequence
9	13	28.3	33	6	AR141220	AR141220 Sequence
10	13	28.3	33	6	AR141457	AR141457 Sequence
11	13	28.3	33	6	HEA37ND2	HEA37ND2 Sequence
12	12.8	27.8	45	6	E60005	E60005 Sequence
13	12.8	27.8	45	6	AX234992	AX234992 Sequence
14	12.8	27.8	45	6	I07868	I07868 Sequence
15	12.6	27.4	38	6	I05266	I05266 Sequence
16	12.6	27.4	45	6	AR033949	AR033949 Sequence
17	12.6	27.4	45	6	AR175082	AR175082 Sequence
18	12.6	27.4	45	6	AX032526	AX032526 Sequence
19	12.6	27.4	45	6	I07867	I07867 Sequence
20	12.4	27.0	47	6	AX194744	AX194744 Sequence
21	12.4	27.0	50	6	AR087173	AR087173 Sequence
22	12.4	27.0	50	6	E36072	E36072 Sequence
23	12.4	27.0	50	6	I49628	I49628 Sequence
24	12.2	26.5	49	6	AR158009	AR158009 Sequence
25	12.2	26.5	49	6	AX279837	AX279837 Sequence
26	12.2	26.5	50	6	A06298	A06298 Sequence
27	12.2	26.5	50	6	A10987	A10987 Sequence
28	12.2	26.5	50	6	A11836	A11836 Sequence
29	12	26.1	38	6	AX219011	AX219011 Sequence
30	12	26.1	38	6	AX219542	AX219542 Sequence
31	12	26.1	38	6	AX219543	AX219543 Sequence
32	12	26.1	38	6	AX219574	AX219574 Sequence
33	12	26.1	38	6	AX227864	AX227864 Sequence
34	12	26.1	41	6	I09032	I09032 Sequence
35	12	26.1	45	6	AX021022	AX021022 Sequence
36	12	26.1	45	6	AX081634	AX081634 Sequence
37	12	26.1	45	6	AX343665	AX343665 Sequence
38	12	26.1	48	6	AR065588	AR065588 Sequence
39	12	26.1	48	6	AR105964	AR105964 Sequence
40	12	26.1	50	6	AX164966	AX164966 Sequence
41	12	26.1	50	6	I42278	I42278 Sequence
42	11.8	25.7	28	6	AR090955	AR090955 Sequence
43	11.8	25.7	36	6	AX010623	AX010623 Sequence
44	11.8	25.7	37	6	AR153417	AR153417 Sequence
45	11.8	25.7	42	6	I22762	I22762 Sequence
46	11.8	25.7	42	6	I47587	I47587 Sequence
47	11.8	25.7	43	10	AB03552510	AB03552510 Sequence
48	11.8	25.7	46	6	A98794	A98794 Sequence
49	11.8	25.7	46	6	AR087647	AR087647 Sequence
50	11.8	25.7	47	6	AR170381	AR170381 Sequence
51	11.8	25.7	48	9	HUMDE06M3	HUMDE06M3 Sequence
52	11.8	25.7	49	6	AR003532	AR003532 Sequence
53	11.8	25.7	49	6	AR087646	AR087646 Sequence
54	11.8	25.7	49	6	AX279743	AX279743 Sequence
55	11.8	25.7	49	6	AX305185	AX305185 Sequence
56	11.8	25.7	49	6	I55645	I55645 Sequence
57	11.6	25.2	26	6	AR156510	AR156510 Sequence
58	11.6	25.2	31	6	AR142157	AR142157 Sequence
59	11.6	25.2	31	6	BD007211	BD007211 Sequence
60	11.6	25.2	34	6	AR031382	AR031382 Sequence
61	11.6	25.2	34	6	BD009750	BD009750 Sequence
62	11.6	25.2	36	6	AR130208	AR130208 Sequence
63	11.6	25.2	36	6	AR174240	AR174240 Sequence
64	11.6	25.2	38	6	AX219059	AX219059 Sequence
65	11.6	25.2	39	6	BD011043	BD011043 Sequence
66	11.6	25.2	40	6	A63304	A63304 Sequence
67	11.6	25.2	40	6	A60185	A60185 Sequence
68	11.6	25.2	45	6	AR040813	AR040813 Sequence
69	11.6	25.2	26	6	AR167267	AR167267 Sequence
70	11.4	24.8	30	6	I33767	I33767 Sequence
71	11.4	24.8	34	6	A67363	A67363 Sequence
72	11.4	24.8	34	6	AR009703	AR009703 Sequence
73	11.4	24.8	34	6	AX137684	AX137684 Sequence

us-09-509-234c-1_1000_1045.primer.rge

Fri Jun 21 14:51:59 2002

FEATURES		Location/Qualifiers	
SOURCE		1..38	
		/organism="synthetic construct"	
		/db_xref="taxon:32630"	
		/note="Nucleic Acid"	
BASE COUNT		13 a 7 c 10 g 8 t	
ORIGIN			
Query Match		30.4%; Score 14; DB 6; Length 38;	
Best Local Similarity		47.2%; Pred. No. 4.6e+04;	
Matches 17; Conservative		0; Mismatches 19; Indels 0; Gaps 0;	
QY		11 acntcaaatnnntnnngcattngcngnagntat 46	
Db		1 ACATGCAACTGATGAGCGGCTTAGCGCGAAGATAT 36	
RESULT 2			
LOCUS		ARI48155 50 bp DNA	
DEFINITION		Sequence 1 from patent US 6225063.	
ACCESSION		ARI48155	
VERSION		ARI48155.1 GI:15112245	
KEYWORDS		Unknown.	
SOURCE		Unknown.	
ORGANISM		Unclassified.	
REFERENCE		1 (bases 1 to 50)	
AUTHORS		Khvorova,A. and Varus,M.	
TITLE		RNA channels in biological membranes	
JOURNAL		Patent: US 6225063-A 1 01-MAY-2001;	
FEATURES		Location/Qualifiers	
		1..50	
BASE COUNT		8 a 11 c 17 g 14 t	
ORIGIN			
Query Match		29.6%; Score 13.6; DB 6; Length 50;	
Best Local Similarity		50.0%; Pred. No. 7.4e+04;	
Matches 16; Conservative		0; Mismatches 16; Indels 0; Gaps 0;	
QY		2 gcngtgagcncatcnaatnnntnnngcattt 33	
Db		17 GCGGGTGACCGCTAATATCTCTCGACACTT 48	
RESULT 3			
LOCUS		AR050507/c 49 bp DNA	
DEFINITION		Sequence 57 from patent US 5827693.	
ACCESSION		AR050507	
VERSION		AR050507.1 GI:5973232	
KEYWORDS		Unknown.	
SOURCE		Unknown.	
ORGANISM		Unclassified.	
REFERENCE		1 (bases 1 to 49)	
AUTHORS		De Angelo,J., Motwani,N.M., Bajwa,W. and Bonaventura,J.	
TITLE		Expression of recombinant hemoglobin and hemoglobin variants in yeast	
JOURNAL		Patent: US 5827693-A 57 27-OCT-1998;	
FEATURES		Location/Qualifiers	
		1..49	
BASE COUNT		12 a 14 c 12 g 11 t	
ORIGIN			
Query Match		28.7%; Score 13.2; DB 6; Length 49;	
Best Local Similarity		42.9%; Pred. No. 1.2e+05;	
Matches 18; Conservative		0; Mismatches 24; Indels 0; Gaps 0;	

ALIGNMENTS

RESULT 1		38 bp mRNA		Linear		PAT 07-SEP-2001	
LOCUS		AX218691					
DEFINITION		Sequence 4133 from Patent WO0159103.					
ACCESSION		AX218691					
VERSION		AX218691.1 GI:15546415					
KEYWORDS		synthetic construct.					
SOURCE		artificial sequence.					
ORGANISM		1 (bases 1 to 38)					
REFERENCE		Blatt,L., McSwiggen,J. and Chowrira,B.M.					
AUTHORS		Method and reagent for the modulation and diagnosis of cd20 and					
TITLE		nogo gene expression					
JOURNAL		Patent: WO 0159103-A 4133 16-AUG-2001;					
		RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;					
		McSwiggen, James (US) ; Chowrira, Bharat M. (US)					

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Page 9

OY 3 cnggtgnaactcnaatnnnnngcancntgncngnagnt 44
| | | | | | | | | | | | | | | | | | | | | |
Db 47 CTCGTGCGACGACTGAGCTTATGCAATGTGATCCAAAGCT 6

RESULT 4
ARI24635/c ARI24635 49 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 57 from patent US 6172039.
ACCESSION ARI24635
VERSION ARI24635.1 GI:14109996
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 49)
AUTHORS De Angelo,J., Motwani,N.M., Bajwa,W. and Bonaventura,J.
TITLE Expression of recombinant hemoglobin and hemoglobin variants in yeast
JOURNAL Patent: US 6172039-A 57 09-JAN-2001;
FEATURES Location/Qualifiers
source 1..49
/organism="unknown"
BASE COUNT 12 a 14 c 12 g 11 t
ORIGIN

Query Match 28.7%; Score 13.2; DB 6; Length 49;
Best Local Similarity 42.9%; Pred. No. 1.2e+05;
Matches 18; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

OY 3 cnggtgnaactcnaatnnnnngcancntgncngnagnt 44
| | | | | | | | | | | | | | | | | | | | | |
Db 47 CTCGTGCGACGACTGAGCTTATGCAATGTGATCCAAAGCT 6

RESULT 5
AX279805 AX279805 49 bp DNA linear PAT 02-NOV-2001
LOCUS Sequence 1138 from Patent WO0175180.
DEFINITION AX279805
ACCESSION AX279805
VERSION AX279805.1 GI:16607259
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequence.

REFERENCE 1 (sites)
AUTHORS Ulanovsky,L., Mugasimangalam,R., Elnat,P., Zezin-Sonkin,D. and Shlomit,G.
TITLE Sequence-dependent gene sorting techniques
JOURNAL Patent: WO 0175180-A 1138 11-OCT-2001;
FEATURES Opi Enterprises Ltd. (US)
source 1..49
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 8 a 13 c 19 g 9 t
ORIGIN

Query Match 28.7%; Score 13.2; DB 6; Length 49;
Best Local Similarity 43.9%; Pred. No. 1.2e+05;
Matches 18; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

OY 2 gcnggtgnaactcnaatnnnnngcancntgncngnag 42
| | | | | | | | | | | | | | | | | | | | | |
Db 2 GCTGCGAGTACGTCGTACCGCGCCGCGTTTCGAAGGAG 42

RESULT 6
AR003749/c

LOCUS AR003749 33 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 39 from patent US 5744580.
ACCESSION AR003749
VERSION AR003749.1 GI:3965008
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.
TITLE Immunotoxins comprising ribosome-inactivating proteins
JOURNAL Patent: US 5744580-A 39 28-APR-1998;
FEATURES Location/Qualifiers
source 1..33
/organism="unknown"

BASE COUNT 9 a 11 c 6 g 7 t
ORIGIN

Query Match 28.3%; Score 13; DB 6; Length 33;
Best Local Similarity 56.5%; Pred. No. 1.4e+05;
Matches 13; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 14 tcnaatnnnnngcancntgc 36
| | | | | | | | | | | | | | | | | | | | | |
Db 23 TCAATGACTGTGCGACGTTGCG 1

RESULT 7
AR010085/c AR010085 33 bp DNA linear PAT 04-DEC-1998
LOCUS Sequence 39 from patent US 5756699.
DEFINITION AR010085
ACCESSION AR010085
VERSION AR010085.1 GI:3968890
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.
TITLE Immunotoxins comprising ribosome-inactivating proteins
JOURNAL Patent: US 5756699-A 39 26-MAY-1998;
FEATURES Location/Qualifiers
source 1..33
/organism="unknown"

BASE COUNT 9 a 11 c 6 g 7 t
ORIGIN

Query Match 28.3%; Score 13; DB 6; Length 33;
Best Local Similarity 56.5%; Pred. No. 1.4e+05;
Matches 13; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 14 tcnaatnnnnngcancntgc 36
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Db 23 TCAATGACTGTGCGACGTTGCG 1

RESULT 8
AR055291/c AR055291 33 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 39 from patent US 5837491.
DEFINITION AR055291
ACCESSION AR055291
VERSION AR055291.1 GI:5980868
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.
TITLE Polynucleotides encoding gelonin sequences
JOURNAL Patent: US 5837491-A 39 17-NOV-1998;
FEATURES Location/Qualifiers

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source          1. .33
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BASE COUNT      9 a 11 c 6 g 7 t
ORIGIN

Query Match      28.3%; Score 13; DB 6; Length 33;
Best Local Similarity 56.5%; Pred. No. 1.4e+05;
Matches 13; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 14 tcnaatnnntnnngcattngc 36
    ||||| | |||||
Db 23 TCAATGACTGTGGCAGATTGGC 1

RESULT 9
LOCUS      ARI141220          33 bp      DNA          linear          PAT 08-AUG-2001
DEFINITION Sequence 39 from patent US 6146631.
ACCESSION  ARI141220
VERSION     ARI141220.1 GI:15100737
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 33)
AUTHORS    Better, M.D., Carroll, S.F. and Studnicka, G.M.
TITLE      Immunotoxins comprising ribosome-inactivating proteins
JOURNAL    Patent: US 6146631-A 39 14-NOV-2000;
FEATURES
    source          1. .33
    /organism="unknown"
BASE COUNT      9 a 11 c 6 g 7 t
ORIGIN

Query Match      28.3%; Score 13; DB 6; Length 33;
Best Local Similarity 56.5%; Pred. No. 1.4e+05;
Matches 13; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 14 tcnaatnnntnnngcattngc 36
    ||||| | |||||
Db 23 TCAATGACTGTGGCAGATTGGC 1

RESULT 10
LOCUS      ARI141457/c          33 bp      DNA          linear          PAT 08-AUG-2001
DEFINITION Sequence 39 from patent US 6146850.
ACCESSION  ARI141457
VERSION     ARI141457.1 GI:15100973
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 33)
AUTHORS    Better, M.D. and Carroll, S.F.
TITLE      Proteins encoding gelonin sequences
JOURNAL    Patent: US 6146850-A 39 14-NOV-2000;
FEATURES
    source          1. .33
    /organism="unknown"
BASE COUNT      9 a 11 c 6 g 7 t
ORIGIN

Query Match      28.3%; Score 13; DB 6; Length 33;
Best Local Similarity 56.5%; Pred. No. 1.4e+05;
Matches 13; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 14 tcnaatnnntnnngcattngc 36
    ||||| | |||||
Db 23 TCAATGACTGTGGCAGATTGGC 1

source          1. .33
/organism="unknown"
BASE COUNT      9 a 11 c 6 g 7 t
ORIGIN

Query Match      28.3%; Score 13; DB 6; Length 33;
Best Local Similarity 56.5%; Pred. No. 1.4e+05;
Matches 13; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 14 tcnaatnnntnnngcattngc 36
    ||||| | |||||
Db 23 TCAATGACTGTGGCAGATTGGC 1

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RESULT 11
LOCUS      HEA37NU2/c          50 bp      DNA          linear          BCT 10-NOV-1993
DEFINITION H.influenzae non-uptake non-binding sequence 37nu2.
ACCESSION  M33438
VERSION     M33438.1 GI:148840
KEYWORDS
SOURCE      H.influenzae (strain Rd) DNA.
ORGANISM    Haemophilus influenzae
            Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
            Haemophilus.
REFERENCE   1 (bases 1 to 50)
AUTHORS    Goodgal, S.H. and Mitchell, M.A.
JOURNAL    Unpublished (1990)
REFERENCE   2 (sites)
AUTHORS    Goodgal, S.H. and Mitchell, M.A.
TITLE      Sequence and uptake specificity of cloned sonicated fragments of
            Haemophilus influenzae DNA
JOURNAL    J. Bacteriol. 172, 5924-5928 (1990)
MEDLINE    91008969
COMMENT     [2] sites. [1] for [2].

Draft entry and computer-readable sequence for [2],[1] kindly
submitted by S.H.Goodgal, 30-MAR-1990.

Author Address: S.H. Goodgal, and M.A. Mitchell, Dept. of
Microbiology, School of Medicine, Rm 346, Johnson Pav.,
Philadelphia, PA 19104-6076.
FEATURES
    source          1. .50
    /organism="Haemophilus influenzae"
    /db_xref="taxon:727"
BASE COUNT      15 a 13 c 15 g 7 t
ORIGIN

Query Match      28.3%; Score 13; DB 1; Length 50;
Best Local Similarity 47.1%; Pred. No. 1.5e+05;
Matches 16; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 3 cngstggaactcnaatnnntnnngcattngc 36
    ||||| | |||||
Db 34 CCGCTGGGACTTCATCCTCAATAGTGGCTTACGC 1

RESULT 12
LOCUS      E60005          45 bp      DNA          linear          PAT 31-JAN-2002
DEFINITION Ceramide-binding peptide.
ACCESSION  E60005
VERSION     E60005.1 GI:18622764
KEYWORDS    JP 2000319296-A/5.
SOURCE      Synthetic construct.
ORGANISM    artificial sequence.
REFERENCE   1 (bases 1 to 45)
AUTHORS    Ishikawa, M., Tanaka, Y., Ogino, K. and Taki, T.
TITLE      Ceramide-binding peptide
JOURNAL    Patent: JP 2000319296-A 5 21-NOV-2000;
            OTSUKA PHARMACEUT CO LTD
COMMENT     OS Artificial Sequence
            PN JP 2000319296-A/5
            PD 21-NOV-2000
            PF 10-MAY-1999 JP 1999128674
            PR MASARU ISHIKAWA, YOSHINORI TANAKA, KOICHI OGINO, TAKAO TAKI
            PI C07K7/00
            CC Key
            FH Location/Qualifiers
            FT source
            FT /organism='Artificial Sequence'.

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5 a	5 c	15 g	20 t
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Query Match	Score	DB 6;	Length
27.88;	12.8;	DB 6;	45;

Best Local Similarity 43.6%; Pred. NO. 1.9e+07;
Matches 17; Conservative 0; Mismatches 22; Indels 0; Gaps 0.

QY 6 gtggnacntcnaatnmtngncanttngcngnagnt 44
||| | | | | | | |
Db 4 GTGGGCGCTATTTTATGCTGTACTTTTCGGATGAT 42

RESULT 13
AX234992
15334002 47 bp DNA linear PAT 11-SEP-2001

LOCUS	AA234992	
DEFINITION	Sequence 7 from Patent WO0162961.	
ACCESSION	AX234992	
VERSION	AX234992.1	GI:15593651

SOURCE ORGANISM	synthetic construct. synthetic construct sequence
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REFERENCE	AUTHORS	TITLE
1 (bases 1 to 47)	Olek, A. and Berlin, K.	Ligase/polymerase method for detecting cytosine methylation in dna

JOURNAL
Patent: WO 0162961-A 7 30-AUG-2001
Epigenomics AG (DE)

FEATURES	Location/Qualifiers
source	1. .47

BASE COUNT	19 a	0 c	13 g	15 t
	/note=" 01lgonukleotid"			

Query Match	27.88;	Score 12.8;	DB 6;	Length 47;
Best Local Similarity	50.0%;	Pred. No. 1.9e+05;		
Matches 14;	Conservative 0;	Mismatches 14;	Indels 0;	Gaps 0

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QY      17  aatnntnngncanttngcngnagnt 44
      |||  |  |  |  |  |  |  |  |
Db      20  AATGTATAAGTAAATTAGAGAAGAGAT 47
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RESULT 14

107866	48 bp
LOCUS	I07866
DEFINITION	Sequence 8 from Patent EP 0130756.

ACCESSION	I07868	
VERSION	I07868.1	GI:589418

SOURCE	Unknown.
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ORGANISM	Unknown. Unclassified.
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REFERENCE	AUTHORS	TITLE
1 (bases 1 to 48)	Bolt, R.R., Ferrari, E., Wells, J.A., Estell, D.A. and Henner, D.J.	Procarboxylic carbonyl hydrolases, methods, DNA, vectors and

transformed hosts for producing nucleic acids containing them
Patent: EP 0130756-A1 8 09-JAN-1985

FEATURES	Location/Qualifiers
source	1. .48

BASE COUNT ORIGIN	9 a	14 c	14 g	8 t	3 others

Query Match	27.8%;	Score 12.8;	DB 6;	Length 48;
Best Local Similarity	43.8%;	Pred. No. 1.9e+05;		
Matches 14;	Conservative	0;	Mismatches 18;	Indels 0;
				Gaps 0;

Qy 8 ggnacntcnaatnntnngncanttngng 39
 10 GGTACGTCANNGCATCTCCGCACGTTGCAGG 41

RESULT	15	
105266		
ROOTS		
T05266		
	36 bp	
	linear	PAT 02-DEC-1994

LOCUS	I05266	36 bp
DEFINITION	Sequence 27 from Patent EP 0251446	
ACCESSION	I05266	
VERSION	I05266.1	GI:591195

KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.

UNCLASSIFIED
REFERENCE
METHODS

Unclassified.
1 (bases 1 to 36)
Wells, J. A., Cunningham, B.C., Caldwell, R.M., Bott, R.R., Estell, D.A.

TITLE Non-human Carbonyl hydrolase mutants, DNA sequences and vectors encoding same and hosts transformed with said vectors
JOURNAL Patent: EP 0251446-A2 27 07-JAN-1988;
and POWELL, S.D.

JOURNAL	Patent: EP 0251446-A2 27 07-JAN-1988;
FEATURES	Location/Qualifiers
	1 36

	source	1. 100	/organism="unknown"	
BASE COUNT		7 a	11 c	11 g
ORIGIN				7 t

Query Match	27.4%	Score 12.6;	DB 6;	Length 36;
Best Local Similarity	46.9%	Pred. No. 2.3e+05;		
Matches 15;	Conservative 0;	Mismatches 17;	Indels 0;	Gaps 0

Qy 8 ggnacntcnaatnntnngncanttngcng 35
 |||||
 Db 1 GGTACCTCAATGGCATCTCCGCACGTTCAGG 32

Search completed: June 20, 2002, 23:42:29
Job time: 17374 sec

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229	10.8	23.5	43	19	AAV10828	Human MSH2 gene PC
230	10.8	23.5	43	22	AAAC82229	Human retrovirus D
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232	10.8	23.5	44	18	AAI45055	Rapamycin-dependent
233	10.8	23.5	45	14	AAQ28446	Target gag region
234	10.8	23.5	45	14	AAQ47079	HIV ENV gene PCR p
235	10.8	23.5	45	14	AAQ46670	Duplex cutting RNA
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237	10.8	23.5	45	18	AAI63969	Human cytochrome P
238	10.8	23.5	45	20	AAI7257	Test sequence from
239	10.8	23.5	45	22	AAI88160	Murine wild-type d
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241	10.8	23.5	46	18	AAI63814	Test sequence from
242	10.8	23.5	46	20	AAI17102	Human serum albumi
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244	10.8	23.5	46	21	AAI93168	Primer HRNA contai
245	10.8	23.5	46	22	AAI26138	Collectin PCR prim
246	10.8	23.5	46	22	AAI91197	PCR primer sequenc
247	10.8	23.5	47	21	AAI15868	Human map-related
248	10.8	23.5	47	21	AAI65990	Human map-related
249	10.8	23.5	47	21	AAI67885	Human map-related
250	10.8	23.5	47	21	AAI68075	Human map-related
251	10.8	23.5	47	21	AAI69196	CNS disorder-relat
252	10.8	23.5	47	21	AAI88580	Deletion mutant 1/
253	10.8	23.5	48	21	AAI93367	Human serum albumi
254	10.8	23.5	48	21	AAI93367	Human serum albumi
255	10.8	23.5	48	21	AAI93367	T cell antigen rec
256	10.8	23.5	48	21	AAI93367	Primer BHA contai
257	10.8	23.5	48	21	AAI93367	Template linker pr
258	10.8	23.5	50	12	AAI2981	HIV template linker
259	10.8	23.5	50	18	AAI74431	Antisense oligo u
260	10.8	23.5	50	20	AAI26185	Antisense oligonuc
261	10.8	23.5	50	22	AAI81433	Human SNP oligonuc
262	10.8	23.5	50	22	AAI34162	Aldehyde dehydrog
263	10.6	23.0	15	24	AAI93377	Primer for B. subt
264	10.6	23.0	29	14	AAI93377	Alpha subunit spec
265	10.6	23.0	29	16	AAI93377	HIV-1 cDNA amplifi
266	10.6	23.0	29	19	AAI54426	Nucleotide sequenc
267	10.6	23.0	29	20	AAI78226	pppG208 primer 2.
268	10.6	23.0	29	21	AAI49047	PCR primer for fas
269	10.6	23.0	29	21	AAI49047	PCR primer for 3' p
270	10.6	23.0	30	14	AAI4375	TH3 promoter 3' p
271	10.6	23.0	30	19	AAI7893	PCR primer TDR3-3'
272	10.6	23.0	30	22	AAI3437	Primer #8. Uniden
273	10.6	23.0	31	19	AAI3437	Target sequence #1
274	10.6	23.0	31	19	AAI3437	Mycobacterium para
275	10.6	23.0	31	20	AAI26345	PCR primer used to
276	10.6	23.0	31	23	AAI6702	Human NCOO DNAzyme
277	10.6	23.0	32	20	AAI6702	P. daieae rRNA oli
278	10.6	23.0	33	15	AAI70256	T. gondii P30.336
279	10.6	23.0	33	16	AAI29167	Bacteriophage T4 g
280	10.6	23.0	33	22	AAI9871	M. tuberculosis rhodoc
281	10.6	23.0	33	22	AAI9871	Rhodococcus rhodoc
282	10.6	23.0	33	22	AAI77372	Human negative reg
283	10.6	23.0	33	22	AAI77372	Human ubiquitin-11
284	10.6	23.0	33	22	AAI77372	Anti-HIV antiselec
285	10.6	23.0	33	22	AAI77372	Myobacterium kans
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287	10.6	23.0	33	22	AAI77372	PCR primer HFR1.2
288	10.6	23.0	33	22	AAI77372	Primer for antihod
289	10.6	23.0	33	22	AAI77372	Th cDNA of ICR-8.1
290	10.6	23.0	33	22	AAI77372	Murine ICR-8.1 ant
291	10.6	23.0	33	22	AAI77372	Murine antibody IC
292	10.6	23.0	33	22	AAI77372	Murine antibody IC
293	10.6	23.0	33	22	AAI77372	DNA del(5-258):4LE
294	10.6	23.0	33	22	AAI77372	Primer 8 for A. th
295	10.6	23.0	33	22	AAI77372	Thermal amplifica
296	10.6	23.0	33	22	AAI77372	Rat GluR4/myc epit
297	10.6	23.0	33	22	AAI77372	Oligo M2 containin
298	10.6	23.0	33	22	AAI77372	Human Chk1 ribozym
299	10.6	23.0	33	22	AAI77372	Human UNC-5 PCR pr
300	10.6	23.0	33	22	AAI77372	E. coli cldCBFG
301	10.6	23.0	33	22	AAI77372	

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959 9.8 21.3 24 24 ABI85761
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 c 964 9.8 21.3 25 14 AAQ49882
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 c 966 9.8 21.3 25 19 AAQ19230
 c 967 9.8 21.3 25 20 AAQ32448
 968 9.8 21.3 25 21 AAQ33666
 969 9.8 21.3 25 22 ABA82310
 970 9.8 21.3 25 22 AAH48846
 c 971 9.8 21.3 26 13 AAQ28502
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 973 9.8 21.3 26 17 AAQ32131
 974 9.8 21.3 26 17 AAQ32106
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 c 979 9.8 21.3 26 21 AAQ15675
 c 980 9.8 21.3 26 22 AAQ17894
 c 981 9.8 21.3 26 22 AAQ13275
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 c 985 9.8 21.3 26 22 AAQ06776
 c 986 9.8 21.3 26 22 AAQ61795
 c 987 9.8 21.3 26 22 AAQ97076
 c 988 9.8 21.3 27 13 AAQ29734
 c 989 9.8 21.3 27 14 AAQ42300
 c 990 9.8 21.3 27 22 AAQ91471
 c 991 9.8 21.3 28 13 AAQ31029
 c 992 9.8 21.3 28 16 AAQ87362
 c 993 9.8 21.3 28 16 AAQ92514
 c 994 9.8 21.3 28 19 AAQ09380
 c 995 9.8 21.3 28 19 AAQ66891
 c 996 9.8 21.3 28 19 AAQ37308
 c 997 9.8 21.3 28 21 AAQ13320
 c 998 9.8 21.3 28 21 AAQ256054
 c 999 9.8 21.3 28 21 AAQ11290
 1000 9.8 21.3 29 19 AAQ11290

ALIGNMENTS

RESULT 1
 ID AAN91962/c
 XX AAN91962; standard; DNA; 50 BP.
 AC AAN91962;
 XX
 DT 13-APR-1990 (first entry)
 XX
 DE Complementary strand of the Neisseria gonorrhoeae Tem-1 beta lactamase
 DE gene combined with lla2c amplifier probe.
 XX
 KW Neisseria gonorrhoeae; beta lactamase Tem-1; capture probe;
 KW amplifier probe lla2c; temkit21.25; TEM-LNH assay.
 XX
 OS Neisseria gonorrhoeae.
 XX
 PH Key Location/Qualifiers
 FT misc_feature 1..30
 FT /*tag- a
 FT /*capture probe"
 FT misc_feature 31..50
 FT /*tag- b
 FT /*lla2c amplifier probe"
 FT
 XX WO8903891-A.
 PN
 XX

PD 05-MAY-1989.
 XX 14-OCT-1988; 88WO-US03644.
 PF 30-SEP-1988; 88US-0252638, US-109282.
 XX
 XX (CHIR-) CHIRON CORP.
 PA Urdea MS, Warner B, Running JA, Kolberg JA, Clyne JM;
 PI Sanchez-Pescador R;
 PI WPI; 1989-150787/20.
 DR Nucleic acid multimer for hybridisation assays
 XX PT - having single-stranded oligo-nucleotide units
 PT capable of binding specifically to sequences of interest.
 XX Fig 10-2; ; 112pp; English.
 XX Partial nucleotide sequences of the capture and amplifier probes used in
 CC the TEM-LNH assay. The capture probe is complementary to the coding
 CC strand of N. gonorrhoeae Tem-1 beta lactamase gene. It is called
 CC temkit21.25.
 XX Sequence 50 BP; 22 A; 10 C; 12 G; 6 T; 0 other;
 SQ
 Query Match 31.7%; Score 14.6; DB 10; Length 50;
 Best Local Similarity 50.0%; Pred. No. 7.4e+02;
 Matches 17; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
 QY 3 cnggtgagcactcaatnnntnnnnncantngc 36
 |||||
 DB 46 CGGCTCTATGCTAAATTTTTCGCGCATTTTC 13
 |||||
 RESULT 2
 ABRK04133
 ID ABRK04133 standard; RNA; 38 BP.
 XX
 AC ABRK04133;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 XX Human NOGO Hammerhead ribozyme substrate sequence #340.
 DE Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease; substrate sequence;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200159103-A2.
 PN
 XX 16-AUG-2001.
 PD 09-FEB-2001; 2001WO-US04273.
 XX 11-FEB-2000; 2000US-181797P.
 XX 28-FEB-2000; 2000US-185516P.
 XX 06-MAR-2000; 2000US-187128P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA

XX	DT	10-SEP-2001 (first entry)
XX	DE	Human map-related biallelic marker SEQ ID NO:1008.
XX	KN	Human genome, biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; genomic map, haplotype; phenotype; polymorphic base; genotyping;

10-SEP-2001	(first entry)	
DT		
DE		
Human map-related	biallelic marker	SEQ ID NO:3207.
XX		
XX		
KW	Human genome; biallelic marker; high density disequilibrium map;	
KW	genomic map; haplotype; phenotype; polymorphic base; genotyping;	
KW	haplotyping; hybridisation; identification; characterisation;	
KW	haplotyping; single nucleotide polymorphism; SNP; ds.	
KW	diagnosis;	

us-09-509-234c-1_1000_1045.primer.rng

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```

XX OS Homo sapiens.
XX FH Location/Qualifiers
XX FT replace(24,T)
XX FT /*tag= a
XX FT /standard_name= "single nucleotide polymorphism"
XX FT
XX PN WO9954500-A2.
XX PD 28-OCT-1999.
XX PF 21-APR-1999; 99WO-IB00822.
XX XX 21-APR-1998; 98US-0082614.
XX PR 23-NOV-1998; 98US-0109732.
XX PA (GIST ) GENSET.
XX PI Cohen D, Blumenfeld M, Chumakov I;
XX PI WPI; 2000-013267/01.
XX DR Novel biallelic markers used to construct a high density disequilibrium
XX PT map of the human genome
XX PS Claim 3; Page 914; 2745pp; English.
XX XX AA65654 to AAZ69578 represent human biallelic markers from the present
XX CC invention, which contain a polymorphic base at position 24 of their
XX CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
XX CC primers for the biallelic markers. The biallelic markers of the
XX CC invention have a variety of uses: they can be used for high density
XX CC mapping of the human genome, and in complex association studies and
XX CC haplotyping studies which are useful in determining the genetic basis
XX CC for disease states. Compositions and methods of the invention can also
XX CC be useful for the identification of the targets for the development of
XX CC pharmaceutical agents and diagnostic methods, as well as the
XX CC characterisation of the differential efficacious responses to and side
XX CC effects from pharmaceutical agents acting on a disease as well as other
XX CC treatment.
XX CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
XX CC and 3367, are not actually given a sequence in the Sequence Listing
XX CC from the present invention.
XX XX Sequence 47 BP; 19 A; 11 C; 9 G; 8 T; 0 other;
XX SQ
XX XX Query Match 30.0%; Score 13.8; DB 21; Length 47;
XX XX Best Local Similarity 51.7%; Pred. No. 1.8e+03;
XX XX Matches 15; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
XX QY 14 tcnaatnnnnnngcncantngcngnag 42
XX DB 2 taataacatgaccacattagcggcag 30
XX XX
XX RESULT 5
XX ID AAA30308 standard; DNA; 48 BP.
XX AC AAA30308;
XX XX 11-SEP-2000 (first entry)
XX DT
XX DE M. tuberculosis Cu, Zn Superoxide dismutase, SOD, gene fragment.
XX XX
XX KW Cu, Zn superoxide dismutase; antibody; tuberculosis; enzyme;
XX KW superoxide radical; macrophage; sodC; bacterium detection; ds.
XX OS Mycobacterium tuberculosis.
XX PN WO200029017-A1.

```

```

XX PD 25-MAY-2000.
XX XX 09-NOV-1999; 99WO-US26372.
XX PR 13-NOV-1998; 98US-0108309.
XX PA (YUNG-) YUNG SHIN PHARM IND CO LTD.
XX PI Lee FS, Wu CH;
XX PI WPI; 2000-387619/33.
XX DR P-PSDB; AAY96264.
XX XX Novel monoclonal antibodies targeted to Mycobacterium tuberculosis
XX PT superoxide dismutase, useful for detecting tuberculosis infection -
XX PS Example 1; Page 14; 28pp; English.
XX XX The present sequence is a gene fragment of Mycobacterium tuberculosis
XX CC Copper, zinc Superoxide dismutase, Cu, ZnSOD. Superoxide dismutase,
XX CC catalyses the conversion of superoxide radicals, which are mutagenic,
XX CC into molecular oxygen and hydrogen peroxide. Cu, ZnSOD is thought to be
XX CC important for bacterial survival in macrophages. Macrophages engulf
XX CC bacteria, and set about destroying them by generating superoxide
XX CC radicals. The bacterium counteracts by releasing SOD, to neutralise the
XX CC superoxide radicals. The present sequence is added to the truncated
XX CC Cu, ZnSOD coding sequence (AAA30303) to produce a full-length version.
XX CC The T of the stop codon of AAA30303 is mutated to an A, to produce a Lys
XX CC codon. The present sequence was then added downstream of the Lys codon.
XX CC Antibodies can be developed which bind specifically to the full-length
XX CC protein. The antibodies are useful for detecting tuberculosis
XX CC infection in animals, and for detecting the presence of Mycobacterium
XX CC tuberculosis. The antibodies are also used to isolate the Mycobacterium
XX CC tuberculosis Cu, Zn SOD.
XX XX Sequence 48 BP; 10 A; 15 C; 13 G; 10 T; 0 other;
XX SQ
XX XX Query Match 30.0%; Score 13.8; DB 21; Length 48;
XX XX Best Local Similarity 45.0%; Pred. No. 1.8e+03;
XX XX Matches 18; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
XX QY 2 gonggtggnacatcnaatnnnnnngcncantngcngnag 41
XX DB 45 GCAGCGGATCCACTAGTAACGGCGCGCCACTGTGTGGAA 6
XX XX
XX RESULT 6
XX ID AAZ47139 standard; RNA; 50 BP.
XX XX AAZ47139;
XX XX 28-MAR-2000 (first entry)
XX DT
XX DE Liposome membrane-binding RNA molecule #2.
XX XX
XX KW Antibiotic; antitumour; cellular membrane; binding; liposome; SELEX; ss;
XX KW Systematic Evolution of Ligands by Exponential enrichment; permeability.
XX OS Synthetic.
XX XX WO9961460-A1.
XX PD 02-DEC-1999.
XX PF 21-MAY-1999; 99WO-US11297.
XX XX 22-MAY-1998; 98US-0086492.
XX PR 20-MAY-1999; 99US-0086492.
XX XX (UYTE-) UNIV TECHNOLOGY CORP.
XX PN

```

New transcription regulating fragments of hexokinase II DNA conty.
 response element - and methods for diagnosis or treatment of
 neoplasias that over-express hexokinase II and for regulating
 glycolysis
 Claim 1; Fig 11; 104pp: English.

The present sequence represents a segment of the hepatoma AS-30D Type
 II hexokinase promoter region. Response elements (transcription factor
 binding site) in this fragment may consist of all or part of the
 present sequence. AS-30D is a new isolated hexokinase II. The present
 DNA fragment is capable of regulating transcription of a downstream
 open reading frame and contains at least one response element. The
 present DNA fragment may be coupled to a reporter gene and used to
 screen for potential drugs that affect regulated transcription of
 tumour hexokinase II. Alternatively it may be coupled to a toxic gene
 and used to treat cells that over-express hexokinase II, such as those
 present in patients with cancer. It may also be used in gene therapy
 to treat diabetes. The DNA fragment increases glycolysis in cells and
 to treat homologous or heterologous protein. Probes of the DNA fragment
 are used in the method for diagnosing a neoplasia that over-expresses
 hexokinase. The new response elements are active only in tumours, not
 in normal cells.

Sequence 49 BP; 9 A; 13 C; 14 G; 13 T; 0 other;

29.1%; Score 13.4; DB 18; Length 49;
 Query Match Best Local Similarity 45.9%; Pred. No.36+03;
 Matches 17; Conservative 0; Mismatches 20; Indels 0; Gaps

5 ggtgacatcnaatnntnnnngcattngcngna 41
 ||||| ||| ||| ||| ||| ||| ||| |||
 44 gctggcactacctttatcagacccttggcggca 8

Db

RESULT	8	
AAV08803/c		
ID	AAV08803 standard; DNA; 49 BP.	
XX		
AC	AAV08803;	
XX		
DT	18-FEB-1999 (first entry)	
XX		
DE	PCR primer for human haemoglobin mutant.	
XX		
XX	Haemoglobin; mutant; human; substitute blood product; synthetic blood.	
KW	beta chain; PCR primer; ss.	
XX		
OS	Synthetic.	
OS	Homo sapiens.	
XX		
PN	US5827693-A.	
PD	27-OCT-1998.	
XX		
XX	07-JUN-1995; 95US-0484686.	
FE		
XX		
XX	29-APR-1992; 92US-0876290.	
PR	16-APR-1990; 90US-0509918.	
PR	14-NOV-1990; 90US-0614359.	
PR	12-APR-1991; 91US-0684611.	
PR	29-DEC-1994; 94US-0368407.	
PR	07-JUN-1995; 95US-0484686.	
XX		
PA	(APEX-) APEX BIOSCIENCE INC.	
PI	Bajwa W, Bonaventura J, De Angelo J, Motwani NM;	
XX		
DR	WPI; 1998-593993/50.	
XX		
PT	Recombinant expression of globin chains - and variants in yeast.	
PT	useful as substitutes for natural blood required for oxygen carriage	

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XX Example 25; Fig 51; 144pp; English.

PS This sequence represents a PCR primer for DNA encoding a human

XX haemoglobin variant. The amplified DNA is used in the recombinant DNA

CC vector of the invention, which expresses a globin chain in a yeast cell,

CC and comprises: (a) a first DNA sequence encoding a globin chain; (b) a

CC yeast transcriptional promoter which promotes the transcription of the

CC first DNA sequence; (c) a second DNA sequence encoding a yeast selectable

CC marker; and (d) a yeast replication origin. The vectors and recombinant

CC yeast cells containing their variants. The products in turn, can be used

CC as substitute blood products, where oxygen carriage is required. The

CC variants are designed to enable generally stable cross-linking of

CC monomers to a tetrameric form, which does not dissociate into dimers.

CC They are also designed to be stable to a certain extent in alkaline

CC conditions compared to normal physiological conditions. The yeast strains

CC used allow recombinant production of correctly processed haemoglobin

CC chains in large quantities. The use of recombinant blood also eliminates

CC risks of contamination of donated blood samples, and also shortages of

CC not having enough donations of a specific blood type.

CC N.B. This sequence was created from the human haemoglobin beta chain

CC sequence given in the specification.

XX Sequence 49 BP; 12 A; 14 C; 12 G; 11 T; 0 other;

SQ

Query Match 28.7%; Score 13.2; DB 19; Length 49;

Best Local Similarity 42.9%; Pred. No. 3.7e+03;

Matches 18; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 3 cnggtggaactcnaatnnnnnncantnngcngnagnt 44

Db 47 CTCGTGGCAGCAGCTGGAGGTTTATGGCAATTGGATCCAGCT 6

RESULT 9

AAF31447/C

ID AAF31447 standard; DNA; 49 BP.

XX AAF31447;

AC AAF31447;

XX 10-APR-2001 (first entry)

DT Primer #18.

DE Hemoglobin; globin; oxygen carrier; ss.

XX Unidentified.

OS US6172039-B1.

XX 09-JAN-2001.

PD 05-JUN-1995; 95US-0463160.

PF 29-DEC-1994; 94US-0368407.

XX 07-JUN-1995; 95US-0484686.

PR 29-APR-1992; 92US-0876290.

XX 16-APR-1990; 90US-0509918.

PR 14-NOV-1990; 90US-0614359.

XX 12-APR-1991; 91US-0684611.

XX (APEX-) APEX BIOSCIENCE INC.

PA De Angelo J, Motwani NM, Bajwa W, Bonaventura J;

PI WPI; 2001-136882/14.

XX Novel globin chain in combination with a source of heme useful for

XX producing hemoglobin, is free of erythrocyte membrane component,

PT mammalian cell components and Escherichia coli endotoxins

PT

PS Example 25; Fig 51; 144pp; English.

XX The present invention relates to a substantially pure globin

CC chain which is free of erythrocyte membrane components,

CC Escherichia coli endotoxins and mammalian cell components.

CC The globin combined with a source of heme is useful for producing

CC hemoglobin, which in turn is useful as physiological oxygen carrier in

CC blood substitute solutions and in plasma expanders or in applications

CC requiring a physiological oxygen carrier.

XX Sequence 49 BP; 12 A; 14 C; 12 G; 11 T; 0 other;

SQ

Query Match 28.7%; Score 13.2; DB 22; Length 49;

Best Local Similarity 42.9%; Pred. No. 3.7e+03;

Matches 18; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 3 cnggtggaactcnaatnnnnnncantnngcngnagnt 44

Db 47 CTCGTGGCAGCAGCTGGAGGTTTATGGCAATTGGATCCAGCT 6

RESULT 10

ABAI0848

ID ABAI0848 standard; DNA; 49 BP.

XX ABAI0848;

AC ABAI0848;

XX 26-FEB-2002 (first entry)

DT Tail adaptor oligonucleotide #217 used in gene sorting method.

XX Gene sorting; PCR primer; disease diagnosis; disease analysis;

XX cell differentiation; gene therapy; ss.

OS Synthetic.

XX WO200175180-A2.

PN 11-OCT-2001.

PD 23-MAR-2001; 2001WO-US09492.

PF 30-MAR-2000; 2000US-0538709.

XX (OBIO-) QBI ENTERPRISES LTD.

PA Ulanovsky L, Mugasimangalam R, Einat P, Zevin-Sonkin D, Shlomit G;

PI WPI; 2001-626451/72.

XX Sorting genes into non-redundant groups, useful e.g. for gene

XX isolation, diagnosis and in gene therapy, by amplifying cDNA fragments

XX attached to selective adaptors

XX Example 2; Fig 18; 67pp; English.

XX The present invention relates to a method for sorting genes. The method

XX comprises producing first double stranded (ds) cDNA from mRNA by reverse

XX transcription using a poly-T primer. The ds cDNA is then digested with a

XX restriction enzyme that generates cohesive ends with overhanging

XX single stranded sequence containing a constant number of nucleotides, and

XX the digestion products are ligated to a set of ds DNA oligonucleotide

XX adaptors. Each adaptor has at one end, a sequence complementary to a

XX possible overhang and the other end a primer-template sequence specific

XX for the adaptor complementary sequence, and between these two ends the

XX same sequence is present for all adaptors. The ligated cDNA molecules are

XX amplified in separate PCR assays, using for each a primer that anneals

XX to polyT and a second primer, from a set that anneals to the cDNA

XX specific primer-template sequences. Amplicons are finally sorted into

XX non-redundant groups defined by the specific primer that annealed to the

XX primer-template sequence and thus primed PCR. The method is useful for

XX producing a collection of non-redundant cDNA groups, especially where

QY 14 tcnatnntnngncantlnc 36

[illegible]

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```
XX 10-MAY-1999; 99JP-0128674.
PF
XX
XX 10-MAY-1999; 99JP-0128674.
PR
XX
XX (SAKA ) OTSUKA PHARM CO LTD.
PA
XX
XX WPI; 2001-184995/19.
DR
XX P-PSDB; AAB46781.
DR
XX
XX A ceramide-combining peptide
PT
XX
XX Disclosure; Page 8; 10pp; Japanese.
PS
XX
XX This invention describes novel ceramide-combining peptides. Such peptides
CC are useful as a tool for elucidating the molecular mechanism of cell
CC signal-transfer and various cell functions and life phenomena accompanied
CC to it.
CC
XX Sequence 45 BP; 5 A; 5 C; 15 G; 20 T; 0 other;
SQ

Query Match 27.8%; Score 12.8; DB 22; Length 45;
Best Local Similarity 43.6%; Pred. No. 5.7e+03;
Matches 17; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Oy 6 gtggnaatcnaatnnnnnncantngcngnagnt 44
    |||| | | | | | | | | | | | | |
Db 4 gtggggcgctattttatgtgttacttttcggatgat 42

RESULT 15
AAZ68716/C
ID AAZ68716 standard; DNA; 47 BP.
XX
XX AAZ68716;
AC
XX
XX 10-SEP-2001 (first entry)
DT
XX
XX Human map-related biallelic marker SEQ ID NO:3067.
DE
XX
XX Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW diagnosis; single nucleotide polymorphism; SNP; ds.
XX
XX Homo sapiens.
OS
XX
XX Location/Qualifiers
FH Key
FT Variation replace(24,G)
FT /tag=a
FT /standard_name="single nucleotide polymorphism"
FT
XX
XX WO9954500-A2.
XX
XX 28-OCT-1999.
PD
XX
XX 21-APR-1999; 99WO-1B00822.
XX
XX 21-APR-1998; 98US-0082614.
XX
XX 23-NOV-1998; 98US-0109732.
XX
XX (GEST ) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX WPI; 2000-013267/01.
XX
XX Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome
XX
XX Claim 3; Page 884; 2745pp; English.
XX
```

```
XX 31-AUG-2001 (first entry)
DT
XX
XX Human prolipoprotein signal peptide 14 probe #1.
DE
XX
XX Human; cytostatic; anti-HIV; immunogenic; antiinflammatory; probe;
KW prolipoprotein signal peptide 14; malignant tumour; haemopathy;
KW HIV infection; immunological disease; inflammation; ss.
XX
XX Homo sapiens.
OS
XX WO200140299-A1.
XX
XX 07-JUN-2001.
PD
XX
XX 27-NOV-2000; 2000WO-CN00514.
PF
XX
XX 30-NOV-1999; 99CN-0124174.
PR
XX
XX (BIOR-) BIROAD GENE DEV LTD SHANGHAI.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2001-374794/39.
DR
XX
XX Human prolipoprotein signal peptide 14 and encoded polynucleotide,
PT applicable in diagnosis and treatment of malignant tumor, hemopathy,
PT HIV infection, immunological diseases and various inflammation
XX
XX Example 6; Page 15; 36pp; Chinese.
XX
XX The present invention relates to human prolipoprotein signal peptide 14
CC and coding sequence (see AAH41269 and AAB91175). The signal peptide and
CC coding sequence are useful in the diagnosis and treatment of malignant
CC tumour, haemopathy, HIV infection, immunological diseases and various
CC inflammation. The present sequence is a probe, which was used in an
CC example from the present invention.
XX
XX Sequence 41 BP; 15 A; 6 C; 8 G; 12 T; 0 other;
SQ

Query Match 27.8%; Score 12.8; DB 22; Length 41;
Best Local Similarity 50.0%; Pred. No. 5.6e+03;
Matches 14; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Oy 9 gnaatcnaatnnnnnncantngc 36
    | | | | | | | | | | | | |
Db 4 gtaaatcagatgattagagacattgc 31

RESULT 14
AAF25923
ID AAF25923 standard; DNA; 45 BP.
XX
XX AAF25923;
AC
XX
XX 19-APR-2001 (first entry)
DT
XX
XX Ceramide affinity peptide CerBP#21 encoding DNA SEQ ID 17.
DE
XX
XX Ceramide; cell signal transfer; cell function; ds.
XX
XX Synthetic.
XX
XX JP2000319296-A.
XX
XX 21-NOV-2000.
PD
```

5

Sequence 47 BP; 15 A; 7 C; 8 G; 17 T; 0 other;

Me

Dh

Search completed: June 20, 2002, 23:09:49
Job time: 30154 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 20, 2002, 23:43:09 ; Search time 66.94 Seconds
(without alignments)
168.795 Million cell updates/sec

Title: US-09-509-234C-1_COPY_1000_1045
Perfect score: 46
Sequence: 1 ngcngtgcgacnctcnaatn.....gncanttcgngnagntat 46

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 506208

Minimum DB seq length: 15
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents.NA.*
1: /cgn2_6/prodata/2/1na/5A_COMB.seq:*
2: /cgn2_6/prodata/2/1na/5B_COMB.seq:*
3: /cgn2_6/prodata/2/1na/6A_COMB.seq:*
4: /cgn2_6/prodata/2/1na/6B_COMB.seq:*
5: /cgn2_6/prodata/2/1na/PCTUS_COMB.seq:*
6: /cgn2_6/prodata/2/1na/backfilssl.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	13.6	29.6	50 4	US-09-315-886C-1 Sequence 1, Appl
2	13.2	28.7	49 1	US-08-484-668B-57 Sequence 57, Appl
3	13.2	28.7	49 4	US-08-463-160B-57 Sequence 13, Appl
4	13.2	28.7	49 5	PCT-US91-02568-13 Sequence 39, Appl
5	13	28.3	33 1	US-08-488-113B-39 Sequence 39, Appl
6	13	28.3	33 1	US-08-477-484B-39 Sequence 39, Appl
7	13	28.3	33 2	US-08-646-360-39 Sequence 39, Appl
8	13	28.3	33 3	US-08-839-765-39 Sequence 39, Appl
9	13	28.3	33 3	US-09-136-389-39 Sequence 39, Appl
10	12.6	27.4	45 2	US-08-596-387B-104 Sequence 104, App
11	12.6	27.4	45 4	US-09-067-615-104 Sequence 104, App
12	12.6	27.4	45 5	PCT-US95-09816A-104 Sequence 104, App
13	12.6	27.4	48 6	RE34606-8 Patent No. RE34,60
14	12.4	27.0	50 1	US-08-088-658-46 Sequence 46, Appl
15	12.4	27.0	50 2	US-08-471-907A-46 Sequence 46, Appl
16	12.2	26.5	30 4	US-09-321-831-12 Sequence 12, Appl
17	12.2	26.5	45 5	PCT-US95-13975-27 Sequence 27, Appl
18	12.2	26.5	49 4	US-08-782-480-91 Sequence 88, Appl
19	12.2	26.5	49 4	US-08-954-211-88 Sequence 104, App
20	12	26.1	38 4	US-09-564-805-104 Sequence 18, Appl
21	12	26.1	48 3	US-07-792-600-18 Sequence 18, Appl
22	12	26.1	48 3	US-09-157-021-18 Sequence 18, Appl
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24	11.8	25.7	50 1	US-08-407-901-91 Sequence 91, Appl
25	11.8	25.7	28 4	US-08-859-998-1075 Sequence 1075, Ap
26	11.8	25.7	28 4	US-09-225-928-1075 Sequence 25, Appl
27	11.8	25.7	37 4	US-09-481-288-25 Sequence 25, Appl
28	11.8	25.7	42 1	US-08-474-542A-250 Sequence 250, App
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31	11.8	25.7	45 3	US-07-998-226F-4 Sequence 4, Appl1
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34	11.8	25.7	46 2	US-08-931-830-4 Sequence 4, Appl1
35	11.8	25.7	46 4	US-09-384-195-4 Sequence 7, Appl1
36	11.8	25.7	47 4	US-09-167-375-7 Sequence 9, Appl1
37	11.8	25.7	49 1	US-08-229-279-9 Sequence 2, Appl1
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39	11.8	25.7	49 1	US-08-608-617-2 Sequence 2, Appl1
40	11.8	25.7	49 2	US-08-931-830-2 Sequence 2, Appl1
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43	11.6	25.2	31 3	US-08-873-437-39 Sequence 446, App
44	11.6	25.2	31 4	US-09-258-754-446 Sequence 13, Appl
45	11.6	25.2	34 2	US-08-627-151A-13 Sequence 9, Appl1
46	11.6	25.2	36 4	US-09-012-097A-9 Sequence 19, Appl
47	11.6	25.2	36 4	US-08-672-213-19 Sequence 63, Appl
48	11.6	25.2	39 4	US-08-169-715-63 Sequence 42, Appl
49	11.6	25.2	25 1	US-08-374-641-42 Sequence 29, Appl
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53	11.4	24.8	26 5	US-09-171-945-119 Sequence 6, Appl1
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56	11.4	24.8	34 4	US-09-445-472-10 Sequence 414, App
57	11.4	24.8	36 1	US-08-411-795B-414 Sequence 25, Appl
58	11.4	24.8	36 1	US-08-469-312A-414 Sequence 6, Appl1
59	11.4	24.8	40 2	US-08-829-876-25 Sequence 9, Appl1
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69	11.2	24.3	41 3	US-08-350-260A-30 Sequence 64, Appl
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75	11.2	24.3	24 6	5180812-3 Sequence 10, Appl
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78	11.2	24.3	33 4	US-09-633-043-18 Sequence 154, App
79	11.2	24.3	36 1	US-08-319-492B-195 Sequence 157, App
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92	10.8	23.5	39 3	US-08-737-708C-29 Sequence 95, Appl
93	10.8	23.5	40 2	US-08-425-684-95 Patent No. 545518
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831	9.6	20.9	37	4	US-09-350-399-65	Sequence 65, App1	c 904	9.6	20.9	50	1	US-08-171-389-20	Sequence 20, App1
832	9.6	20.9	37	5	PCT-US93-11198-509	Sequence 509, App	c 905	9.6	20.9	50	1	US-08-171-389-352	Sequence 352, App
833	9.6	20.9	37	5	PCT-US93-11198-513	Sequence 513, App	c 906	9.6	20.9	50	1	US-08-171-389-534	Sequence 534, App
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843	9.6	20.9	39	3	US-08-470-535-17	Sequence 227, App	c 916	9.6	20.9	50	3	US-08-482-080A-352	Sequence 546, App
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850	9.6	20.9	40	3	US-08-970-740-49	Sequence 49, App1	c 923	9.6	20.9	50	5	PCT-US93-12388-20	Sequence 352, App
851	9.6	20.9	41	1	US-08-721-458B-60	Sequence 60, App1	c 924	9.6	20.9	50	5	PCT-US93-12388-352	Sequence 534, App
852	9.6	20.9	41	1	US-08-268-679E-6	Sequence 6, App1	c 925	9.6	20.9	50	5	PCT-US93-12388-534	Sequence 546, App
853	9.6	20.9	41	1	US-08-231-342-9	Sequence 9, App1	c 926	9.6	20.9	50	5	PCT-US93-12388-546	Sequence 6, App1
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857	9.6	20.9	42	2	US-08-194-981E-63	Sequence 63, App1	c 930	9.6	20.9	50	5	US-08-758-306-443	Sequence 943, App
858	9.6	20.9	42	2	US-08-290-577-7	Sequence 7, App1	c 931	9.6	20.9	50	5	US-08-758-306-458	Sequence 584, App
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ALIGNMENTS

```

sequence 3//, applications/087967
GENERAL INFORMATION:
Patent No. 5827693
APPLICANT: De Angelo, Joseph
APPLICANT: Motwani, Nalini
APPLICANT: Bajwa, Wajeeb
TITLE OF INVENTION: Expressive
TITLE OF INVENTION: Hemoglobin
NUMBER OF SEQUENCES: 71

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ALIGNMENTS

```

sequence 3//, applications/087967
GENERAL INFORMATION:
Patent No. 5827693
APPLICANT: De Angelo, Joseph
APPLICANT: Motwani, Nalini
APPLICANT: Bajwa, Wajeeb
TITLE OF INVENTION: Expressive
TITLE OF INVENTION: Hemoglobin
NUMBER OF SEQUENCES: 71

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RESULT. 3
 US-08-463-160B-57/c
 Sequence 57, Application US/08463160B
 Patent No. 6172039
 GENERAL INFORMATION:
 APPLICANT: De Angelo, Joseph
 APPLICANT: Motwani, Nalini
 APPLICANT: Bajwa, Wajeeh
 TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HEMOGLOBIN
 TITLE OF INVENTION: AND HEMOGLOBIN VARIANTS IN YEAST
 NUMBER OF SEQUENCES: 71
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: Pennie & Edmonds LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,160B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/368,407
FILING DATE: 29-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/876,290
FILING DATE: 29-APR-1992
PRIOR APPLICATION DATA: US 07/684,611
APPLICATION NUMBER: US 07/684,611
FILING DATE: 12-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Flintoft, Gerald J.
REGISTRATION NUMBER: 20,823
REFERENCE/DOCKET NUMBER: 6666-044-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-463-160B-57

Query Match 28.7%; Score 13.2; DB 4; Length 49;
Best Local Similarity 42.9%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

OY 3 cngtggacnctnaatnntnngcancnttngcngnagt 44
DB 47 CTCGTGCACGACTGAGCTTTATGCAATTGATCCAACT 6

RESULT 4
PCT-US91-02568-13/C
Sequence 13, Application PC/TUS9102568
GENERAL INFORMATION:
APPLICANT: De Angelo, Joseph
APPLICANT: Motwani, Nalini M
APPLICANT: Baiwa, Wajeeh
TITLE OF INVENTION: Expression Of Recombinant Hemoglobin
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: N.Y.
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02568
FILING DATE: 19910415
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Flintoft, Gerald J.
REGISTRATION NUMBER: 20,823
REFERENCE/DOCKET NUMBER: 6666-008-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090

TELEFAX: 212 869-9741
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PCT-US91-02568-13

Query Match 28.7%; Score 13.2; DB 5; Length 49;
Best Local Similarity 42.9%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

OY 3 cngtggacnctnaatnntnngcancnttngcngnagt 44
DB 47 CTCGTGCACGACTGAGCTTTATGCAATTGATCCAACT 6

RESULT 5
US-08-488-113B-39/C
Sequence 39, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Stankula, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs

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Query Match          28.3%; Score 13; DB 1; Length 33;
Best Local Similarity 56.5%; Pred. No. 4.1e+02;
Matches 13; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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Qy 14 tcnaatnntnnnnngncanttngc 36
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Db 23 TCAAAATGACTGTGGACAGTTGGC 1

7 RESULT

US-08-646-360-39/c
; Sequence 39, Application US/08646360
: patent No. 5837491

; GENERAL INFORMATION: Marc D.
 ; APPLICANT: Better, Stephen F.
 ; APPLICANT: Carroll, Stephen F.
 ; APPLICANT: Studnika, Gary M.
 ; TITLE OF INVENTION: Immunotoxi
 ; TITLE OF INVENTION: Proteins

```

:
: CORRESPONDENCE ADDRESS:
:
: ADDRESSEE: McAndrews, Held & Malloy, Ltd.
:
: STREET: 500 West Madison Street, 34th floor
:
: CITY: Chicago
:
: STATE: Illinois
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: COUNTRY: USA
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: ZIP: 60661
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FILING DATE: 12-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/064,691
 FILING DATE: 12-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/988,430
 FILING DATE: 09-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/901,707
 FILING DATE: 19-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/787,567
 FILING DATE: 04-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: MCNICHOLAS, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE/DOCKET NUMBER: 200-70-P

ATTORNEY/AGENT INFORMATION:
NAME: Menicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70-P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 39

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Query Match

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Qy      14 tcnatnntnngncantngc 36
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Db      23 TCAATGACTGTGACAGTTGCC 1
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US-08-839-765-39/c
; Sequence 39, Application US/08839765

Patent No 6146631
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studinka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939,765
FILING DATE: 15-APR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-839-765-39

Query Match	28.38;	Score 13;	DB 3;	Length 33;
Best Local Similarity	56.58;	Pred. No. 4.1e+02;		
Matches 13; Conservative		0; Mismatches 10;	Indels 0;	Gaps 0;

QY 14 tcnatnntnngncantngc 36

Db 23 TCAATGACTGTGGACAGTTGCC 1

US-09-136-389-39/c
; Sequence 39, Application US/09136389

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Patent No 6146850
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Bettoli, Stephen F.
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSER: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-136-389-39

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Query Match	28.3%	Score 13;	DB 3;	Length 33;
Best Local Similarity	56.5%;	Pred. No. 4.1e+02;		
Matches 13; Conservative		0; Mismatches 10; Indels 0; Gaps 0;		

QY 14 tcnaatnntnngncanttngc 36
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Db 23 TCAATGACTGTGGACAGTTGCC 1

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RESULT 10
; US-08-596-387B-104
; Sequence 104, Application US/08596387B
; Patent No. 5869270
; GENERAL INFORMATION:
; APPLICANT: Rhode, Peter R.
; APPLICANT: Jiao, Jin-An
; APPLICANT: Burkhardt, Martin
; APPLICANT: Wong, Hing
; TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dade International, Inc.
; STREET: 1717 Deerfield Road
; CITY: Deerfield
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60015
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/596,387B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: PCT/US95/09816
; FILING DATE: 31-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/382,454
; FILING DATE: 01-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/283,302
; FILING DATE: 29-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Pearson, Louise S.
; REGISTRATION NUMBER: 32,369
; REFERENCE/DOCKET NUMBER: STR-4665-CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708) 267-5300
; TELEFAX: (708) 267-5376
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; US-08-596-387B-104

Query Match 27.4%; Score 12.6; DB 2; Leng
Best Local Similarity 48.4%; Pred. No. 7, 5e+02;
Matches 15; Conservative 0; Mismatches 16; Inc

Qy 3 cnggtggnaactnaatnnnnnngpcaatt 33
Db 5 CAGGTGGCACTCCAGACACCCAGGGCCTTT 35

RESULT 11
US-09-067-615-104
; Sequence 104, Application US/09067615
; Patent No. 6309645
; GENERAL INFORMATION:
; APPLICANT: Rhode, Peter R.
; APPLICANT: Jiao, Jin-An
; APPLICANT: Burkhardt, Martin
; APPLICANT: Wong, Hing
; TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF

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us-09-509-234c-1_1000_1045.primer.rn1

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.300
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09816A
FILING DATE: 31-JUL-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/382,454
FILING DATE: 01-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,302
FILING DATE: 29-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Pearson, Louise S.
REGISTRATION NUMBER: 37,369
REFERENCE/DOCKET NUMBER: STR-4665-CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 267-5300
TELEFAX: (708) 267-5376
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
PCT-US95-09816A-104

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	Query Match	Local Similarity	Best Local Similarity	Matches	Conservative	Indels	Gaps
QY	3	cnngtgcgaactcmaactnnnnnnngcatt	33				
db	5	cagctgcacactctccagacacccacagggcccttt	35				

RESULT 13
RE34606-8
PATENT NO. RE34,606
APPLICANT: ESPELL, DAVID A.; WELLS, JAMES A.; BOTT,
RICHARD R.
TITLE OF INVENTION: MODIFIED ENZYMES AND METHODS FOR
MAKING SAME
NUMBER OF SEQUENCES: 27
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/556,918
FILING DATE: 20-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 614,612
FILING DATE: 29-MAY-1984
SEQ ID NO: 8
LENGTH: 48
RE34606-8

Query Match	27.48;	Score 12.6;	DB 6;	Length 48;
Best Local Similarity	46.98;	Pred. No. 7.7e-02;		
Matches 15: Conservative	0;	Mismatches 17;	Indels 0;	Gaps 0;
Qy	8	ggaactcnaactnnmngcancnngcng	39	
	11	11 11 11 11 11 11 11 11		
db	10	ggtaactgcaatggcactccgcacgtgtccgg	41	

RESULT 14
US-08-086-658-46
; Sequence 46, Application US/0808658
; Patent No. 5641625
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; APPLICANT: Buchardt, Ole

APPLICANT: Egholm, Michael
 APPLICANT: Nielsen, Peter E.
 APPLICANT: Berg, Rolf H.
 APPLICANT: M llesgaard, Niels E.
 TITLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE
 TITLE OF INVENTION: NUCLEIC ACIDS
 NUMBER OF SEQUENCES: 56
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5641625riss
 STREET: One Liberty Place - 46th Floor
 City: Philadelphia
 STATE: PA
 COUNTRY: U.S.A.
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/088,658
 FILING DATE: 19930702
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/054,363
 FILING DATE: 26-APRIL-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Luccl, Joseph
 REGISTRATION NUMBER: 33,307
 REFERENCE/DOCKET NUMBER: ISIS-1052
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-568-3100
 TELEFAX: 215-568-3439
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 50
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear

	Query Match	Score	DB 1:	Length	50:
	Best Local Similarity	43.28;	Ped. No. 1e-03;		
	Matches	16;	Conservative	0;	Mismatches
					Indices
					Gaps
Qy	8	ggaacatcmaactmnnngcgttngcgttngat	44		
Db	12	GAAGACGACATTTCTTTAAATTAGCAGGAGAT	48		

RESULT 15
 US-08-471-907A-46
 Sequence 46, Application US/08471907A
 Patent No. 5386053
 GENERAL INFORMATION:
 APPLICANT: Ecker, David J.
 APPLICANT: Buchardt, Ole
 APPLICANT: Echolm, Michael
 APPLICANT: Nielsen, Peter E.
 APPLICANT: Berg, Rolf H.
 APPLICANT: M. Ilegard, Niels E.
 TITLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE
 TITLE OF INVENTION: NUCLEIC ACIDS
 NUMBER OF SEQUENCES: 56
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5986033r1s
 STREET: One Liberty Place - 46th Floor
 CITY: Philadelphia
 STATE: PA
 COUNTRY: U.S.A.
 ZIP: 19103
 COMPUTER READABLE FORM:

us-09-509-234c-l_1000_1045.primer.rni

Fri Jun 21 14:52:00 2002

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/471,907A
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/088,658
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Lucchi, Joseph
 REGISTRATION NUMBER: 33,307
 REFERENCE/DOCKET NUMBER: ISIS-1052
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-568-3100
 TELEFAX: 215-568-3439
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 50
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 US-08-471-907A-46

Query Match 27.0%; Score 12.4; DB 2; Length 50;
 Best Local Similarity 43.2%; Pred. No. 1e+03;
 Matches 16; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

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 Db 12 GAAACAGCATATTTCTTTTAAATATTAGCAGGAGAT 48

Search completed: June 20, 2002, 23:43:22
 Job time: 5182 sec

Fri Jun 21 14:52:02 2002

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Page 1

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2002, 23:05:02 ; Search time 2574.69 Seconds
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241.140 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 88996

Minimum DB seq length: 15
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
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SUMMARIES

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Fri Jun 21 14:52:02 2002

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REFERENCE 1. (bases 1 to 50)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCT, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: adunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0435 row: F column: 20
Seq primer: CACACAGGACACAGCATGACC
Class: plasmid ends
High quality sequence stop: 50.
Location/Qualifiers
1.50
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0435F20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: pMD42hv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi14732114|gb|AF129072.1), a copy-number

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AUI04804 AUI04804
AUI05303 AUI05303
AUI05803 AUI05803
AUI05828 AUI05828
AUI05829 AUI05829
AUI05906 AUI05906
AUI06408 AUI06408
AUI06528 AUI06528
AUI06641 AUI06641
AUI06700 AUI06700
AUI06770 AUI06770
AUI06774 AUI06774
AUI06825 AUI06825
AUI06897 AUI06897
AUI06984 AUI06984
AUI07036 AUI07036
AUI07094 AUI07094
AUI07138 AUI07138
AUI07182 AUI07182
AUI07399 AUI07399
AUI07883 AUI07883
AUI08071 AUI08071
B1860234 603386939
BM069804 189612.Y
BM155745 f26g12.Y
N70569 ze76d10.s1
R70221 Y180F12.r1
R96970 Y462C03.r1
AZ312790 1M0028B20
AZ313593 1M0030B05
AZ514823 1M0361114
AZ795488 2M0049D16
AZ802822 2M0061C23
BH227672 100614ID0
RESULT 1
TA37H07Q 50 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 37h07, reverse sequence,
DEFINITION genomic survey sequence.
ACCESSION AL455404
VERSION AL455404.1 GI:11855590
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 50)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GURAT 10.1) was mechanically sheared
to give a tight size distribution (
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nh@sanger.ac.uk
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers

```

FEATURES

Inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 12 a 10 c 14 g 14 t
ORIGIN

Query Match 31.7%; Score 14.6; DB 12; Length 50;
Best Local Similarity 50.0%; Pred. No. 1.7e+04;
Matches 17; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 2 cgggtgagcactcaatnntnnngcactg 35
DB 17 GCTGTGGAATTCGAACTGATATAGGACTCTG 50

RESULT 3
AZ800459/c 46 bp DNA linear GSS 16-FEB-2001
LOCUS 2M058A04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0058A04 R, DNA sequence.

ACCESSION AZ800459
VERSION AZ800459.1 GI:12952596
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus.

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 46)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Kelly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0058 row: A column: 04
Seq primer: CACACAGAAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 46.

FEATURES

source

1. 46
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_1db="UUGC2M0058A04"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nr; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid RL. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 9 a 14 c 11 g 12 t
ORIGIN

Query Match 31.3%; Score 14.4; DB 12; Length 46;
Best Local Similarity 47.4%; Pred. No. 2e+04;
Matches 18; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 5 ggtgagcactcaatnntnnngcactgag 42
DB 41 GGTGCACTACCTTATATCTACGACTCAGAGCGAG 4

RESULT 4
AJ239756 43 bp mRNA linear EST 10-AUG-1999
LOCUS AJ239756 Aspergillus niger ATCC6275 Aspergillus niger cDNA clone
DEFINITION AN01C03, mRNA sequence.

ACCESSION AJ239756
VERSION AJ239756.1 GI:5443747
KEYWORDS EST.
SOURCE Aspergillus niger.
ORGANISM Aspergillus niger.

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
1 (bases 1 to 43)
AUTHORS Choi,J.Y., Lee,D.W., Koh,J.S., Kim,J.H., Yang,M.S. and Chae,K.S.
TITLE Identification of expressed sequence tags (ESTs) of the highly
transcribed genes in Aspergillus niger
Biotechnol. Lett. 21, 381-384 (1999)

JOURNAL Contact: Chae KS
Faculty of Biological Sciences
Chonbuk National University
Chonju 561-756, Republic of Korea.

COMMENT Location/Qualifiers

1. 43
/organism="Aspergillus niger"
/strain="ATCC6275"
/db_xref="taxon:5061"
/clone_1db="AN01C03"

BASE COUNT 10 a 8 c 7 g 10 t 8 others
ORIGIN

Query Match 29.6%; Score 13.6; DB 9; Length 43;
Best Local Similarity 51.3%; Pred. No. 4.3e+04;
Matches 20; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 3 cnggtgagcactcaatnntnnngcactgag 41
DB 2 CGGCTGATCAATTCAGANNATTTNCCCTTGCCTGNA 40

RESULT 5
BF340017 49 bp mRNA linear EST 22-NOV-2000
LOCUS 602036953p1 NCI CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184917
DEFINITION 5', mRNA sequence.

ACCESSION BF340017
VERSION BF340017.1 GI:11286479
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

REFERENCE 1 (bases 1 to 49)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L149503 row: 1 column: 14
High quality sequence stop: 49.
Location/Qualifiers
1. .49
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI_CGAP_Brn64"
/tissue_type="glioblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: brain; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

FEATURES
source
Query Match 29.6%; Score 13.6; DB 10; Length 49;
Best Local Similarity 50.0%; Pred. No. 4.5e+04;
Matches 16; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 2 gcggtggnactnaatnntnnngcactt 33
| ||||| || | | | | | | | | | |
Db 18 GGTGGTGGCAGTGTCTTCATTCGCCGCCACTT 49

RESULT 6
LOCUS BF340526 49 bp mRNA linear EST 22-NOV-2000
DEFINITION 602037162F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184990
5', mRNA sequence.
ACCESSION BF340526
VERSION BF340526.1 GI:11286988
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 49)
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI_CGAP_Brn64"
/tissue_type="glioblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: brain; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

FEATURES
source
Query Match 29.6%; Score 13.6; DB 10; Length 49;
Best Local Similarity 50.0%; Pred. No. 4.5e+04;
Matches 16; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 2 gcggtggnactnaatnntnnngcactt 33
| ||||| || | | | | | | | | | |
Db 18 GGTGGTGGCAGTGTCTTCATTCGCCGCCACTT 49

RESULT 7
LOCUS A2946842/c 41 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0208M18R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
Clone UUGC2M0208M18 R, DNA sequence.
ACCESSION A2946842
VERSION A2946842.1 GI:13817212
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 41)
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Ti-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative

```

```

/tissue_type="glioblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: brain; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 5 a 16 c 16 g 12 t
ORIGIN

Query Match 29.6%; Score 13.6; DB 10; Length 49;
Best Local Similarity 50.0%; Pred. No. 4.5e+04;
Matches 16; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 2 gcggtggnactnaatnntnnngcactt 33
| ||||| || | | | | | | | | | |
Db 18 GGTGGTGGCAGTGTCTTCATTCGCCGCCACTT 49

RESULT 7
LOCUS A2946842/c 41 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0208M18R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
Clone UUGC2M0208M18 R, DNA sequence.
ACCESSION A2946842
VERSION A2946842.1 GI:13817212
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 41)
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Ti-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative

```

of pMD42 (g114732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT
ORIGIN

9 a 12 c 11 g 9 t

Query Match 29.1%; Score 13.4; DB 12; Length 41;
Best Local Similarity 45.9%; Pred. No. 5.1e+04;
Matches 17; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

OY 6 gtgagacatcnaatnntnngcancntngcngnag 42
|||||
Db 41 GTGGCAGACGCTTTATATCCACACTGTGTAGCAG 5

RESULT 8
A2489704/c 41 bp DNA linear GSS 05-OCT-2000
LOCUS A2489704
DEFINITION 1M0322L14F Mouse 10kb plasmid U06C1M library Mus musculus genomic
ACCESSION A2489704
VERSION A2489704.1 GI:10659714
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 41)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Baecorn, T., Duval, B., Hamli, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0322 row: L column: 14
Seq primer: CGTGTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 41.
Location/Qualifiers
1. 41
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U06C1M0322L14"
/clone_1lb="Mouse 10kb plasmid U06C1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42mv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel

FEATURES
SOURCE

1. 41
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U06C1M0322L14"
/clone_1lb="Mouse 10kb plasmid U06C1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42mv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel

BASE COUNT
ORIGIN

15 a 7 c 12 g 7 t

Query Match 28.7%; Score 13.2; DB 12; Length 41;
Best Local Similarity 51.7%; Pred. No. 6.3e+04;
Matches 15; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 5 gttgagacatcnaatnntnngcancnt 33
|||||
Db 30 GGTGTACATCCTTTATATCCACACTT 2

RESULT 9
AA933930 46 bp mRNA linear EST 23-JUN-1998
LOCUS AA933930
DEFINITION on94909.s1 Soares-NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1564384 3' similar to SW:UAF4_HUMAN P51826 LAF-4 PROTEIN ;,
mRNA sequence.
ACCESSION AA933930
VERSION AA933930.1 GI:3090198
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 46)
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/nciccap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
This clone is available royalty-free through ILNt; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 570 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. 46
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1564384"
/clone_1lb="Soares-NFL_T_GBC_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site.1: Not I; Site.2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBH19W, testis NH7, and B-cell
NCI-GAP GC81) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo.

FEATURES
SOURCE

1. 46
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1564384"
/clone_1lb="Soares-NFL_T_GBC_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site.1: Not I; Site.2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBH19W, testis NH7, and B-cell
NCI-GAP GC81) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo.

BASE COUNT
ORIGIN

9 a 7 c 15 g 15 t

Query Match 28.7%; Score 13.2; DB 9; Length 46;
Best Local Similarity 43.9%; Pred. No. 6.5e+04;
Matches 18; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Best Local Similarity 48.4%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Oy 5 ggtggaactcaatnntnnngcncanting 35
|||||
Db 8 GGTGACACATGCTTAAATCCAGCACTGG 38

RESULT 12

A2769953

43 bp

DNA

linear GSS 16-FEB-2001

LOCUS

DEFINITION

A2769953 1M0571E10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0571E10 F, DNA sequence.

ACCESSION

A2769953

VERSION

A2769953.1

GI:12890633

GSS.

KEYWORDS

SOURCE

ORGANISM

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 43)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly

Islam, H., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.

and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA

Tel.: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0209 row: P column: 13

Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 43.

Location/Qualifiers

1..43

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0571E10"

/clone_1lb="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The ligated DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g114732114[9b]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

ORIGIN

7 a 14 c 13 g 9 t

Query Match 27.4%; Score 12.6; DB 12; Length 43;
Best Local Similarity 41.9%; Pred. No. 1.2e+05;
Matches 18; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Oy 2 gcngatgnaactcaatnntnnngcncanting 44
|||||
Db 1 GCAGCAGATGCTTAAATCCAGCACTGG 43

RESULT 13

A2427403

41 bp

DNA

linear GSS 03-OCT-2000

LOCUS

DEFINITION

A2427403 1M0209P13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0209P13 F, DNA sequence.

ACCESSION

A2427403

VERSION

A2427403.1

GI:10551416

GSS.

KEYWORDS

SOURCE

ORGANISM

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 41)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly

Islam, H., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.

and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

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84112, USA

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Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0209 row: P column: 13

Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 41.

Location/Qualifiers

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/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The ligated DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g114732114[9b]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

ORIGIN

5 a 7 c 11 g 18 t

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0571 row: E column: 10
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 43.
Location/Qualifiers

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/sex="Male"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The ligated DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g114732114[9b]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

ORIGIN

7 a 14 c 13 g 9 t

BASE COUNT
ORIGIN

7 a 14 c 13 g 9 t

BASE COUNT
ORIGIN

5 a 7 c 11 g 18 t

Fri Jun 21 14:52:02 2002

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 50)

REFERENCE AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE

JOURNAL COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0012 row: L column: 13

Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends

High quality sequence stop: 50.
Location/Qualifiers

FEATURES source

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/clone="UUCG1M0012L13"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114[gb]AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 13 a 14 c 6 g 17 t
ORIGIN

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Best Local Similarity 44.4%; Pred. No. 1.5e+05;
Matches 16; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 11 acntcnaatnnnnnnncantngcngnagntat 46
Db 49 AATCAAGGTAAAGCTGTTCATTTGGTGAAGCTGT 14

Search completed: June 20, 2002, 23:05:46
Job time: 31111 sec

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Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 13; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 19 tnnntnnnncantngcngnagnt 44
Db 3 TCTCTGTGTGTCAGTTTTCAGGGAGTT 28

RESULT 14

AW768769 50 bp mRNA linear EST 04-MAY-2000
LOCUS hl53a03.x1 NCI_CGAP_Col4 Homo sapiens cDNA clone IMAGE:3004876 3',
DEFINITION mRNA sequence.

ACCESSION AW768769
VERSION AW768769.1 GI:7700792

KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 50)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-femail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov

Seq primer: -400P from Gibco.

Location/Qualifiers

FEATURES source

1..50
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/db_xref="taxon:9606"
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/clone_lib="NCI_CGAP_Col4"
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/lab_host="DH10B"
/note="Organ: colon; Vector: pCMV-SPORT6; Site:1: SalI;
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.7 kb. Life Technologies catalog #:
11531-019"

BASE COUNT 20 a 5 c 9 g 16 t
ORIGIN

Query Match 27.0%; Score 12.4; DB 9; Length 50;
Best Local Similarity 43.2%; Pred. No. 1.5e+05;
Matches 16; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 9 gnaactcnaatnnnnnnncantngcngnagnta 45
Db 7 GAATATTAAATTTTATTAACTTTCCAGAAAGGTA 43

RESULT 15

AZ308860/c 50 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0012L13F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
DEFINITION clone UUCG1M0012L13 F, DNA sequence.

ACCESSION AZ308860

VERSION AZ308860.1 GI:10349274

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

Fri Jun 21 14:52:02 2002

us-09-509-234c-1_1000_1045.primer.rst

Page 15

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2002, 23:42:29 ; Search time 1932.32 Seconds
(without alignments)
314.063 Million cell updates/sec

Title: US-09-509-234c-1_COPY_1300_1328

Perfect score: 29
Sequence: 1 nnnnnnataattacagagtttaann 29

Scoring table: IDENTITY_NTIC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463368293 residues

Total number of hits satisfying chosen parameters: 663590

Minimum DB seq length: 15
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : GenEmb1:*
1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pal:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pal:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htgo_inv:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query Match Length DB ID Description

1	19	65.5	19	6	A97472	A97472 Sequence 28
2	14	48.3	27	6	AX117627	AX117627 Sequence
3	14	48.3	33	6	AR174977	AR174977 Sequence
4	14	48.3	33	6	AR174978	AR174978 Sequence
5	14	48.3	45	6	AR174999	AR174999 Sequence
6	14	48.3	45	6	AR175000	AR175000 Sequence
7	13	44.8	19	6	AX130141	AX130141 Sequence
8	13	44.8	19	6	AX130142	AX130142 Sequence
9	13	44.8	19	6	AX130143	AX130143 Sequence
10	12.8	44.1	24	6	AR043211	AR043211 Sequence
11	12.8	44.1	24	6	AR050529	AR050529 Sequence
12	12.8	44.1	28	6	AR166684	AR166684 Sequence
13	12.8	44.1	35	6	AR12544	AR12544 polypeptide
14	12.8	44.1	35	6	AR97446	AR97446 polypeptide 2
15	12.8	44.1	25	6	AX117715	AX117715 Sequence
16	12.6	43.4	31	6	AX249110	AX249110 Sequence
17	12.6	43.4	32	6	AX306909	AX306909 Sequence
18	12.6	43.4	46	6	AR032594	AR032594 Sequence
19	12.6	43.4	46	6	I29334	I29334 Sequence 20
20	12.6	43.4	46	6	I91008	I91008 Sequence 20
21	12.6	43.4	46	6	AR038791	AR038791 Sequence
22	12.4	42.8	22	6	AR059677	AR059677 Sequence
23	12.4	42.8	44	6	AR071971	AR071971 Sequence
24	12.4	42.8	44	6	A97447	A97447 Sequence 3
25	12.2	42.1	25	6	AR119427	AR119427 Sequence
26	12.2	42.1	32	6	AR174969	AR174969 Sequence
27	12.2	42.1	39	6	AR048796	AR048796 Sequence
28	12.2	42.1	39	6	AR103237	AR103237 Sequence
29	12.2	42.1	40	6	A83615	A83615 Sequence 44
30	12.2	42.1	40	6	AX249196	AX249196 Sequence
31	12	41.4	31	6	AX040130	AX040130 Sequence
32	12	41.4	20	6	A92003	A92003 Sequence 6
33	11.8	40.7	20	6	AR112676	AR112676 Sequence
34	11.8	40.7	20	6	AX278656	AX278656 Sequence
35	11.8	40.7	24	6	AX155918	AX155918 Sequence
36	11.8	40.7	30	6	AR089388	AR089388 Sequence
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47	11.8	40.7	50	6	AX147901	AX147901 Sequence
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57	11.6	40.0	32	6	AR102833	AR102833 Sequence
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ALIGNMENTS

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LOCUS Sequence 28 from Patent WO9916780.
DEFINITION A97472
ACCESSION A97472
VERSION A97472.1 GI:6780818
KEYWORDS unidentified.
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Gala,J. and Vannuffel,P.
TITLE GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND
JOURNAL DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS
Patent: WO 9916780-A 28 08-APR-1999;
GALA JEAN LOC (BE); UNIV LOUVAIN (BE)
FEATURES Location/Qualifiers

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Db 1 ATGAATTTACAGACTTAA 19
|||||
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AX117627/c 27 bp DNA linear PAT 11-MAY-2001
LOCUS AX117627
DEFINITION Sequence 2750 from Patent WO0129262.
ACCESSION AX117627
VERSION AX117627.1 GI:14034578
KEYWORDS synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 27)
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 2750 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES Location/Qualifiers
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/db_xref="taxon:32630"
/note="primer"
BASE COUNT 5 a 9 c 1 g 12 t
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QY 9 tgaattacacag 22
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Db 19 TGAATTTACAGAG 6
|||||
RESULT 3
AR174977/c 33 bp DNA linear PAT 17-DEC-2001
LOCUS AR174977
DEFINITION Sequence 23 from patent US 6309644.
ACCESSION AR174977
VERSION AR174977.1 GI:17916276
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Chandrashekar,R. and Mehta,K.
TITLE Parasitic nematode transglutaminase proteins and uses thereof
JOURNAL Patent: US 6309644-A 23 30-OCT-2001;
Location/Qualifiers
FEATURES
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/organism="unknown"
BASE COUNT 7 a 10 c 4 g 12 t
ORIGIN
Query Match 48.3%; Score 14; DB 6; Length 33;
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QY 8 atgaattacaga 21
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 Db 33 ATGAATTACAGA 20

RESULT 4
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 LOCUS
 DEFINITION Sequence 24 from patent US 6309644.
 ARI74978
 ACCESSION
 VERSION ARI74978.1 GI:17916277
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 33)
 AUTHORS Chandrasekar, R. and Mehta, K.
 TITLE Parasitic nematode transglutaminase proteins and uses thereof
 JOURNAL Patent: US 6309644-A 24 30-OCT-2001;
 FEATURES Location/Qualifiers
 source 1..33
 BASE COUNT 11 a 7 c 9 g 6 t
 ORIGIN

Query Match 48.3%; Score 14; DB 6; Length 33;
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 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 atgaattacaga 21
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 Db 13 ATGAATTACAGA 26

RESULT 5
 ARI74999 45 bp DNA linear PAT 17-DEC-2001
 LOCUS
 DEFINITION Sequence 51 from patent US 6309644.
 ARI74999
 ACCESSION
 VERSION ARI74999.1 GI:17916298
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 45)
 AUTHORS Chandrasekar, R. and Mehta, K.
 TITLE Parasitic nematode transglutaminase proteins and uses thereof
 JOURNAL Patent: US 6309644-A 51 30-OCT-2001;
 FEATURES Location/Qualifiers
 source 1..45
 BASE COUNT 14 a 5 c 16 g 10 t
 ORIGIN

Query Match 48.3%; Score 14; DB 6; Length 45;
 Best Local Similarity 100.0%; Pred. No. 6.3e+04;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 atgaattacaga 21
 |||||||
 Db 13 ATGAATTACAGA 26

RESULT 6
 ARI75000 45 bp DNA linear PAT 17-DEC-2001
 LOCUS
 DEFINITION Sequence 53 from patent US 6309644.
 ARI75000
 ACCESSION
 VERSION ARI75000.1 GI:17916299
 KEYWORDS

SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.

REFERENCE 1 (bases 1 to 45)
 AUTHORS Chandrasekar, R. and Mehta, K.
 TITLE Parasitic nematode transglutaminase proteins and uses thereof
 JOURNAL Patent: US 6309644-A 53 30-OCT-2001;
 FEATURES Location/Qualifiers
 source 1..45
 BASE COUNT 10 a 16 c 5 g 14 t
 ORIGIN

Query Match 48.3%; Score 14; DB 6; Length 45;
 Best Local Similarity 100.0%; Pred. No. 6.3e+04;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 atgaattacaga 21
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 Db 33 ATGAATTACAGA 20

RESULT 7
 AX130141 19 bp DNA linear PAT 15-MAY-2001
 LOCUS
 DEFINITION Sequence 1359 from Patent WO0130362.
 AX130141
 ACCESSION
 VERSION AX130141.1 GI:14136446
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 19)
 AUTHORS Robbins, J.M. and Tritz, R.
 TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
 JOURNAL Patent: WO 0130362-A 1359 03-MAY-2001;
 FEATURES Location/Qualifiers
 source 1..19
 BASE COUNT 7 a 4 c 3 g 5 t
 ORIGIN

Query Match 44.8%; Score 13; DB 6; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.2e+05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 aattacagagt 24
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 Db 7 AATTACAGGTT 19

RESULT 8
 AX130142 19 bp DNA linear PAT 15-MAY-2001
 LOCUS
 DEFINITION Sequence 1360 from Patent WO0130362.
 AX130142
 ACCESSION
 VERSION AX130142.1 GI:14136447
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 19)
 AUTHORS Robbins, J.M. and Tritz, R.
 TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases

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JOURNAL Patent: WO 0130362-A 1360 03-MAY-2001;
IMMUSOL, INC. (US)

FEATURES
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BASE COUNT 7 a 3 c 4 g 5 t
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 aattacagatt 24
Db 6 AATTACAGATT 18

RESULT 9
LOCUS AX130143 19 bp DNA PAT 15-MAY-2001
DEFINITION Sequence 1361 from Patent WO0130362.
ACCESSION AX130143
VERSION AX130143.1 GI:14136448
KEYWORDS human.
SOURCE

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 1361 03-MAY-2001;
IMMUSOL, INC. (US)

FEATURES
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="Cdk-we-hu ribozyme binding site"

BASE COUNT 7 a 3 c 4 g 5 t
ORIGIN

Query Match 44.8%; Score 13; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 aattacagatt 24
Db 5 AATTACAGATT 17

RESULT 10
LOCUS AR043211/c 24 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 95 from patent US 5814453.
ACCESSION AR043211
VERSION AR043211.1 GI:5964219
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Beck,J.Joseph.
TITLE Detection of fungal pathogens using the polymerase chain reaction
JOURNAL Patent: US 5814453-A 95 29-SEP-1998;
FEATURES Location/Qualifiers
source 1. .24
/organism="unknown"

BASE COUNT 7 a 4 c 2 g 11 t

ORIGIN

Query Match 44.1%; Score 12.8; DB 6; Length 24;
Best Local Similarity 87.5%; Pred. No. 2.5e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 11 aaattacagagttaa 26
Db 17 AAATTACAGAGTTTA 2

RESULT 11
LOCUS AR050529 24 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 15 from patent US 5827695.
ACCESSION AR050529
VERSION AR050529.1 GI:5973254
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Beck,J.Joseph.
TITLE Detection of wheat fungal pathogens using the polymerase chain reaction
JOURNAL Patent: US 5827695-A 15 27-OCT-1998;
FEATURES Location/Qualifiers
source 1. .24
/organism="unknown"

BASE COUNT 7 a 4 c 2 g 11 t
ORIGIN

Query Match 44.1%; Score 12.8; DB 6; Length 24;
Best Local Similarity 87.5%; Pred. No. 2.5e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 11 aaattacagagttaa 26
Db 17 AAATTACAGAGTTTA 2

RESULT 12
LOCUS AR166684 28 bp DNA PAT 17-OCT-2001
DEFINITION Sequence 34 from patent US 6281346.
ACCESSION AR166684
VERSION AR166684.1 GI:16242098
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Hess,J.W., Caskey,C.Thomas., Liu,Q. and Phillips,M.Sea.
TITLE Rat ob-receptors and nucleotides encoding them
JOURNAL Patent: US 6281346-A 34 28-AUG-2001;
FEATURES Location/Qualifiers
source 1. .28
/organism="unknown"

BASE COUNT 12 a 6 c 4 g 6 t
ORIGIN

Query Match 44.1%; Score 12.8; DB 6; Length 28;
Best Local Similarity 87.5%; Pred. No. 2.4e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 11 aaattacagagttaa 26
Db 6 AAATTACAGAGTTAA 21

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RESULT 13
LOCUS A12544 35 bp DNA linear PAT 07-DEC-1993
DEFINITION polypeptide actin.
ACCESSION A12544
VERSION A12544.1 GI:491391
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 35)
AUTHORS
TITLE ENHANCED SECRETION OF HETEROLOGOUS PROTEINS BY HOSTS USING
SUBSTITUTED PROMOTERS
JOURNAL Patent: WO 8703300-A 15 04-JUN-1987;
FEATURES
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/db_xref="taxon:32630"
BASE COUNT 13 a 4 c 7 g 11 t
ORIGIN

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Best Local Similarity 87.5%; Pred. No. 2.3e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 aaattacagagtaa 26
||||| |||||
DB 7 AAATTACTGAATTAA 22

RESULT 14
LOCUS A97446 35 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 2 from Patent WO916780.
ACCESSION A97446
VERSION A97446.1 GI:6780792
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 35)
AUTHORS Gala,J. and Vannuffel,P.
TITLE GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND
DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS
JOURNAL Patent: WO 916780-A 2 08-APR-1999;
GALA JEAN LUC (BE); UNIV LOUVAIN (BE)
FEATURES
source 1..35
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 12 a 3 c 3 g 9 t 8 others
ORIGIN

Query Match 44.1%; Score 12.8; DB 6; Length 35;
Best Local Similarity 73.7%; Pred. No. 2.3e+05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 8 atgaattacagagtaa 26
||||| ||||| |||
DB 4 ATGAATTACNAATTNA 22

RESULT 15
LOCUS A12546 39 bp DNA linear PAT 07-DEC-1993
DEFINITION polypeptide pex-8.
ACCESSION A12546
VERSION A12546.1 GI:491393
KEYWORDS
SOURCE synthetic construct.

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ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 39)
AUTHORS
TITLE ENHANCED SECRETION OF HETEROLOGOUS PROTEINS BY HOSTS USING
SUBSTITUTED PROMOTERS
JOURNAL Patent: WO 8703300-A 17 04-JUN-1987;
FEATURES
source 1..39
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 15 a 5 c 6 g 13 t
ORIGIN

Query Match 44.1%; Score 12.8; DB 6; Length 39;
Best Local Similarity 87.5%; Pred. No. 2.2e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 aaattacagagtaa 26
||||| ||||| |||
DB 7 AAATTACTGAATTAA 22

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Search completed: June 20, 2002, 23:42:42
 Job time: 17387 sec

us-09-509-234c-1_1300_1328.primer.rge

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2002, 23:09:49 ; Search time 286.45 Seconds

(Without alignments)
173.819 Million cell updates/sec

Title: US-09-509-234c-1_COPY_1300_1328
Sequence: 1 nnnnnnataaattacagagtaann 29

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Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1042728

Minimum DB seq length: 15
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Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	65.5	19	AA33776	Staphylococcus sp.
2	62.1	29	AA33792	Staphylococcus sp.
3	48.3	27	AA33954	SNP specific lower
4	48.3	33	AA33029	Dicofilaria immiti
5	48.3	33	AA33030	Dicofilaria immiti
6	48.3	33	AA33037	D. immitis transgl
7	48.3	33	AA33038	D. immitis transgl
8	48.3	45	AA33039	D. immitis transgl
9	48.3	45	AA33040	Complementary stra

10	13.4	46.2	15	AA33714	IGF-1 oligonucleot
11	13	44.8	19	AA33773	cdk-we-hu ribozyme
12	13	44.8	21	AA33774	cdk-we-hu ribozyme
13	13	44.8	19	AA33775	cdk-we-hu ribozyme
14	13	44.8	19	AA33776	cdk-we-hu ribozyme
15	13	44.8	19	AA33777	cdk-we-hu ribozyme
16	13	44.8	19	AA33778	cdk-we-hu ribozyme
17	13	44.8	19	AA33779	cdk-we-hu ribozyme
18	13	44.8	19	AA33780	cdk-we-hu ribozyme
19	13	44.8	19	AA33781	cdk-we-hu ribozyme
20	13	44.8	19	AA33782	cdk-we-hu ribozyme
21	13	44.8	19	AA33783	cdk-we-hu ribozyme
22	13	44.8	19	AA33784	cdk-we-hu ribozyme
23	13	44.8	19	AA33785	cdk-we-hu ribozyme
24	13	44.8	19	AA33786	cdk-we-hu ribozyme
25	13	44.8	19	AA33787	cdk-we-hu ribozyme
26	13	44.8	19	AA33788	cdk-we-hu ribozyme
27	13	44.8	19	AA33789	cdk-we-hu ribozyme
28	13	44.8	19	AA33790	cdk-we-hu ribozyme
29	13	44.8	19	AA33791	cdk-we-hu ribozyme
30	13	44.8	19	AA33792	cdk-we-hu ribozyme
31	13	44.8	19	AA33793	cdk-we-hu ribozyme
32	13	44.8	19	AA33794	cdk-we-hu ribozyme
33	13	44.8	19	AA33795	cdk-we-hu ribozyme
34	13	44.8	19	AA33796	cdk-we-hu ribozyme
35	13	44.8	19	AA33797	cdk-we-hu ribozyme
36	13	44.8	19	AA33798	cdk-we-hu ribozyme
37	13	44.8	19	AA33799	cdk-we-hu ribozyme
38	13	44.8	19	AA33800	cdk-we-hu ribozyme
39	13	44.8	19	AA33801	cdk-we-hu ribozyme
40	13	44.8	19	AA33802	cdk-we-hu ribozyme
41	13	44.8	19	AA33803	cdk-we-hu ribozyme
42	13	44.8	19	AA33804	cdk-we-hu ribozyme
43	13	44.8	19	AA33805	cdk-we-hu ribozyme
44	13	44.8	19	AA33806	cdk-we-hu ribozyme
45	13	44.8	19	AA33807	cdk-we-hu ribozyme
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78	13	44.8	19	AA33840	cdk-we-hu ribozyme
79	13	44.8	19	AA33841	cdk-we-hu ribozyme
80	13	44.8	19	AA33842	cdk-we-hu ribozyme
81	13	44.8	19	AA33843	cdk-we-hu ribozyme
82	13	44.8	19	AA33844	cdk-we-hu ribozyme

us-09-509-234c-1_1300_1328.primer.rng

Fri Jun 21 14:52:03 2002

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667	AAA06064	26	10.2	35.2	+	2500	10.2	740	10.2	35.2	+	2500	10.2	
668	AAH01446	26	10.2	35.2	+	2500	10.2	741	10.2	35.2	+	2500	10.2	
669	PAC92034	26	10.2	35.2	+	2500	10.2	742	10.2	35.2	+	2500	10.2	
670	AAH19132	26	10.2	35.2	+	2500	10.2	743	10.2	35.2	+	2500	10.2	
671	AAH23002	27	10.2	35.2	+	2500	10.2	744	10.2	35.2	+	2500	10.2	
672	AAH2936	27	10.2	35.2	+	2500	10.2	745	10.2	35.2	+	2500	10.2	
673	AAH24241	27	10.2	35.2	+	2500	10.2	746	10.2	35.2	+	2500	10.2	
674	AAH10670	28	10.2	35.2	+	2500	10.2	747	10.2	35.2	+	2500	10.2	
675	AAH09946	28	10.2	35.2	+	2500	10.2	748	10.2	35.2	+	2500	10.2	
676	AAH38782	28	10.2	35.2	+	2500	10.2	749	10.2	35.2	+	2500	10.2	
677	AAH37598	28	10.2	35.2	+	2500	10.2	750	10.2	35.2	+	2500	10.2	
678	AAH28067	28	10.2	35.2	+	2500	10.2	751	10.2	35.2	+	2500	10.2	
679	AAH24875	28	10.2	35.2	+	2500	10.2	752	10.2	35.2	+	2500	10.2	
680	AAH04421	29	10.2	35.2	+	2500	10.2	753	10.2	35.2	+	2500	10.2	
681	AAH20168	29	10.2	35.2	+	2500	10.2	754	10.2	35.2	+	2500	10.2	
682	AAH14301	29	10.2	35.2	+	2500	10.2	755	10.2	35.2	+	2500	10.2	
683	AAH04138	30	10.2	35.2	+	2500	10.2	756	10.2	35.2	+	2500	10.2	
684	AAH02533	30	10.2	35.2	+	2500	10.2	757	10.2	35.2	+	2500	10.2	
685	AAH60583	30	10.2	35.2	+	2500	10.2	758	10.2	35.2	+	2500	10.2	
686	AAH34723	30	10.2	35.2	+	2500	10.2	759	10.2	35.2	+	2500	10.2	
687	AAH27311	30	10.2	35.2	+	2500	10.2	760	10.2	35.2	+	2500	10.2	
688	AAH07496	30	10.2	35.2	+	2500	10.2	761	10.2	35.2	+	2500	10.2	
689	AAH64644	30	10.2	35.2	+	2500	10.2	762	10.2	35.2	+	2500	10.2	
690	AAH05882	30	10.2	35.2	+	2500	10.2	763	10.2	35.2	+	2500	10.2	
691	AAH17951	30	10.2	35.2	+	2500	10.2	764	10.2	35.2	+	2500	10.2	
692	AAH16728	30	10.2	35.2	+	2500	10.2	765	10.2	35.2	+	2500	10.2	
693	AAH95863	30	10.2	35.2	+	2500	10.2	766	10.2	35.2	+	2500	10.2	
694	AAH11129	30	10.2	35.2	+	2500	10.2	767	10.2	35.2	+	2500	10.2	
695	AAH63028	30	10.2	35.2	+	2500	10.2	768	10.2	35				

813	10	34.5	21	19	AAV5153	Homo sapiens P-TEN
814	10	34.5	21	22	AAV58995	FKHf gene specific
815	10	34.5	21	22	AAV57105	Human gene single
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817	10	34.5	22	19	AAO9780	Bacillus thuringie
818	10	34.5	22	19	AAO9754	Bacillus thuringie
819	10	34.5	22	22	AAO82441	Zmxi gene region
820	10	34.5	22	22	AAO7059	Pig c-KIT gene PCR
821	10	34.5	23	18	AAO1233	Cellular apoptosis
822	10	34.5	23	19	AAV57862	Human chromosome 1
823	10	34.5	23	20	AAV72653	Streptococcus pneu
824	10	34.5	23	22	AAO9739	Immunostimulatory
825	10	34.5	23	22	AAO9739	Immunostimulatory
826	10	34.5	24	14	AAO52020	B-cell mRNA ribozy
827	10	34.5	24	18	AAO47419	Primer #2 for ganc
828	10	34.5	24	19	AAV24211	Homo sapiens BARD1
829	10	34.5	24	21	AAO6760	Dog genomic marker
830	10	34.5	24	22	AAO5088	Mutagenic primer (
831	10	34.5	25	12	AAO91956	T-cell receptor pr
832	10	34.5	25	16	AAO91956	Primer B (Group 13
833	10	34.5	25	16	AAO91956	Aequorea victoria
834	10	34.5	25	18	AAO92753	Bacillus thuringie
835	10	34.5	25	19	AAO92753	Bacillus thuringie
836	10	34.5	25	19	AAO92753	Bacillus thuringie
837	10	34.5	25	21	AAO6729	B. thuringiensis p
838	10	34.5	25	21	AAO6729	B. thuringiensis p
839	10	34.5	25	21	AAO6729	B. thuringiensis p
840	10	34.5	25	21	AAO6729	B. thuringiensis p
841	10	34.5	25	21	AAO6729	B. thuringiensis p
842	10	34.5	25	21	AAO6729	B. thuringiensis p
843	10	34.5	25	21	AAO6729	B. thuringiensis p
844	10	34.5	25	21	AAO6729	B. thuringiensis p
845	10	34.5	25	21	AAO6729	B. thuringiensis p
846	10	34.5	25	21	AAO6729	B. thuringiensis p
847	10	34.5	25	21	AAO6729	B. thuringiensis p
848	10	34.5	25	21	AAO6729	B. thuringiensis p
849	10	34.5	25	21	AAO6729	B. thuringiensis p
850	10	34.5	25	21	AAO6729	B. thuringiensis p
851	10	34.5	25	21	AAO6729	B. thuringiensis p
852	10	34.5	25	21	AAO6729	B. thuringiensis p
853	10	34.5	25	21	AAO6729	B. thuringiensis p
854	10	34.5	25	21	AAO6729	B. thuringiensis p
855	10	34.5	25	21	AAO6729	B. thuringiensis p
856	10	34.5	25	21	AAO6729	B. thuringiensis p
857	10	34.5	25	21	AAO6729	B. thuringiensis p
858	10	34.5	25	21	AAO6729	B. thuringiensis p
859	10	34.5	25	21	AAO6729	B. thuringiensis p
860	10	34.5	25	21	AAO6729	B. thuringiensis p
861	10	34.5	25	21	AAO6729	B. thuringiensis p
862	10	34.5	25	21	AAO6729	B. thuringiensis p
863	10	34.5	25	21	AAO6729	B. thuringiensis p
864	10	34.5	25	21	AAO6729	B. thuringiensis p
865	10	34.5	25	21	AAO6729	B. thuringiensis p
866	10	34.5	25	21	AAO6729	B. thuringiensis p
867	10	34.5	25	21	AAO6729	B. thuringiensis p
868	10	34.5	25	21	AAO6729	B. thuringiensis p
869	10	34.5	25	21	AAO6729	B. thuringiensis p
870	10	34.5	25	21	AAO6729	B. thuringiensis p
871	10	34.5	25	21	AAO6729	B. thuringiensis p
872	10	34.5	25	21	AAO6729	B. thuringiensis p
873	10	34.5	25	21	AAO6729	B. thuringiensis p
874	10	34.5	25	21	AAO6729	B. thuringiensis p
875	10	34.5	25	21	AAO6729	B. thuringiensis p
876	10	34.5	25	21	AAO6729	B. thuringiensis p
877	10	34.5	25	21	AAO6729	B. thuringiensis p
878	10	34.5	25	21	AAO6729	B. thuringiensis p
879	10	34.5	25	21	AAO6729	B. thuringiensis p
880	10	34.5	25	21	AAO6729	B. thuringiensis p
881	10	34.5	25	21	AAO6729	B. thuringiensis p
882	10	34.5	25	21	AAO6729	B. thuringiensis p
883	10	34.5	25	21	AAO6729	B. thuringiensis p
884	10	34.5	25	21	AAO6729	B. thuringiensis p
885	10	34.5	25	21	AAO6729	B. thuringiensis p

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c 959 10 34.5 43 20 AAX91971
 c 960 10 34.5 43 21 AAA44765
 c 961 10 34.5 43 22 AAX56268
 c 962 10 34.5 44 16 AAX94911
 c 963 10 34.5 44 16 AAX94912
 c 964 10 34.5 44 20 AAX07741
 c 965 10 34.5 44 22 AAD18014
 c 966 10 34.5 45 17 AAT27250
 c 967 10 34.5 45 17 AAT18488
 c 968 10 34.5 45 22 AAX90926
 c 969 10 34.5 45 22 AAC89589
 c 970 10 34.5 46 17 AAT27347
 c 971 10 34.5 46 20 AAZ23234
 c 972 10 34.5 46 22 AAD09000
 c 973 10 34.5 46 22 AAD09028
 c 974 10 34.5 46 22 AAH41738
 c 975 10 34.5 47 15 AAX69399
 c 976 10 34.5 47 18 AAX63861
 c 977 10 34.5 47 20 AAZ01052
 c 978 10 34.5 47 20 AAX17149
 c 979 10 34.5 47 21 AAZ65974
 c 980 10 34.5 47 21 AAZ66334
 c 981 10 34.5 47 21 AAZ66376
 c 982 10 34.5 47 21 AAZ66481
 c 983 10 34.5 47 21 AAZ66566
 c 984 10 34.5 47 21 AAZ66641
 c 985 10 34.5 47 21 AAZ66676
 c 986 10 34.5 47 21 AAZ66705
 c 987 10 34.5 47 21 AAZ66749
 c 988 10 34.5 47 21 AAZ66890
 c 989 10 34.5 47 21 AAZ67155
 c 990 10 34.5 47 21 AAZ67637
 c 991 10 34.5 47 21 AAZ67785
 c 992 10 34.5 47 21 AAZ67814
 c 993 10 34.5 47 21 AAZ67823
 c 994 10 34.5 47 21 AAZ67865
 c 995 10 34.5 47 21 AAZ67902
 c 996 10 34.5 47 21 AAZ67933
 c 997 10 34.5 47 21 AAZ67981
 c 998 10 34.5 47 21 AAZ68082
 c 999 10 34.5 47 21 AAZ68508
 1000 10 34.5 47 21 AAZ68679

ALIGNMENTS

RESULT 1
 AAX37776
 ID AAX37776 standard; DNA; 19 BP.
 XX
 AC AAX37776;
 XX
 DT 09-JUL-1999 (first entry)
 XX
 DE Staphylococcus sp. detecting oligonucleotide femA1.
 XX
 KW femA; primer; identification; detection; therapy; infection; femB;
 KW amplification; genotyping; gram-positive bacteria; vaccine; ss.
 XX
 OS Synthetic.
 XX Staphylococcus sp.
 XX WO9916780-A2.
 XX
 PN 08-APR-1999.
 XX
 PD 28-SEP-1998; 98WO-BE00141.
 XX
 PF 26-SEP-1997; 97EP-0870146.
 XX
 PR (BENA-) BELGIAN MIN NAT DEFENCE.
 XX (UYLO-) UNIV CATHOLIQUE LOUVAIN.
 PA

XX Gala J, Vannuffel P;
 PI WPI; 1999-287521/24.
 XX
 DR New Staphylococcus-specific oligonucleotides
 XX
 PT Claim 5; Page 9; 48pp; English.
 XX
 PS This invention describes novel Staphylococcus-specific oligonucleotides
 CC based on the consensus femA nucleotide sequence which are used to
 CC develop products for the identification, detection and therapy of
 CC infections. The oligonucleotides can be used for the genetic
 CC amplification, the identification and/or quantification of various femA
 CC sequences which are specific to known or unknown Staphylococci species.
 CC Since the femA sequence is similar to the femB sequence, the
 CC oligonucleotides can also be used for the molecular genotyping of femB
 CC genes of different Staphylococci species or other gram-positive bacteria.
 CC The femA nucleic acids can also be used in therapeutic applications.
 CC They can also be used to identify inhibitors, e.g. antibodies or
 CC antisense oligonucleotides, for blocking expression of the femA
 CC nucleotide sequences. They can also be used for producing vaccines
 CC against Staphylococci infections.
 XX
 SQ Sequence 19 BP; 9 A; 1 C; 3 G; 6 T; 0 other;
 Query Match 65.5%; Score 19; DB 20; Length 19;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 8 atgaattacagaggttaa 26
 DB 1 atgaattacagaggttaa 19
 |||||
 RESULT 2
 AAX37792/C
 ID AAX37792 standard; DNA; 29 BP.
 XX
 AC AAX37792;
 XX
 DT 09-JUL-1999 (first entry)
 XX
 DE Staphylococcus sp. detecting oligonucleotide 27.
 XX
 KW femA; primer; identification; detection; therapy; infection; femB;
 KW amplification; genotyping; gram-positive bacteria; vaccine; ss.
 XX
 OS Synthetic.
 XX Staphylococcus sp.
 XX WO9916780-A2.
 XX
 PN 08-APR-1999.
 XX
 PD 28-SEP-1998; 98WO-BE00141.
 XX
 PF 26-SEP-1997; 97EP-0870146.
 XX
 PR (BENA-) BELGIAN MIN NAT DEFENCE.
 XX (UYLO-) UNIV CATHOLIQUE LOUVAIN.
 XX
 PI Gala J, Vannuffel P;
 XX
 DR WPI; 1999-287521/24.
 XX
 PT New Staphylococcus-specific oligonucleotides
 XX
 PS Example 1; Fig 1; 48pp; English.
 XX
 CC This invention describes novel Staphylococcus-specific oligonucleotides
 CC based on the consensus femA nucleotide sequence which are used to

CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC amygallobulinemia, diabetes insipidus, Leisch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC diseases of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a PCR primer specific
CC for a human SNP containing DNA sequence.
XX
Sequence 27 BP; 5 A; 9 C; 1 G; 12 T; 0 other;

Query Match	48.3%	Score 14	DB 22	Length 27
Best Local Similarity	100.0%	Pred. No. 2.4e+03		
Matches 14	Conservative 0	Mismatches 0	Indels 0	Gaps 0
OY	9 tgaattacagag 22			
cb	19 tcaaatTTACAGG 6			

RESULT : 4
AAV33029/C
ID AAV33029 standard; cDNA; 33 BP.
XX
XX AAV33029;
XX
XX
DT 18-NOV-1998 (first entry)
DE
XX Dirofilaria immitis transglutaminase DNA nd1G143 antisense primer.
XX
XX
XX Dirofilaria immitis transglutaminase; TG; parasitic nematode infection;
KM Brugia malayi transglutaminase; Onchocerca volvulus transglutaminase;
XX PCR; primer; amplification; ss.
XX
OS Synthetic.
XX Dirofilaria immitis.
XX
PN M09824887-R2.
XX
ED 11-JUN-1998.
XD
PF 02-DEC-1997; 97MO-US21999.
XX
PR 03-DEC-1996; 96US-0781420.
XX
PA (HESK-) HESKA CORP.
XX Chandrashekar R, Mehta K;
PI WPI: 1998-33309/29.
XX
DR
XX New isolated parasitic nematode transglutaminase genes - used to
PT develop products for the detection, prevention and treatment of
PT Infections by parasitic nematodes
XX
PS Example 10; Page 63; 12pp; English.

The antisense and sense (AAV33028) primers were used to amplify
CC A dirofilaria immitis transglutaminase (TG) DNA molecule, denoted
CC nd1G143, from D. immitis adult female cDNA. The sequence of nd1G143
CC was found to overlap with that of nd1G1472 (see AAV33025-V33027) and
CC nd1G1407 (see AAV33030 and AAV33031), allowing the construction of a
CC full length D. immitis TG encoding DNA sequence denoted as nd1G1881
CC (AAV33017 and AAV33033). The nd1G1881 DNA sequence encodes a 495
CC residue TG protein (AAM70270). The invention also claims for TG protein
CC sequences and the corresponding DNA sequences encoding these proteins

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC isolated from Brugia malayi (AAV33018, AAV33019, AAW70271 and AAW70272)
 CC and Onchocerca volvulus (AAV33020 and AAW70273). The nematode TG DNA and
 CC protein sequences are claimed to be useful for the diagnosis, prevention
 CC and treatment of parasitic nematode infection.

XX Sequence 33 BP; 7 A; 10 C; 4 G; 12 T; 0 other;

Query Match 48.3%; Score 14; DB 19; Length 33;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 atgaattacaga 21
 |||||
 Db 33 ATGAATTACAGA 20

RESULT 5
 AAV33030
 ID AAV33030 standard; cDNA; 33 BP.

XX AAV33030;

XX 18-NOV-1998 (first entry)

DT Dirofilaria immitis transglutaminase DNA nDITG1407 sense primer.

XX Dirofilaria immitis transglutaminase; TG; parasitic nematode infection;
 XX Brugia malayi transglutaminase; Onchocerca volvulus transglutaminase;
 KW PCR; primer; amplification; ss.

XX Synthetic.

XX Dirofilaria immitis.

XX WO9824887-A2.

XX 11-JUN-1998.

XX 02-DEC-1997; 97WO-US21999.

XX 03-DEC-1996; 96US-0781420.

XX (HESK-) HESKA CORP.

XX Chandrashekar R, Mehta K;

XX WPI; 1998-333309/29.

XX New isolated parasitic nematode transglutaminase genes - used to
 PT develop products for the detection, prevention and treatment of
 PT infections by parasitic nematodes

XX Example 11; Page 64; 129pp; English.

XX The sense and antisense (AAV33031) primers were used to amplify
 CC a Dirofilaria immitis transglutaminase (TG) DNA molecule, denoted
 CC nDITG1407, from D. immitis adult female cDNA. The sequence of
 CC nDITG1407 was found to overlap with that of nDITG1472 (see AAV33025-
 CC AAV33027) and nDITG143 (see AAV33028 and AAV33029), allowing the
 CC construction of a full length D. immitis TG encoding DNA sequence
 CC as nDITG1881 (AAV33017 and AAV33033). The invention also claims for TG
 CC a 495 residue TG protein (AAW70270). The nDITG1881 DNA sequence
 CC protein sequences and the corresponding DNA sequences encoding these
 CC proteins isolated from Brugia malayi (AAV33018, AAV33019, AAW70271 and
 CC AAW70272) and Onchocerca volvulus (AAV33020 and AAW70273). The nematode
 CC TG DNA and protein sequences are claimed to be useful for the diagnosis,
 CC prevention and treatment of parasitic nematode infection.

XX Sequence 33 BP; 11 A; 7 C; 9 G; 6 T; 0 other;

Query Match 48.3%; Score 14; DB 19; Length 33;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;

RESULT 6

AAI67837/C

ID AAI67837 standard; DNA; 33 BP.

XX AAI67837;

XX 27-FEB-2002 (first entry)

DT D. immitis transglutaminase cDNA amplifying antisense primer.

XX Transglutaminase protein; disulfide isomerase; antiparasite; vaccine;
 KW nematode; heartworm; PCR primer; ss.

XX Dirofilaria immitis.

XX US6309644-B1.

XX 30-OCT-2001.

XX 12-JUN-1997; 97US-0874102.

XX 03-DEC-1996; 96US-0781420.

XX (HESK-) HESKA CORP.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Chandrashekar R, Mehta K;

XX WPI; 2002-040231/05.

XX Novel Dirofilaria immitis transglutaminase protein which also has
 PT protein disulfide isomerase activity, used to identify transglutaminase
 PT activity inhibitors that are useful for protecting animals from
 PT heartworm

XX Example 10; Column 43; 66pp; English.

XX The invention relates to parasitic nematode transglutaminase proteins and
 CC polynucleotides encoding them. The transglutaminase proteins are useful
 CC for identifying a compound capable of inhibiting transglutaminase or
 CC protein disulfide isomerase activity. The proteins represent novel
 CC targets for antiparasite vaccines and drugs. The products inhibit the
 CC crucial steps in nematode molting that involve nematode transglutaminase.
 CC The proteins are also useful for preventing an animal (a dog) from
 CC heartworm, a disease condition caused by D. immitis. The nematode protein
 CC disulfide isomerase or transglutaminase activity inhibitors identified
 CC are useful for protecting an animal from heartworm. The proteins are
 CC useful as diagnostic agents to detect infection by parasitic nematodes.
 CC Sequences AAI67836-39 represent PCR primers for amplifying nematode
 CC transglutaminase nucleic acid molecules from D. immitis female adult
 CC cDNA library.

XX Sequence 33 BP; 7 A; 10 C; 4 G; 12 T; 0 other;

Query Match 48.3%; Score 14; DB 24; Length 33;

Best Local Similarity 100.0%; Pred. No. 2.5e+03; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 atgaattacaga 21

|||||

Db 33 ATGAATTACAGA 20

RESULT 7

AAI67838

```

ID  AA167838 standard; DNA; 33 BP.
XX
XX  AA167838;
AC
XX  27-FEB-2002 (first entry)
DT
XX
XX  D. immitis transglutaminase cDNA amplifying sense primer.
DE
XX
XX  Transglutaminase protein; disulfide isomerase; antiparasite; vaccine;
KW  nematode; heartworm; PCR primer; ss.
XX
XX  Dirofilaria immitis.
OS
XX  US6309644-B1.
PN
XX  30-OCT-2001.
PD
XX  12-JUN-1997; 97US-0874102.
PF
XX  03-DEC-1996; 96US-0781420.
PR
XX
XX  (HESK-) HESKA CORP.
PA  (TEXA ) UNIV TEXAS SYSTEM.
XX
XX  Chandrashekar R, Mehra K;
PI
XX  WPI; 2002-040231/05.
DR
XX
XX  Novel Dirofilaria immitis transglutaminase protein which also has
PT  protein disulfide isomerase activity, used to identify transglutaminase
PT  activity inhibitors that are useful for protecting animals from
PT  heartworm
XX
XX  Example 11; Column 43; 66pp; English.
PS
XX  The invention relates to parasitic nematode transglutaminase proteins and
XX  polynucleotides encoding them. The transglutaminase proteins are useful
XX  for identifying a compound capable of inhibiting transglutaminase or
XX  protein disulfide isomerase activity. The proteins represent novel
XX  targets for antiparasite vaccines and drugs. The products inhibit the
XX  crucial steps in nematode molting that involve nematode transglutaminase.
XX  Transglutaminase, a disease condition caused by D. immitis. The nematode protein
XX  disulfide isomerase or transglutaminase activity inhibitors identified
XX  are useful for protecting an animal from heartworm. The proteins are
XX  are useful as diagnostic agents to detect infection by parasitic nematodes.
XX  Sequences AA167835-39 represent PCR primers for amplifying nematode
XX  transglutaminase nucleic acid molecules from D. immitis female adult
XX  cDNA library.
XX
XX  Sequence 33 BP; 11 A; 7 C; 9 G; 6 T; 0 other;
SO

```

```

Query Match      48.3%; Score 14; DB 24; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY  8 atgaattacaga 21
    |||
DB  13 atgaattacaga 26

```

RESULT 8

AA167859 standard; cDNA; 45 BP.

```

XX
XX  AA167859;
AC
XX  27-FEB-2002 (first entry)
DT
XX
XX  D. immitis transglutaminase protein PD1ng15 coding sequence.
DE
XX  Transglutaminase protein; disulfide isomerase; antiparasite; vaccine;
KW

```

```

KM  nematode; heartworm; ss.
XX
XX  Dirofilaria immitis.
OS
XX  Location/Qualifiers
XX  Key 1..45
XX  CDS /*tag=a
XX  /product="mature transglutaminase"
XX
XX  US6309644-B1.
PN
XX  30-OCT-2001.
PD
XX  12-JUN-1997; 97US-0874102.
PF
XX  03-DEC-1996; 96US-0781420.
PR
XX
XX  (HESK-) HESKA CORP.
PA  (TEXA ) UNIV TEXAS SYSTEM.
XX
XX  Chandrashekar R, Mehra K;
PI
XX  WPI; 2002-040231/05.
DR
XX  P-PSDB; AAG66112.
DR
XX
XX  Novel Dirofilaria immitis transglutaminase protein which also has
PT  protein disulfide isomerase activity, used to identify transglutaminase
PT  activity inhibitors that are useful for protecting animals from
PT  heartworm
XX
XX  Claim 3; Columns 113-114; 66pp; English.
PS
XX
XX  The invention relates to parasitic nematode transglutaminase proteins and
XX  polynucleotides encoding them. The transglutaminase proteins are useful
XX  for identifying a compound capable of inhibiting transglutaminase or
XX  protein disulfide isomerase activity. The proteins represent novel
XX  targets for antiparasite vaccines and drugs. The products inhibit the
XX  crucial steps in nematode molting that involve nematode transglutaminase.
XX  Transglutaminase, a disease condition caused by D. immitis. The nematode protein
XX  disulfide isomerase or transglutaminase activity inhibitors identified
XX  are useful for protecting an animal from heartworm. The proteins are
XX  are useful as diagnostic agents to detect infection by parasitic nematodes.
XX  The present sequence represents a D. immitis nucleotide sequence encoding
XX  a transglutaminase protein PD1ng15, the mature form of PD1ng40.
XX
XX  Sequence 45 BP; 14 A; 5 C; 16 G; 10 T; 0 other;
SO

```

```

Query Match      48.3%; Score 14; DB 24; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY  8 atgaattacaga 21
    |||
DB  13 atgaattacaga 26

```

RESULT 9

AA167860/c standard; cDNA; 45 BP.

```

XX
XX  AA167860;
AC
XX  27-FEB-2002 (first entry)
DT
XX
XX  Complementary strand of transglutaminase protein PD1ng15 coding DNA.
DE
XX  Transglutaminase protein; disulfide isomerase; antiparasite; vaccine;
KW  nematode; heartworm; ss.
XX
XX  Dirofilaria immitis.
OS

```

XX	PF	21-JUN-2000; 2000WO-AUO0693.
XX	PR	21-JUN-1999; 99US-0140345.
XX	PA	(MURD-) MURDOCH CHILDRENS RES INST.
XX	PI	Wright CJ, Werther GA, Edmondson SR;
XX	WI	WPI; 2001-041421/05.
XX	DR	Ameliorating the effects of a disorder, e.g. psoriasis, by
XX	PT	administering UV (ultra-violet) treatment (optional) and an antisease
XX	PT	nucleic acid that inhibits or reduces growth factor mediated cell
XX	PT	proliferation and/or inflammation -
XX	PS	Example 8; Page 91; 20pp; English.
XX	CC	The present invention relates to a method for ameliorating the effects
XX	CC	of skin disorders. The method comprises contacting the skin with an
XX	CC	antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX	CC	receptor, IGF binding protein [IGFBP]-2 or IGFBP), which is capable of
XX	CC	inhibiting or reducing growth factor mediated cell proliferation,
XX	CC	inflammation and/or other disorders. The present sequence is an
XX	CC	oligonucleotide which can be used to design the antisense
XX	CC	oligonucleotides of the present invention (see AAF45151 and
XX	CC	AAF45153-F45161). The method is useful for ameliorating the effects of
XX	CC	psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids,
XX	CC	keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the
XX	CC	skin, a hyperneovascular condition such as a neovascular condition of the
XX	CC	retina, brain or skin, growth factor-mediated malignancies, other
XX	CC	sclerotic disease, kidney disease, hyperproliferation of the inside of
XX	CC	'blood vessels or any other hyperplasia.
XX	SS	Sequence 15 BP; 8 A; 1 C; 2 G; 4 T; 0 other;
XX	SQ	
XX	QY	Query Match 46.2%; Score 13.4; DB 22; Length 15;
XX	DB	Best Local Similarity 93.3%; Pred. No. 4.5e+03;
XX		Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX		QY 8 atgaatttaccagag 22
XX		
XX		DB 1 atgaatttaccagag 15
XX	RESULT 11	
XX	AAAF3773	
XX	ID	AAAF3773 standard; DNA; 19 BP.
XX	AC	AAAF3773;
XX	DT	04-DEC-2000 (first entry).
XX	DE	cdk-we-hu ribozyme binding site #248.
XX	KW	Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;
XX	KW	restenosis; ss.
XX	OS	Mammalia.
XX	PN	WO2000032765-A2.
XX	PD	08-JUN-2000.
XX	PF	06-DEC-1999; 99WO-US28772.
XX	PR	04-DEC-1998; 98US-0110954.
XX	PA	(IMMU-) IMMUSOL INC.
XX	PI	Tritz R, Welch PJ, Barber JR, Robbins JW;
XX	PX	
XX	US	US6309644-B1.
XX	30-OCT-2001.	
XX	12-JUN-1997; 97US-0874102.	
XX	03-DEC-1996; 96US-0781420.	
XX	(HESK-) HESKA CORP.	
XX	(TEXA) UNIV TEXAS SYSTEM.	
XX	Chandrashekar R, Mehta K;	
XX	WPI; 2002-040231/05.	
XX	Novel Dirofilaria immitis transglutaminase protein which also has	
XX	protein disulfide isomerase activity, used to identify transglutaminase	
XX	activity inhibitors that are useful for protecting animals from	
XX	heartworm -	
XX	Example 10; Columns 113-114; 66pp; English.	
XX	CC	The invention relates to parasitic nematode transglutaminase proteins and
XX	CC	polynucleotides encoding them. The transglutaminase proteins are useful
XX	CC	for identifying a compound capable of inhibiting transglutaminase or
XX	CC	protein disulfide isomerase activity. The proteins represent novel
XX	CC	targets for antiparasite vaccines and drugs. The products inhibit the
XX	CC	crucial steps in nematode molting that involve nematode transglutaminase.
XX	CC	The proteins are also useful for preventing an animal (a dog) from
XX	CC	heartworm, a disease condition caused by D. immitis. The nematode protein
XX	CC	disulfide isomerase or transglutaminase activity inhibitors identified
XX	CC	are useful for protecting an animal from heartworm. The proteins are
XX	CC	useful as diagnostic agents to detect infection by parasitic nematodes.
XX	CC	The present sequence represents the complementary strand of a D. immitis
XX	CC	nucleotide sequence encoding a transglutaminase protein PDING15, the
XX	CC	mature form of PDITG40.
XX	SS	Sequence 45 BP; 10 A; 16 C; 5 G; 14 T; 0 other;
XX	SQ	
XX	QY	Query Match 48.3%; Score 14; DB 24; Length 45;
XX	DB	Best Local Similarity 100.0%; Pred. No. 2.5e+03;
XX		Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX		QY 8 atgaatttaccaga 21
XX		
XX	DB	33 ATGAATTATCAGA 20
XX	RESULT 10	
XX	AAAF3714	
XX	ID	AAAF3714 standard; DNA; 15 BP.
XX	AC	AAAF3714;
XX	DT	30-MAR-2001 (first entry)
XX	DE	IGF-I oligonucleotide #4674.
XX	KW	Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX	KW	cytostatic; dermatological; cardiant; viricide; ophthalmological; keloid;
XX	KW	skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX	KW	IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX	KW	growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
XX	KW	keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX	KW	hyperneovascular condition; hyperplasia; kidney disease;
XX	KW	neovascular condition of the retina; ss.
XX	OS	Homo sapiens.
XX	PX	WO2000078341-A1.
XX	PN	

DR WPI; 2000-412314/35.
 XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
 PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
 PT PCNA and Cyclin B1 -
 XX
 XX Disclosure: Page 66; 109pp; English.
 PS
 CC The present invention relates to a hairpin or hammerhead ribozyme,
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
 CC Representative examples of ribozyme recognition sites are given in
 CC AA82415 to AA86787. The ribozyme of the invention is useful for
 CC inhibiting restenosis by introduction of the ribozyme into cells.
 CC The ribozyme is resistant to endonuclease activity and hence is
 CC efficient in restenosis treatment.
 CC
 SO Sequence 19 BP; 7 A; 4 C; 3 G; 5 T; 0 other;

Query Match 44.8%; Score 13; DB 21; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.9e+03; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 0;
 QY 12 aattacagagtt 24
 |||||
 DB 7 aattacagagtt 19

RESULT 12
 AAA83774
 ID AAA83774 standard; DNA; 19 BP.
 AC AAA83774;
 DT 04-DEC-2000 (first entry)
 DE cdk-we-hu ribozyme binding site #249.
 XX
 KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;
 KM restenosis; ss.
 XX
 OS Mammalia.
 XX
 PN WO200032765-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 06-DEC-1999; 99WO-US28772.
 XX
 PR 04-DEC-1998; 98US-0110954.
 XX
 PA (IMMU-) IMMUSOL INC.
 XX
 PI Tritz R, Welch PJ, Barber JR, Robbins JM;
 XX
 DR WPI; 2000-412314/35.
 XX
 PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
 PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
 PT PCNA and Cyclin B1 -
 XX
 XX Disclosure: Page 66; 109pp; English.
 PS
 CC The present invention relates to a hairpin or hammerhead ribozyme,
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 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
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 CC AA82415 to AA86787. The ribozyme of the invention is useful for
 CC inhibiting restenosis by introduction of the ribozyme into cells.
 CC The ribozyme is resistant to endonuclease activity and hence is
 CC efficient in restenosis treatment.
 CC

SO Sequence 19 BP; 7 A; 3 C; 4 G; 5 T; 0 other;
 Query Match 44.8%; Score 13; DB 21; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.9e+03; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 0;
 QY 12 aattacagagtt 24
 |||||
 DB 6 aattacagagtt 18

RESULT 13
 AAA83775
 ID AAA83775 standard; DNA; 19 BP.
 AC AAA83775;
 DT 04-DEC-2000 (first entry)
 DE cdk-we-hu ribozyme binding site #250.
 XX
 KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;
 KM restenosis; ss.
 XX
 OS Mammalia.
 XX
 PN WO200032765-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 06-DEC-1999; 99WO-US28772.
 XX
 PR 04-DEC-1998; 98US-0110954.
 XX
 PA (IMMU-) IMMUSOL INC.
 XX
 PI Tritz R, Welch PJ, Barber JR, Robbins JM;
 XX
 DR WPI; 2000-412314/35.
 XX
 PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
 PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
 PT PCNA and Cyclin B1 -
 XX
 XX Disclosure: Page 66; 109pp; English.
 PS
 CC The present invention relates to a hairpin or hammerhead ribozyme,
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
 CC Representative examples of ribozyme recognition sites are given in
 CC AA82415 to AA86787. The ribozyme of the invention is useful for
 CC inhibiting restenosis by introduction of the ribozyme into cells.
 CC The ribozyme is resistant to endonuclease activity and hence is
 CC efficient in restenosis treatment.
 CC
 SO Sequence 19 BP; 7 A; 3 C; 4 G; 5 T; 0 other;
 Query Match 44.8%; Score 13; DB 21; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.9e+03; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 0;
 QY 12 aattacagagtt 24
 |||||
 DB 5 aattacagagtt 17

RESULT 14
 AAH58935
 ID AAH58935 standard; DNA; 19 BP.
 AC AAH58935;

XX 10-SEP-2001 (first entry)
 XX Cdk-we-hu ribozyme binding site SEQ ID NO:1359.
 XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 KW recognition site; target; ribozyme binding site; eye disease; vulnary;
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
 KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
 KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seboreic wart; vitreoretinopathy; scar;
 KW sickle cell retinopathy; ss.
 XX Homo sapiens.
 OS Synthetic.
 OS WO200130362-A2.
 PN 03-MAY-2001.
 XX 26-OCT-2000; 2000WO-US29500.
 XX 26-OCT-1999; 99US-0161532.
 XX (IMMU-) IMMUSOL INC.
 XX Robbins JM, Tritz R;
 XX WPI; 2001-300427/31.
 DR Treating proliferative skin or eye diseases and scarring, using
 PT ribozymes that cleave RNA encoding cytokines involved in inflammation,
 PT matrix metalloproteinases, growth factors and cell-cycle dependent
 PT kinases -
 XX Example 1; Page 170; 408pp; English.
 PS The present invention describes a method for treating a proliferative
 XX skin or eye disease and scarring. The method involves administering a
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
 CC dermatological, vulnary, antiseborrheic, antidiabetic, antisickling,
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative
 CC skin diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 CC squamous or basal cell carcinoma and viral or seboreic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 CC scar. AAH57577 to AAH62099 represent sequences used in the
 CC exemplification of the present invention.
 XX Sequence 19 BP; 7 A; 4 C; 3 G; 5 T; 0 other;

Query Match 44.8%; Score 13; DB 22; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.9e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 aattacagagtt 24
 Db 7 aattacagagtt 19
 |||||

RESULT 15

AAH58936
 ID AAH58936 standard; DNA; 19 BP.
 XX AC AAH58936;
 XX 10-SEP-2001 (first entry)
 XX Cdk-we-hu ribozyme binding site SEQ ID NO:1360.
 XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 KW recognition site; target; ribozyme binding site; eye disease; vulnary;
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
 KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
 KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seboreic wart; vitreoretinopathy; scar;
 KW sickle cell retinopathy; ss.
 XX Homo sapiens.
 OS Synthetic.
 OS WO200130362-A2.
 PN 03-MAY-2001.
 XX 26-OCT-2000; 2000WO-US29500.
 XX 26-OCT-1999; 99US-0161532.
 XX (IMMU-) IMMUSOL INC.
 XX Robbins JM, Tritz R;
 XX WPI; 2001-300427/31.
 DR Treating proliferative skin or eye diseases and scarring, using
 PT ribozymes that cleave RNA encoding cytokines involved in inflammation,
 PT matrix metalloproteinases, growth factors and cell-cycle dependent
 PT kinases -
 XX Example 1; Page 170; 408pp; English.
 PS The present invention describes a method for treating a proliferative
 XX skin or eye disease and scarring. The method involves administering a
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
 CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative
 CC skin diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 CC squamous or basal cell carcinoma and viral or seboreic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 CC scar. AAH57577 to AAH62099 represent sequences used in the
 CC exemplification of the present invention.
 XX Sequence 19 BP; 7 A; 3 C; 4 G; 5 T; 0 other;

Query Match 44.8%; Score 13; DB 22; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.9e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 aattacagagtt 24
 |||||

Fri Jun 21 14:52:03 2002

Db 6 aattacagagt 18

Search completed: June 20, 2002, 23:10:05
Job time: 30170 sec

us-09-509-234c-1_1300_1328.primer.rng

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OM nucleic - nucleic search, using sw model

Run on: June 20, 2002, 23:43:22 ; Search time 66.94 Seconds
(without alignments)
106.414 Million cell updates/sec

Title: US-09-509-234c-1_COPY_1300_1328
Perfect score: 29
Sequence: 1 nnnnnatgaattacagagtaannn 29

Scoring table: IDENTITY_NTC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 506208

Minimum DB seq length: 15
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

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3: /cgn2_6/ptodata/2/1na/6a_COMB.seq:*
4: /cgn2_6/ptodata/2/1na/6b_COMB.seq:*
5: /cgn2_6/ptodata/2/1na/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/1na/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	48.3	33	4	US-08-874-102-23
2	14	48.3	33	4	US-08-874-102-24
3	14	48.3	45	4	US-08-874-102-51
4	14	48.3	45	4	US-08-874-102-53
5	12.8	44.1	24	1	US-08-887-480-95
6	12.8	44.1	24	1	US-08-905-314A-15
7	12.8	44.1	28	4	US-08-803-346-34
8	12.6	43.4	32	4	US-09-117-860-56
9	12.6	43.4	46	1	US-08-121-936-206
10	12.6	43.4	46	1	US-08-121-936-206
11	12.6	43.4	46	2	US-08-475-228A-206
12	12.6	43.4	46	2	US-08-482-080A-206
13	12.6	43.4	46	5	PCT-US93-12388-206
14	12.4	42.8	22	1	US-08-833-883-97
15	12.4	42.8	22	2	US-08-833-883-97
16	12.4	42.8	44	2	US-08-713-557B-1
17	12.4	42.8	44	2	US-09-660-552-20
18	12.2	42.1	30	5	PCT-US95-01944-8
19	12.2	42.1	32	4	US-08-781-420-15
20	12.2	42.1	32	4	US-08-874-102-15
21	12.2	42.1	32	4	US-08-445-065-15
22	12.2	42.1	39	1	US-08-959-524-15
23	11.8	40.7	17	4	US-08-584-040-2836
24	11.8	40.7	20	3	US-09-157-177-4
25	11.8	40.7	20	3	US-09-157-177-4
26	11.8	40.7	20	3	US-09-358-384-40
27	11.8	40.7	24	3	US-08-781-891-86

28	11.8	40.7	30	2	US-08-743-637B-147	Sequence 147, App
29	11.8	40.7	30	3	US-08-526-840B-147	Sequence 147, App
30	11.6	40.0	32	4	US-09-153-555-8	Sequence 8, App1
31	11.6	40.0	33	3	US-08-884-324-29	Sequence 29, App1
32	11.6	40.0	33	3	US-08-996-338-30	Sequence 30, App1
33	11.6	40.0	34	1	US-08-387-315A-11	Sequence 11, App1
34	11.6	40.0	34	2	US-08-754-559-11	Sequence 11, App1
35	11.6	40.0	35	3	US-08-965-477-21	Sequence 21, App1
36	11.6	40.0	36	1	US-08-442-063A-5	Sequence 5, App1
37	11.6	40.0	37	3	US-08-884-324-34	Sequence 34, App1
38	11.6	40.0	47	1	US-08-723-896-20	Sequence 20, App1
39	11.4	39.3	21	1	US-08-049-783-13	Sequence 13, App1
40	11.4	39.3	21	1	US-08-158-232-27	Sequence 27, App1
41	11.4	39.3	21	1	US-08-304-626-27	Sequence 27, App1
42	11.4	39.3	21	1	US-08-316-301A-34	Sequence 34, App1
43	11.4	39.3	21	1	US-08-611-928-27	Sequence 27, App1
44	11.4	39.3	21	3	US-09-224-024-11	Sequence 11, App1
45	11.4	39.3	21	3	US-09-173-891-27	Sequence 27, App1
46	11.4	39.3	21	4	US-09-076-137-34	Sequence 34, App1
47	11.4	39.3	21	5	PCT-US92-03624-34	Sequence 34, App1
48	11.4	39.3	21	5	PCT-US94-07902-11	Sequence 11, App1
49	11.4	39.3	22	1	US-07-992-618-1	Sequence 1, App1
50	11.4	39.3	22	1	US-08-100-118-1	Sequence 1, App1
51	11.4	39.3	22	2	US-08-474-450A-18	Sequence 18, App1
52	11.4	39.3	22	2	US-08-983-466-49	Sequence 49, App1
53	11.4	39.3	28	3	US-08-544-381B-66	Sequence 86, App1
54	11.4	39.3	30	1	US-08-352-818-14	Sequence 14, App1
55	11.4	39.3	34	1	US-08-399-696-34	Sequence 34, App1
56	11.4	39.3	35	2	US-08-850-049-97	Sequence 97, App1
57	11.4	39.3	35	2	US-08-050-478-97	Sequence 97, App1
58	11.4	39.3	35	4	US-09-414-117-97	Sequence 185, App
59	11.4	39.3	36	3	US-08-781-891-165	Sequence 24, App1
60	11.4	39.3	44	2	US-08-441-887A-24	Sequence 25, App1
61	11.4	39.3	44	3	US-08-544-381B-121	Sequence 121, App
62	11.4	39.3	44	3	US-08-544-381B-122	Sequence 122, App
63	11.4	39.3	17	1	US-08-477-110A-3	Sequence 3, App1
64	11.2	38.6	18	3	US-09-205-143-81	Sequence 81, App1
65	11.2	38.6	22	2	US-08-739-069-14	Sequence 14, App1
66	11.2	38.6	22	3	US-09-313-121-14	Sequence 14, App1
67	11.2	38.6	28	1	US-08-629-939-11	Sequence 11, App1
68	11.2	38.6	28	1	US-08-759-873-11	Sequence 11, App1
69	11.2	38.6	30	1	US-08-435-350-74	Sequence 74, App1
70	11.2	38.6	30	4	US-09-177-268-4	Sequence 4, App1
71	11.2	38.6	30	4	US-08-208-885-6	Sequence 6, App1
72	11.2	38.6	39	1	US-08-462-177-6	Sequence 6, App1
73	11.2	38.6	39	2	US-08-833-622-6	Sequence 6, App1
74	11.2	38.6	39	2	US-08-874-186-70	Sequence 70, App1
75	11.2	38.6	39	2	US-08-895-939-1	Sequence 1, App1
76	11.2	38.6	41	2	US-09-188-820-1	Sequence 1, App1
77	11.2	38.6	44	2	US-08-882-083-13	Sequence 13, App1
78	11.2	38.6	44	2	US-08-558-107-13	Sequence 13, App1
79	11.2	38.6	44	3	US-09-243-539-13	Sequence 13, App1
80	11.2	38.6	47	1	US-08-171-389-165	Sequence 165, App
81	11.2	38.6	47	1	US-08-123-936-165	Sequence 165, App
82	11.2	38.6	47	2	US-08-475-228A-165	Sequence 165, App
83	11.2	38.6	47	3	US-08-482-080A-165	Sequence 165, App
84	11.2	38.6	47	5	PCT-US93-12388-165	Sequence 84, App1
85	11.2	38.6	17	3	US-08-985-162-84	Sequence 85, App1
86	11.2	37.9	17	3	US-08-985-162-85	Sequence 85, App1
87	11.2	37.9	17	3	US-08-985-162-86	Sequence 86, App1
88	11.2	37.9	21	1	US-08-379-081B-403	Sequence 403, App
89	11.2	37.9	21	1	US-08-379-078-403	Sequence 403, App
90	11.2	37.9	25	4	US-09-018-584A-125	Sequence 125, App
91	11.2	37.9	25	4	US-09-117-860-53	Sequence 53, App1
92	11.2	37.9	27	4	US-08-584-040-1406	Sequence 106, App
93	11.2	37.9	33	4	US-09-191-852-10	Sequence 10, App1
94	11.2	37.9	33	5	PCT-US95-13376-10	Sequence 8, App1
95	11.2	37.9	36	4	US-09-491-362-8	Sequence 319, App
96	11.2	37.9	38	4	US-09-025-769B-319	Sequence 40, App1
97	11.2	37.9	41	3	PCT-US96-50747-40	Sequence 84, App1
98	11.2	37.9	41	3	US-08-813-5047-84	Sequence 84, App1
99	11.2	37.9	41	4	US-09-464-453-84	Sequence 84, App1
100	11.2	37.9	41	4		

539	9.8	33.8	46	5	PCT-US93-12388-206	Sequence 206, App	C 612	9.6	33.1	24	4	US-09-397-537-18	Sequence 18, Appl
540	9.8	33.8	46	5	PCT-US95-16916-51	Sequence 51, Appl	C 613	9.6	33.1	24	5	PCT-US93-03034-18	Sequence 18, Appl
541	9.8	33.8	47	1	US-08-032-869A-4	Sequence 4, Appl1	C 614	9.6	33.1	25	1	US-08-316-293-34	Sequence 34, Appl
542	9.8	33.8	47	1	US-08-122-433-7	Sequence 7, Appl1	C 615	9.6	33.1	25	1	US-08-316-993-70	Sequence 70, Appl
543	9.8	33.8	47	1	US-08-122-433-7	Sequence 7, Appl1	C 616	9.6	33.1	25	1	US-08-442-542-29	Sequence 29, Appl
544	9.8	33.8	47	1	US-08-472-673-4	Sequence 4, Appl1	C 617	9.6	33.1	25	2	US-08-769-176-17	Sequence 17, Appl
545	9.8	33.8	47	1	US-08-475-782-4	Sequence 4, Appl1	C 618	9.6	33.1	25	3	US-08-554-385-32	Sequence 32, Appl
546	9.8	33.8	47	2	US-08-472-678-4	Sequence 4, Appl1	C 619	9.6	33.1	25	3	US-08-765-469-29	Sequence 29, Appl
547	9.8	33.8	48	2	US-08-484-503-4	Sequence 4, Appl1	C 620	9.6	33.1	25	3	US-09-181-745-17	Sequence 17, Appl
548	9.8	33.8	48	2	US-08-472-172-8	Sequence 8, Appl1	C 621	9.6	33.1	25	3	US-09-397-537-17	Sequence 17, Appl
549	9.8	33.8	49	2	US-08-392-771-3	Sequence 3, Appl1	C 622	9.6	33.1	25	4	US-09-476-124-29	Sequence 29, Appl
550	9.8	33.8	50	2	US-08-980-071-21	Sequence 21, Appl	C 623	9.6	33.1	25	4	US-09-147-751-12	Sequence 12, Appl
551	9.8	33.8	50	2	US-08-980-071-71	Sequence 71, Appl	C 624	9.6	33.1	25	5	PCT-US93-03034-17	Sequence 17, Appl
552	9.8	33.8	50	2	US-08-980-071-72	Sequence 72, Appl	C 625	9.6	33.1	25	6	US-08-477-7-2	Patent No. 5428147
553	9.8	33.8	50	2	US-08-757-536-21	Sequence 21, Appl	C 626	9.6	33.1	26	1	US-08-544-819-94	Sequence 94, Appl
554	9.8	33.8	50	3	US-09-314-093-21	Sequence 21, Appl	C 627	9.6	33.1	26	3	US-08-755-587-71	Sequence 71, Appl
555	9.8	33.8	50	3	US-09-314-093-72	Sequence 72, Appl	C 628	9.6	33.1	26	3	US-09-526-935-15	Sequence 15, Appl
556	9.8	33.8	50	3	US-09-314-093-72	Sequence 21, Appl	C 629	9.6	33.1	26	4	US-09-526-935-15	Sequence 15, Appl
557	9.8	33.8	50	3	US-09-251-885-21	Sequence 21, Appl	C 630	9.6	33.1	26	6	US-08-640-517A-81	Sequence 81, Appl
558	9.8	33.8	50	4	US-09-337-635-21	Sequence 21, Appl	C 631	9.6	33.1	27	1	US-08-640-517A-81	Sequence 81, Appl
559	9.8	33.8	50	4	US-09-337-635-71	Sequence 71, Appl	C 632	9.6	33.1	27	4	US-09-176-666-36	Sequence 36, Appl
560	9.8	33.8	50	4	US-09-337-635-72	Sequence 72, Appl	C 633	9.6	33.1	27	4	US-09-358-972-93	Sequence 93, Appl
561	9.8	33.8	50	4	US-09-337-635-72	Sequence 72, Appl	C 634	9.6	33.1	27	4	US-09-406-065-81	Sequence 81, Appl
562	9.6	33.1	16	1	US-08-753-147-129	Sequence 129, App	C 635	9.6	33.1	27	5	PCT-US95-05161-4	Sequence 4, Appl1
563	9.6	33.1	17	1	US-08-373-124A-2085	Sequence 2085, Ap	C 636	9.6	33.1	27	5	PCT-US95-05161-5	Sequence 5, Appl1
564	9.6	33.1	17	1	US-08-435-628-2085	Sequence 2085, Ap	C 637	9.6	33.1	28	1	US-08-601-435-5	Sequence 5, Appl1
565	9.6	33.1	17	4	US-08-584-040-7740	Sequence 7740, Ap	C 638	9.6	33.1	28	2	US-08-931-047-5	Sequence 5, Appl1
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567	9.6	33.1	18	4	US-09-290-452-14	Sequence 14, Appl	C 640	9.6	33.				

c 977	9.4	32.4	37	4	US-09-153-310-25-	Sequence 25, Appl
978	9.4	32.4	38	1	US-08-283-067-9	Sequence 9, Appl
c 979	9.4	32.4	38	1	US-08-283-067-38	Sequence 38, Appl
c 980	9.4	32.4	38	1	US-08-283-067-47	Sequence 47, Appl
981	9.4	32.4	38	1	US-08-428-370A-1	Sequence 1, Appl
982	9.4	32.4	38	2	US-08-600-764-1	Sequence 1, Appl
c 983	9.4	32.4	38	3	US-08-721-458B-29	Sequence 29, Appl
c 984	9.4	32.4	38	4	US-09-476-299-48	Sequence 48, Appl
c 985	9.4	32.4	38	4	US-09-609-154-48	Sequence 1, Appl
986	9.4	32.4	39	1	US-08-349-867-1	Sequence 1, Appl
987	9.4	32.4	39	1	US-08-239-476-1	Sequence 1, Appl
988	9.4	32.4	39	1	US-08-239-474A-1	Sequence 1, Appl
989	9.4	32.4	39	1	US-07-854-603-5	Sequence 5, Appl
990	9.4	32.4	39	1	US-08-598-305A-1	Sequence 1, Appl
991	9.4	32.4	39	2	US-08-639-923A-1	Sequence 1, Appl
992	9.4	32.4	39	2	US-08-732-495-1	Sequence 1, Appl
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c 994	9.4	32.4	39	3	US-08-109-037-37	Sequence 37, Appl
c 995	9.4	32.4	39	3	US-08-109-037-38	Sequence 38, Appl
c 996	9.4	32.4	39	3	US-08-109-037-39	Sequence 39, Appl
c 997	9.4	32.4	39	4	US-09-358-036-21	Sequence 21, Appl
c 998	9.4	32.4	39	4	US-09-358-036-68	Sequence 68, Appl
999	9.4	32.4	39	5	PT-0595-05431-1	Sequence 1, Appl
1000	9.4	32.4	40	2	US-08-628-422-8	Sequence 8, Appl

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Query Match          48.3%; Score 14; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels

QY      8 atgaattaccaga 21
|||||
DbB     33 ATGAATTTACAGA 20

RESULT 2
US-08-874-102-24
; Sequence 24, Application US/08874102
; Patent No. 6309644
; GENERAL INFORMATION:
; APPLICANT: Ramaswamy Chandrashekar
; APPLICANT: Kapil Mehta
; TITLE OF INVENTION: PARASITIC NEMATODE TRANSGLUCEMINASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
```

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ZIP: 00720
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/874,102
FILING DATE: 12-JUN-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-2-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: primer
HS-08-874-102-24

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Query Match      48.3%; Score 14; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels

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        ||| ||| ||| ||| ||| ||| ||| ||| |||
Db       13 ATGAATTTACAGA 26

RESULT      3
US-08-874-102-51
; Sequence 51, Application US/08874102
; Patent No. 6309644
; GENERAL INFORMATION:
; APPLICANT: Ramaswamy Chandrashekar
; APPLICANT: Kapil Mehta
; TITLE OF INVENTION: PARASITIC NEMATODE TRANSGLUTAMINASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES,

```

;; TITLE OF INVENTION: AND USES THEREOF
;; NUMBER OF SEQUENCES: 59
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Carol Talkington Verser, Ph.D.
;; ADDRESSEE: Heska Corporation
;; STREET: 1825 Sharp Point Drive
;; CITY: Fort Collins
;; STATE: Colorado
;; COUNTRY: USA
;; ZIP: 80525
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: Windows 95
;; SOFTWARE: Wordperfect for Windows, Version 7.0
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/874,102
;; FILING DATE: 12-JUN-1997
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Verser, Carol Talkington
;; REGISTRATION NUMBER: 37,459
;; REFERENCE/DOCKET NUMBER: HW-2-C1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 970/493-7272
;; TELEFAX: 970/484-9505
;;
;; INFORMATION FOR SEQ ID NO: 51:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 45 nucleotides
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..45
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US-08-874-102-51

Query Match 48.3%; Score 14; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 atgaattacaga 21
Db 13 ATGAATTACAGA 26

RESULT 4
US-08-874-102-53/C
; Sequence 53, Application US/08874102
; Patent No. 6309544
; GENERAL INFORMATION:
; APPLICANT: Ramaswamy Chandrasekar
; TITLE OF INVENTION: PARASITIC NEMATODE TRANSGUTAMINASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/874,102
;; FILING DATE: 12-JUN-1997
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Verser, Carol Talkington
;; REGISTRATION NUMBER: 37,459
;; REFERENCE/DOCKET NUMBER: HW-2-C1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 970/493-7272
;; TELEFAX: 970/484-9505
;;
;; INFORMATION FOR SEQ ID NO: 53:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 45 nucleotides
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
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US-08-874-102-53

Query Match 48.3%; Score 14; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 atgaattacaga 21
Db 33 ATGAATTACAGA 20

RESULT 5
US-08-887-480-95/C
; Sequence 95, Application US/08887480
; Patent No. 5814453
; GENERAL INFORMATION:
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5814453artis Corporation
; STREET: 520 White Plains Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,480
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/722,187
; FILING DATE: 15-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mel9s, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer JB614"
;;
US-08-887-480-95

us-09-509-234c-1_1300_1328.primr.rni

Fri Jun 21 14:52:04 2002

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; TITLE OF INVENTION: ENCODING THEM
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JOANNE M. GIESSEY - MERCK & CO., INC.
; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ FOR WINDOWS VERSION 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/803,346
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: GIESSEY, JOANNE M
; REGISTRATION NUMBER: 32,838
; REFERENCE/DOCKET NUMBER: 19642Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-3046
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-803-346-34

Query Match 44.1%; Score 12.8; DB 4; Length 28;
Best Local Similarity 87.5%; Pred. No. 8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 aaattacagagtaa 26
    ||| ||||| |||||
Db 6 AAATTACAGAGTTAA 21

RESULT 8
US-09-117-860-56
; Sequence 36, Application US/09117860A
; Patent No. 6338955
; GENERAL INFORMATION:
; APPLICANT: OGURI, Suguru
; APPLICANT: MINOWA, Mari
; APPLICANT: YOSHIDA, Aruto
; APPLICANT: TAKEUCHI, Naoyuki
; APPLICANT: TANGUCHI, Makoto
; TITLE OF INVENTION: NOVEL 1-4 N-ACETYLGLUCOSAMINYLTRANSFERASE AND GENE
; FILE REFERENCE: 081356/0119
; CURRENT APPLICATION NUMBER: US/09/117,860A
; CURRENT FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: WO PCT/JP97/04546
; EARLIER FILING DATE: 1997-12-10
; EARLIER APPLICATION NUMBER: JP 161462/1997
; EARLIER FILING DATE: 1997-06-18
; EARLIER APPLICATION NUMBER: JP 332411/1996
; EARLIER FILING DATE: 1996-12-12
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 56
; LENGTH: 32

Query Match 44.1%; Score 12.8; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 aaattacagagtaa 26
    ||| ||||| |||||
Db 17 AAATTACAGAGTTAA 2

RESULT 7
US-08-803-346-34
; Sequence 34, Application US/08803346
; Patent No. 6281346
; GENERAL INFORMATION:
; APPLICANT: HESS, JOHN W.
; APPLICANT: CASKEY, C. THOMAS
; APPLICANT: LIU, QINGYUN
; APPLICANT: PHILLIPS, MICHAEL SEAN
; TITLE OF INVENTION: RAT OB RECEPTORS AND NUCLEOTIDES

```

Fri Jun 21 14:52:04 2002

us-09-509-234c-1_1300_1328.primr.nrl

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-117-860-56

Query Match 43.4%; Score 12.6; DB 4; Length 32;
Best Local Similarity 78.9%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 atgaattacagagttaa 26
||| ||| | ||| |||
DB 3 atgattataagagttaa 21

RESULT 9
US-08-171-389-206/c
Sequence 206, Application US/08171389
Patent No. 5578444
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,389
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA: US 08/081,070
APPLICATION NUMBER:
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175/G19P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0980
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 206:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE

INDIVIDUAL ISOLATE: Human interleukin-2 (IL-2) gene
US-08-171-389-206

Query Match 43.4%; Score 12.6; DB 1; Length 46;
Best Local Similarity 78.9%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 atgaattacagagttaa 26
||| ||| | ||| |||
DB 32 ATGCAATTACTACTGTTAA 14

RESULT 10
US-08-123-936-206/c
Sequence 206, Application US/08123936
Patent No. 5726014
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Screening Assay for the Detection of
TITLE OF INVENTION: DNA-Binding Molecules
NUMBER OF SEQUENCES: 640
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,936
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0075.32/G19P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0980
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 206:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human interleukin-2 (IL-2) gene
US-08-123-936-206

Query Match 43.4%; Score 12.6; DB 1; Length 46;
Best Local Similarity 78.9%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 atgaattacagagttaa 26
||| ||| | ||| |||

Db 32 ATGCAATTATACGTGTTAA 14

RESULT 11

US-08-475-228A-206/c

; Sequence 206, Application US/08475228A

; Patent No. 5869241

GENERAL INFORMATION:

APPLICANT: Edwards, Cynthia A.

APPLICANT: Cantor, Charles R.

APPLICANT: Andrews, Beth M.

APPLICANT: Turin, Lisa M.

TITLE OF INVENTION: Sequence-Directed DNA Binding

TITLE OF INVENTION: Molecules, Compositions and Methods

NUMBER OF SEQUENCES: 664

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genelabs Technologies, Inc.

STREET: 505 Penobscot Drive

CITY: Redwood City

STATE: CA

COUNTRY: USA

ZIP: 94063

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/475,228A

FILING DATE: 06-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/123,936

FILING DATE: 17-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/996,783

FILING DATE: 23-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/723,618

FILING DATE: 27-JUN-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/081,070

FILING DATE: 22-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Stratford, Carol A.

REGISTRATION NUMBER: 34,444

REFERENCE/DOCKET NUMBER: 4600-0175.21/G19P3D2

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 206:

SEQUENCE CHARACTERISTICS:

LENGTH: 46 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: Human Interleukin-2 (IL-2) gene

US-08-475-228A-206

Query Match 43.4%; Score 12.6; DB 2; Length 46;

Best Local Similarity 78.9%; Pred. No. 1e+03;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 atgaattacagagttaa 26

Db 32 ATGCAATTATACGTGTTAA 14

RESULT 12

US-08-482-080A-206/c

; Sequence 206, Application US/08482080A

; Patent No. 6010849

GENERAL INFORMATION:

APPLICANT: Edwards, Cynthia A.

APPLICANT: Cantor, Charles R.

APPLICANT: Andrews, Beth M.

APPLICANT: Turin, Lisa M.

TITLE OF INVENTION: Sequence-Directed DNA Binding

TITLE OF INVENTION: Molecules, Compositions and Methods

NUMBER OF SEQUENCES: 664

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genelabs Technologies, Inc.

STREET: 505 Penobscot Drive

CITY: Redwood City

STATE: CA

COUNTRY: USA

ZIP: 94063

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/482,080A

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/171,389

FILING DATE: 20-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/123,936

FILING DATE: 17-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/996,783

FILING DATE: 23-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/723,618

FILING DATE: 27-JUN-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/081,070

FILING DATE: 22-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Brady, John F.

REGISTRATION NUMBER: 39,118

REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1

TELEPHONE: (650) 324-0880

TELEFAX: (650) 324-0960

INFORMATION FOR SEQ ID NO: 206:

SEQUENCE CHARACTERISTICS:

LENGTH: 46 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: Human interleukin-2 (IL-2) gene

US-08-482-080A-206

Query Match 43.4%; Score 12.6; DB 3; Length 46;

Best Local Similarity 78.9%; Pred. No. 1e+03;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 atgaattacagagttaa 26

Db 32 ATGCAATTATACGTGTTAA 14

RESULT 13

PCT-US93-12388-206/c

Sequence 206, Application PC/TUS9312388
GENERAL INFORMATION:
APPLICANT: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12388
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175.41/G19PCT2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0960
TELEFAX: (415) 324-0880
INFORMATION FOR SEQ ID NO: 206:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human Interleukin-2 (IL-2) gene
PCT-US93-12388-206

Query Match 43.4%; Score 12.6; DB 5; Length 46;
Best Local Similarity 78.9%; Pred. No. 1e+03; 4; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 atgaattacagattaa 26
||| ||||| |||||
Db 32 AGCAATTACTGTAA 14

RESULT 14
US-08-832-883-97/c
Sequence 97, Application US/08832883
Patent No. 5807681
GENERAL INFORMATION:
APPLICANT: Giordano, Antonio
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS
OF CANCER
NUMBER OF SEQUENCES: 115
CORRESPONDENCE ADDRESS:
ADDRESSEE: SETDEL, GONDA, LAVORGNA & MONACO, P. C.
STREET: Suite 1800 Two Penn Center Plaza
CITY: Philadelphia
STATE: PA
COUNTRY: USA

ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,883
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-13 US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-5549
TELEFAX: (215) 568-8383
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: other nucleic acid
US-08-832-883-97

Query Match 42.8%; Score 12.4; DB 1; Length 22;
Best Local Similarity 92.9%; Pred. No. 1.2e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 attacagattaa 26
| ||||| |||||
Db 20 AGTACAGATTAA 7

RESULT 15
US-08-832-877-97/c
Sequence 97, Application US/08832877
Patent No. 5840506
GENERAL INFORMATION:
APPLICANT: Giordano, Antonio
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS OF
CANCER
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSEE: SETDEL, GONDA, LAVORGNA & MONACO, P. C.
STREET: Suite 1800 Two Penn Center Plaza
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,877
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-13 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-5549
TELEFAX: (215) 568-8383
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

us-09-509-234c-l_1300_1328.primer.rni

Fri Jun 21 14:52:04 2002

; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-832-877-97

Query Match 42.8%; Score 12.4; DB 2; Length 22;
Best Local Similarity 92.9%; Pred. NO. 1.2e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Caps 0;
QY 13 attacagaggttaa 26
Db 20 AGTTACAGAGTTAA 7

Search completed: June 20, 2002, 23:43:31
Job time: 5191 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2002, 23:05:46 ; Search time 2574.69 Seconds
(Without alignments)
152.023 Million cell updates/sec

Title: US-09-509-234c-1_COPY_1300_1328

Perfect score: 29

Sequence: 1 nnnnnnataaattacagagtaann 29

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues 88996

Total number of hits satisfying chosen parameters:
Minimum DB seq length: 15
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :
ESR:*
1: em_estda:*
2: em_estdm:*
3: em_estln:*
4: em_estlnu:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl1:*
10: gb_estl2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	12.6	43.4	45	10	BE369365 601220740
5	12.6	43.4	49	10	BJ045819 BJ045819
6	12.2	42.1	41	12	A2462621 1M0269C07
7	12.2	42.1	48	10	BJ052421 BJ052421
8	12.2	42.1	49	10	BJ034980 BJ034980
9	11.8	40.7	34	12	A2764028 1M0559G13
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19	11.6	40.0	50	9	AU105067 AU105067
20	11.6	40.0	50	9	AU105078 AU105078
21	11.6	40.0	50	9	AU105081 AU105081
22	11.4	39.3	34	12	BH146174 BG02743-3
23	11.4	39.3	25	12	A2761537 1M0555123
24	11.4	39.3	41	9	AM335152 SA339 AGS
25	11.4	39.3	42	10	DI1033 HDMS02016
26	11.4	39.3	44	12	A2341932 1M0074K12
27	11.2	38.6	21	12	A2798977 2M0056P01
28	11.2	38.6	27	12	A2433270 1M0219K02
29	11.2	38.6	30	12	A2628643 1M0480B20
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31	11.2	38.6	37	10	C00973 HDMS000334
32	11.2	38.6	40	10	DI1037 HDMS02020
33	11.2	38.6	40	12	A2769030 1M0569M13
34	11.2	38.6	42	12	A2442090 1M0234D10
35	11.2	38.6	47	12	A2428175 1M0480R08
36	11.2	38.6	48	12	A2492954 1M0327C22
37	11.2	38.6	49	10	BJ043594 BJ043594
38	11.2	38.6	50	9	AU103680 AU103680
39	11.2	38.6	50	9	AU103680 AU103680
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41	11.2	38.6	50	9	AU103680 AU103680
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87	11.2	38.6	50	9	AU103680 AU103680
88	11.2	38.6	50	9	AU103680 AU103680
89	11.2	38.6	50	9	AU103680 AU103680
90	11.2	38.6	50	9	AU103680 AU103680

91	10.4	35.9	31	9	AU009970	AU009970	10	34.5	43	12	TA53C02Q	AL456734 T. brucei
92	10.4	35.9	31	9	AU009989	AU009989	10	34.5	45	12	AZ666608	IM0348D23
93	10.4	35.9	34	12	AZ466488	IM0277A13	10	34.5	46	10	BE914990	601668031
94	10.4	35.9	34	12	AZ796078	2M0051F03	10	34.5	47	10	D20660	HUMGS01636
95	10.4	35.9	35	12	AZ41A1A10P		10	34.5	47	12	AZ490582	IM0323F12
96	10.4	35.9	36	12	AZ317022	IM0035P20	10	34.5	48	10	D18211	MUSGS00482
97	10.4	35.9	37	9	AA742638	ny91a06.s	10	34.5	48	12	AZ331576	IM0059005
98	10.4	35.9	42	9	AA610176	ny91a06.s	10	34.5	49	9	AI303303	u167c01.y
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100	10.4	35.9	43	9	AI048043	vm201f12.r	10	34.5	49	9	AV844468	AV844468 AV844468
101	10.4	35.9	43	12	BH623071	1007085F0	10	34.5	49	9	AI30381	AU103081
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124	10.2	35.2	45	12	AZ806160	2M0068I02	10	34.5	50	9	AI105037	AU105037
125	10.2	35.2	47	10	BF084126	BJ084126	10	34.5	50	9	AI105038	AU105038
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157	10.2	35.2	53	12	AL474511	T. brucei	10	34.5	50	9	AI106291	AI106291
158	10.2	35.2	53	12	AL496200	T. brucei	10	34.5	50	9	AA566984	1038 Lob1
159	10.2	35.2	53	12	AA179309	zp45c09.s	10	34.5	50	10	BJ066224	BJ066224
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538	9.4	32.4	50	12	AZ424190	C 611	9.2	31.7	41	12	AZ869678
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540	9.4	32.4	50	12	AZ769249	C 613	9.2	31.7	42	12	AZ604085
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542	9.4	32.4	50	12	AZ860602	C 615	9.2	31.7	42	12	AZ822505
543	9.4	32.4	50	12	BH631106	C 616	9.2	31.7	42	12	BH023748
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548	9.2	31.7	20	12	AZ818725	C 621	9.2	31.7	43	12	A0025688
549	9.2	31.7	22	12	FA82E070	C 622	9.2	31.7	43	12	AZ333179
550	9.2	31.7	23	10	DA5827	C 623	9.2	31.7	44	10	AZ778538
551	9.2	31.7	23	10	AZ346779	C 624	9.2	31.7	44	12	D20693
552	9.2	31.7	23	12	AZ332511	C 625	9.2	31.7	44	12	AZ591404
553	9.2	31.7	24	12	AZ420211	C 626	9.2	31.7	44	12	TA189C01P
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562	9.2	31.7	28	12	AZ824349	C 635	9.2	31.7	47	10	LA6923
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571	9.2	31.7	32	9	AV851547	C 644	9.2	31.7	49	10	BE916026
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973	8.6	29.7	23	12	AZ388663
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ALIGNMENTS

RESULT 1	AZ853600/c	45 bp	DNA	linear	GSS 21-FEB-2001
LOCUS	2M0156E23R	Mouse 10kb	plasmid	UUGC1M library	Mus musculus genomic
DEFINITION	clone UUGC2M0156E23 R, DNA sequence.				
ACCESSION	AZ853600				
VERSION	AZ853600.1	GI:13041885			
KEYWORDS	GSS.				
SOURCE	house mouse.				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 45)				
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0156 row: E column: 23 Seq primer: CACACAGGAACAGCTATGACC Class: plasmid ends High quality sequence stop: 45. Location/Qualifiers				

1. 45	source	/organism="Mus musculus"
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		/clone.lib="Mouse 10kb plasmid UUGC1M library"
		/sex="Male"
		/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
		/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gi14732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
9 a	9 c	10 g
BASE COUNT	9 a	9 c
ORIGIN	9 a	9 c
Query Match	49.0%	Score 14.2; DB 12; Length 45;
Best Local Similarity	84.2%	Pred. No. 2e+04; 3; Indels 0; Gaps 0;
Matches	16; Conservative	0; Mismatches
QY	8 atgaattattacagaggttaa 26	
DB	21 ATGAAATGTGCAGAGTGAA 3	
RESULT 2		
AZ801977	46 bp	DNA
LOCUS	2M0050K08R	Mouse 10kb plasmid UUGC1M library
DEFINITION	clone UUGC2M0050K08 R, DNA sequence.	
ACCESSION	AZ801977	
VERSION	AZ801977.1	GI:12954300
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	1 (bases 1 to 46)	
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.	
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	
JOURNAL	Unpublished (2000)	
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0060 row: K column: 08 Seq primer: CACACAGGAACAGCTATGACC Class: plasmid ends High quality sequence stop: 46.	

FEATURES

source

Location/Qualifiers

1. 46
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U0000000000000000"
/clone_lib="Mouse 10kb plasmid U0000000000000000"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42mV; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g11473211419b)AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

13 a 6 c 8 g 19 t

ORIGIN

Query Match 45.5%; Score 13.2; DB 12; Length 46;
Best Local Similarity 83.3%; Pred. No. 5.5e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 atgaattacagatt 25
|||||
Db 24 ATGCAATTTACAGATT 41

RESULT 3

AA154640/c

LOCUS

AA154640 49 bp mRNA linear EST 11-DEC-1996
m44g11.r1 Bedington mouse embryonic region Mus musculus cDNA
clone IMAGE:540836 5' similar to SW:PAP_BOVIN P25500 POLY(A)

ACCESSION

AA154640
AA154640.1 GI:1726278

VERSION

EST.

KEYWORDS

house mouse.

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 49)
Matta, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Thelning, B., Wyllie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.

AUTHORS

The WashU-HMNI Mouse EST Project
Unpublished (1996)

TITLE

WashU-HMNI Mouse EST Project
Contact: Marra M/Mouse EST Project

JOURNAL

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

COMMENT

Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:327772

Trace considered overall poor quality

FEATURES

source

Possible reversed clone: similarity on wrong strand
Seq primer: -40ml3 ET
High quality sequence stop: 1.
Location/Qualifiers

1. 49
/organism="Mus musculus"
/strain="C57BL6 x DBA"
/db_xref="taxon:10090"
/clone="IMAGE:540836"
/clone_lib="Bedington mouse embryonic region"
/sex="pooled"
/tissue_type="embryo"
/dev_stage="7.5dpc"
/lab_host="DH12S"
/note="Organ: whole embryo; Vector: PCMV-SPORT; Site:1;
Sali; Site:2; NotI; Cloned unidirectionally. Primer:
Oligo dT. Gastrulating embryos were collected at 7.5dpc
from C57BL6 x DBA matings, excluding embryos that had
developed head folds and all extraembryonic tissues.
Average insert size: 1.3 kb (range: 0.5 - 3.0 kb).
Referenced in Development 121, 2479-2489 (1995)."

BASE COUNT

19 a 10 c 8 g 12 t

ORIGIN

Query Match 44.1%; Score 12.8; DB 9; Length 49;
Best Local Similarity 87.5%; Pred. No. 8.2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 tgaattacagatt 24
|||||
Db 35 TGAGATTTACAGATT 20

RESULT 4

BE369365

LOCUS

BE369365 45 bp mRNA linear EST 21-JUL-2000
601220740F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3589857 5',
mRNA sequence.

ACCESSION

BE369365
BE369365.1 GI:9314728

VERSION

EST.

KEYWORDS

house mouse.

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 45)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

AUTHORS

Contact: Robert Strausberg, Ph.D.
Email: cga@bbs.fda.gov

TITLE

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

JOURNAL

DNA Sequencing by: Incyte Genomics, Inc.
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

COMMENT

Plate: L1AM8756 row: 0 column: 10
High quality sequence stop: 45.

FEATURES

Location/Qualifiers

source

1. 45
/organism="Mus musculus"
/strain="C2EHC II (fetal)"
/db_xref="taxon:10090"
/clone="IMAGE:3589857"
/clone_lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary."
Stem cell origin.

TITLE

/lab_host="DH10B"
/note="Organ: lung; Vector: PCMV-SPORT6; Site:1; Sali;
Site:2; NotI; Cloned unidirectionally. Primer: Oligo dT.

JOURNAL

Stem cell origin.

COMMENT

Stem cell origin.

ORIGIN

Stem cell origin.

BASE COUNT

Stem cell origin.

Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH

BASE COUNT 25 a 2 c 6 g 12 t

Query Match 43.4%; Score 12.6; DB 10; Length 45;
Best Local Similarity 78.9%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 atgaattacagagttaa 26
||||| | | | |

Db 7 ATGAATTTAAACATTAA 25

RESULT 5
BJ045819/c
LOCUS
DEFINITION BJ045819 NTBB Mochii normalized Xenopus neurula library Xenopus
laevis cDNA clone XL005902 3', mRNA sequence.

ACCESSION BJ045819
VERSION BJ045819.1 GI:17372516
KEYWORDS EST.

SOURCE African clawed frog.

ORGANISM
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopodinae; Xenopus.

REFERENCE 1 (bases 1 to 49)
AUTHORS Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara, Y.

TITLE Expressed genes in X. laevis embryo
JOURNAL Unpublished (2001).
COMMENT Contact: Tadasu Shin-i
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.

FEATURES
Location/Qualifiers
1..49

/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL005902"
/clone_lib="NTBB Mochii normalized Xenopus neurula library"
/tissue_type="whole embryo"
/dev_stage="stage 15"

BASE COUNT 9 a 6 c 4 g 30 t

Query Match 43.4%; Score 12.6; DB 10; Length 49;
Best Local Similarity 78.9%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 atgaattacagagttaa 26
||||| | | | |

Db 36 AAGAACTTACATAATTAA 18

RESULT 6
A2462621/c
LOCUS
DEFINITION A2462621 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0269C07 R, DNA sequence.

ACCESSION A2462621
VERSION A2462621.1 GI:10620662
KEYWORDS GSS.
SOURCE house mouse.

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 41)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.
and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah
Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plates: 0269 row: C column: 07

Seq primer: CACACGAGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 41.

Location/Qualifiers

1..41

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0269C07"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 14 a 13 c 3 g 11 t

Query Match 42.1%; Score 12.2; DB 12; Length 41;
Best Local Similarity 82.4%; Pred. No. 1.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 atgaattacagagtt 24

||||| | | | |

Db 19 ATGAATTTATAGATT 3

RESULT 7
BJ052421
LOCUS
DEFINITION BJ052421 NTBB Mochii normalized Xenopus neurula library Xenopus
laevis cDNA clone XL041h10 3', mRNA sequence.

ACCESSION BJ052421

VERSION BJ052421.1 GI:17498469

KEYWORDS EST.

SOURCE African clawed frog.

ORGANISM Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae;
 Xenopodinae; Xenopus.
 1 (bases 1 to 48)
 Kityama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-I,T. and Kohara
 Y.
 Expressed genes in X. laevis embryo
 Unpublished (2001)
 Contact: Tadasu Shin-I
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshin@genes.nig.ac.jp.
 Location/Qualifiers
 1..48
 /organism="Xenopus laevis"
 /db_xref="taxon:8355"
 /clone_id="NIBB Mochii normalized Xenopus neurula
 library"
 /tissue_type="whole embryo"
 /dev_stage="stage 15"
 BASE COUNT 21 a 10 c 6 g 9 t 2 others
 ORIGIN

Query Match 42.1%; Score 12.2; DB 10; Length 48;
 Best Local Similarity 77.8%; Pred. No. 1.5e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 8 atgaattacagagta 25
 ||||| ||||| |||||
 Db 31 ATTAATGTACACAGNTA 48

RESULT 8 49 bp mRNA linear EST 06-DEC-2001
 LOCUS BJ034980
 DEFINITION BJ034980 NIBB Mochii normalized Xenopus neurula library Xenopus
 laevis cDNA clone XL031107 5', mRNA sequence.
 ACCESSION BJ034980
 VERSION BJ034980.1 GI:17396724
 KEYWORDS EST.
 SOURCE African clawed frog.
 ORGANISM Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae;
 Xenopodinae; Xenopus.
 1 (bases 1 to 49)
 Kityama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-I,T. and Kohara
 Y.
 Expressed genes in X. laevis embryo
 Unpublished (2001)
 Contact: Tadasu Shin-I
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshin@genes.nig.ac.jp.
 Location/Qualifiers
 1..49
 /organism="Xenopus laevis"
 /db_xref="taxon:8355"
 /clone_id="NIBB Mochii normalized Xenopus neurula
 library"
 /tissue_type="whole embryo"
 /dev_stage="stage 15"
 BASE COUNT 17 a 9 c 9 g 13 t 1 others
 ORIGIN

Query Match 42.1%; Score 12.2; DB 10; Length 49;
 Best Local Similarity 82.4%; Pred. No. 1.5e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 8 atgaattacagagt 24
 ||||| ||||| |||||
 Db 40 ATGTCATTAGAGAGTT 24

RESULT 9 34 bp DNA linear GSS 16-FEB-2001
 LOCUS A2764028
 DEFINITION 1K0539G13R Mouse 10kb plasmid UUCGM library Mus musculus genomic
 clone UUCGM0559G13 R, DNA sequence.
 ACCESSION A2764028
 VERSION A2764028.1 GI:12878546
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 34)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0539 row: G column: 13
 Seq primer: CACACAGCAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 34.
 Location/Qualifiers
 1..34
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCGM0559G13"
 /clone_id="Mouse 10kb plasmid UUCGM library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD22ny. Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD24 (g11473114.9b1AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 12 a 6 c 5 g 11 t

us-09-509-234c-l_1300_1328.primer.rst

Fri Jun 21 14:52:06 2002

```

BASE COUNT      10 a      4 c      0 g      15 t
ORIGIN

Query Match      40.0%; Score 11.6; DB 12; Length 29;
Best Local Similarity 77.8%; Pred. No. 2.6e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 9 tgaattattacagagttaa 26
    ||||| ||| |||||
Db 26 TAAAAATTAGTGAGTTAA 9

RESULT 11
D18718/c 33 bp mRNA linear EST 12-DEC-1995
LOCUS MUSGS01780 Mouse 3'-directed Mus musculus domesticus CDNA clone
DEFINITION md1545 3', mRNA sequence.
ACCESSION D18718 GI:1100687
VERSION D18718.1
KEYWORDS EST.
SOURCE western European house mouse.
ORGANISM Mus musculus domesticus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 33)
JOURNAL Kawamoto, S., Okubo, K., Yoshi, J., Katsuki, M. and Matsubara, K.
COMMENT Analysis of gene expression in mouse embryogenesis by 3'-directed
CDNA sequencing
Unpublished (1995)
Contact: Kawamoto, S., Okubo, K., Yoshi, J., Katsuki, M. and Matsubara, K.
Institute for Cellular and Molecular Biology
Osaka University
3-1 Yamada-oka, Suita, Osaka 565, Japan.

FEATURES
source
1..33
/organism="Mus musculus domesticus"
/strain="C57BL/6J"
/db_xref="taxon:10092"
/clone="md1545"
/clone_lib="Mouse 3'-directed"
/tissue_type="decidual tissue (day 6.5-8.5 of gestation)"

BASE COUNT      12 a      4 c      1 g      16 t
ORIGIN

Query Match      40.0%; Score 11.6; DB 10; Length 33;
Best Local Similarity 77.8%; Pred. No. 2.7e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 9 tgaattattacagagttaa 26
    ||||| ||| |||||
Db 31 TGAATTTTAAAGAAAAA 14

RESULT 12
TA392A110/c 36 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 392a11, reverse sequence,
DEFINITION genomic survey sequence.
ACCESSION AL498238
VERSION AL498238.1 GI:11873960
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
REFERENCE Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
AUTHORS 1 (bases 1 to 36)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
TITLE

us-09-509-234c-l_1300_1328.primer.rst

BASE COUNT      10 a      4 c      0 g      15 t
ORIGIN

Query Match      40.7%; Score 11.8; DB 12; Length 34;
Best Local Similarity 86.7%; Pred. No. 2.2e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 tgaattattacagagt 23
    ||||| ||| |||||
Db 16 TGAATTTTAAAGAGT 2

RESULT 10
AZ345539/c 29 bp DNA linear GSS 29-SEP-2000
LOCUS IM0080P03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0080P03 F, DNA sequence.
ACCESSION AZ345539
VERSION AZ345539.1 GI:10424776
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 29)
JOURNAL Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
COMMENT Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
and Wright, D., Weis, R., Stokes, R., Tingey, A., von Niederhausen, A.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: P column: 03
Seq primer: GGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers
1..29
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0080P03"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

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Fri Jun 21 14:52:06 2002

us-09-509-234c-1_1300_1328.primer.rst

```

JOURNAL      Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
              Project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
              Cambridge CB10 1SA, E-mail: barreil@sanger.ac.uk and
              nh@sanger.ac.uk
COMMENT      Constructed at the Institute for Genomic Research (TIGR),
              Rockville, MD. Genomic DNA isolated from a cloned population of
              Trypanosoma brucei (TRED927/4 G04at 10.1) was mechanically sheared
              to give a tight size distribution (
              4 kb). The v + i method used for the library construction is
              described in detail in Smith, H. and Venter, J.C. (Making small
              insert libraries for whole genome shotgun sequencing projects. In
              Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
              Barrell, Oxford University Press, 1999).
              Email: nelsayed@tigr.org
              Details of T. brucei sequencing at the Sanger Centre are available
              at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES     source
              1..36
              /organism="Trypanosoma brucei"
              /strain="TRED927"
              /db_xref="taxon:5691"
              /clone="392a11"

BASE COUNT   10 a      6 c      7 g      13 t

ORIGIN
Query Match      40.0%; Score 11.6; DB 10; Length 36;
Best Local Similarity 77.8%; Pred. No. 2.7e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY      8 atgaattcacagatga 25
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Db      35 ATGACTCTCAAGTCA 18

RESULT 13
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LOCUS      BJ014578 MF01SSA cDNA Oryzias latipes cDNA clone MF01SSM010F09 3',
DEFINITION      mRNA sequence.
ACCESSION      BJ014578
VERSION      BJ014578.1 GI:17375122
KEYWORDS      EST.
SOURCE      Japanese medaka.
ORGANISM      Oryzias latipes
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              Eukaryota; Metazoa;
              Actinopterygii; Neopterygii; Teleostei; Euteleostei;
              Acanthomorphi; Acanthopterygii; Percomorphi; Atherinomorpha;
              Belontiiformes; Adrianiichthyidae; Oryziinae; Oryzias.
              1 (bases 1 to 37)
              Kohara,Y., Shin-I,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.
              Medaka EST project in Takeda's lab
              Unpublished (2001)
              Contact: Tadasu Shin-I
              Center For Genetic Resource Information
              National Institute of Genetics
              1111 Yata, Mishima, Shizuoka 411-8540, Japan
              Tel: 81-559-81-6855
              Fax: 81-559-81-6855
              Email: tshin@genes.nig.ac.jp.
              Location/Qualifiers
              1..37
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BASE COUNT   16 a      7 c      7 g      7 t

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Query Match      40.0%; Score 11.6; DB 10; Length 37;
Best Local Similarity 77.8%; Pred. No. 2.7e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY      8 atgaattcacagatga 25
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Db      20 ATGACTTTCAAGACTGA 37

RESULT 14
C00973      37 bp      mRNA      linear      EST 23-JUL-1996
LOCUS      C00973 HMG5000342 Human adult (K.Okubo) Homo sapiens cDNA, mRNA
DEFINITION      sequence.
ACCESSION      C00973
VERSION      C00973.1 GI:1433203
KEYWORDS      EST.
SOURCE      human.
              Homo sapiens
              Chordata; Craniata; Vertebrata; Euteleostomi;
              Eukaryota; Metazoa;
              Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
              1 (bases 1 to 37)
              Okubo,K.
              BodyMap: human gene expression database
              Unpublished (1995)
              Contact: Okubo,K.
              Institute for Molecular and Cellular Biol
              Osaka University
              Osaka University Suita, Osaka Pref. 565, Japan
              1-3,Yamada-Oka,Suita, Osaka Pref. 565, Japan
              Tel: 06-877-5111(ex.3315)
              Email: kousaku@imcb.osaka-u.ac.jp
              Human gene signature, 3'-directed cDNA sequence. We are not
              submitting the same cDNA sequence redundantly to DDBJ since 1993.
              For the abundance information of clones with this sequence in this
              library and as well as in other 3'-directed libraries, see
              http://www.imcb.osaka-u.ac.jp/bodymap/. The sequences of the clones
              represented by this GS sequences is also found there.
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              1..37
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Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db      34 ATTAATTTATTAATTTA 17

RESULT 15
D19990      37 bp      mRNA      linear      EST 30-JUL-1996
LOCUS      D19990 HMG500957 Human promyelocyte Homo sapiens cDNA clone mp0576 3',
DEFINITION      mRNA sequence.
ACCESSION      D19990
VERSION      D19990.1 GI:500887
KEYWORDS      EST.
SOURCE      human.
              Homo sapiens
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              Eukaryota; Metazoa;
              Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
              1 (bases 1 to 37)
              Okubo,K., Fukushima,A., Yoshii,J., Miyama,T., Kojima,Y., Yoshinari
              ,H., Arimoto,J. and Matsubara,K.
              Gene expression of human promyelocytic cell line HL60 before and
              TITLE

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us-09-509-234c-l_1300_1328.primr.rst

Fri Jun 21 14:52:06 2002

after induction of differentiation. A new application of 3'directed

cDNA sequencing

JOURNAL
COMMENT

Unpublished (1993)
Contact: Okubo, K., Fukushima, A., Yoshii, J., Niiyama, T., Kojima, Y.,
Yoshinari, H., Arimoto, J. and Matsubara, K.
Institute for Molecular and Cellular Biology
Osaka University
3-1 Yamada-oka, Suita, Osaka 565, Japan.

FEATURES

Location/Qualifiers

1..37

source

/organism="Homo sapiens"
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BASE COUNT 15 a 4 c 2 g 16 t

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Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 9 tgaattacagagttaa 26
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Db 31 TGAATTAAAGAAAAA 14

Search completed: June 20, 2002, 23:06:13
Job time: 31138 sec

Fri Jun 21 08:38:18 2002

us-09-509-234c-46.rgc

Page 1

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2002, 22:09:12 ; Search time 12428.6 Seconds
(without alignments)
2160.230 Million cell updates/sec

Title: US-09-509-234C-46
Perfect score: 1283
Sequence: 1 acagctaaagaattagctga.....tatgaattacagagattaa 1283

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : GenEmbl.*
1: gb-da.*
2: gb-hlg.*
3: gb-in.*
4: gb-om.*
5: gb-ov.*
6: gb-pat.*
7: gb-ph.*
8: gb-pl.*
9: gb-pr.*
10: gb-ro.*
11: gb-sts.*
12: gb-sy.*
13: gb-un.*
14: gb-vl.*
15: em-da.*
16: em-fun.*
17: em-hum.*
18: em-in.*
19: em-mu.*
20: em-om.*
21: em-ov.*
22: em-pat.*
23: em-ph.*
24: em-pl.*
25: em-ro.*
26: em-roi.*
27: em-sts.*
28: em-un.*
29: em-vl.*
30: em-hlg-hum.*
31: em-hlg-inv.*
32: em-hlg-other.*
33: em-higo-inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Query
No. Score Match Length DB ID Description

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3	902.2	70.3	4434	1	AF269697	AF269697 Staphyloc
4	902.2	70.3	4434	6	AX145015	AX145015 Sequence
5	900.6	70.2	1877	1	SE023713	U23713 Staphylococ
6	876.2	68.3	1257	6	I32344	I32344 Sequence 1
7	833.4	65.0	1179	6	AX141471	AX141471 Sequence
8	811	63.2	1257	1	AF144663	AX144663 Staphyloc
9	810.6	63.2	1343	1	SHY12874	Y12874 Staphylococ
10	810.2	63.1	1305	6	A97484	A97484 Sequence 40
11	809.6	63.1	1343	6	A97496	A97496 Sequence 52
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16	797	62.1	1263	1	SHU23711	U23711 Staphylococ
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18	774.2	60.7	1263	1	AF144661	AF144661 Staphyloc
19	749.6	58.4	1295	6	A97488	A97488 Sequence 44
20	741.8	57.8	1263	6	AF099965	AF099965 Staphyloc
21	741.2	57.8	1371	6	A97497	A97497 Sequence 53
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DEFINITION	A97490				
ACCESSION	A97490				
VERSION	A97490.1	GI:6780836			
KEYWORDS					
SOURCE					
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Staphylococcus capitis.					
Bacteria; Firmicutes; Bacillus/Clostridium group;					
Bacillus/Staphylococcus group; Staphylococcus.					
REFERENCE					
1 (bases 1 to 1283)					
GALE, J. and Vannuffel, P.					
GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND					
DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS					
PATENT: WO 9916780-A 46 08-APR-1999;					
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SUMMARIES

us-09-509-234c-46.rge

Fri Jun 21 08:38:18 2002

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DEFINITION FEMA (fema) gene, complete cds.
ACCESSION AF099964
VERSION AF099964.1 GI:3820627
KEYWORDS Staphylococcus capitis.
SOURCE Staphylococcus capitis.
ORGANISM Staphylococcus capitis;
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
REFERENCE 1. (bases 1 to 1254)
AUTHORS Vannuffel,P., Heusterspreute,M., Bouyer,M., Philippe,M. and Gala
J.-L.
TITLE Molecular characterization of femA from Staphylococcus hominis,
Staphylococcus saprophyticus and Staphylococcus haemolyticus and
femA-based discrimination of staphylococcal species
JOURNAL Res. Microbiol. (1998) In press
AUTHORS 2. (bases 1 to 1254)
Vannuffel,P., Heusterspreute,M. and Gala,J.-L.
REFERENCE Direct Submission
AUTHORS Submitted (21-OCR-1998) LBCM, UCL, Cios Chapelle-aux Champs
JOURNAL 30/3046, Bruxelles 1200, Belgium
FEATURES
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AF269697
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Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
REFERENCE
1 (bases 1 to 4434)
Kimberly W.J., Taylor J., David, Nelsen, A.J., Godlevski, M.M.,
Rubino, M.A., Nelson, F.J., Rivers, P.R., Torruella-Miller, I.,
Listendee, S., Ashanti, C., Altschuler, G., Mammo, L., Shepherd, N.S.,
Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D.H., Miller, G.S. and
Furdon, P.J.
Transposon-mediated sequencing of the Staphylococcus epidermidis
genome
TITLE
Unpublished
2 (bases 1 to 4434)
Taylor J., David, Kimberly W.J., Nelsen, A.J., Godlevski, M.M.,
Rubino, M.A., Nelson, F.J., Rivers, P.R., Torruella-Miller, I.,
Listendee, S., Ashanti, C., Altschuler, G., Mammo, L., Shepherd, N.S.,
Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D.H., Miller, G.S. and
Furdon, P.J.
Direct Submission
Submitted (22-MAY-2000) Departments of Genomic Sciences and
Bioinformatics, Genetics Directorate, Glaxo Wellcome, Inc., 5 Moore
Drive, Research Triangle Park, North Carolina 27709-3390, USA
LOCATION/Qualifiers
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ACCESSION AX145015			
VERSION AX145015.1 GI:14283580			
KEYWORDS synthetic construct.			
SOURCE synthetic construct.			
ORGANISM artificial sequence.			
REFERENCE 1 (bases 1 to 434).			
AUTHORS Kimmerly,W.J.			
TITLE Staphylococcus epidermidis nucleic acids and proteins			
JOURNAL Patent: WO 0134809-A 3737 17-MAY-2001;			
GLAXO GROUP LIMITED (GB)			
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RESULT 6
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 ACCESSION 132344
 VERSION 132344.1 GI:1823135
 KEYWORDS Unknown.
 SOURCE

ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 1257)
 AUTHORS Alborn,W.E. Jr., Hoskins,J., Skatrud,P.L. and Unal,S.
 TITLE fema gene of staphylococcus epidermidis, fema protein, and vectors
 and microorganisms comprising the fema gene
 JOURNAL Patent: US 5587307-A 1 24-DEC-1996;
 FEATURES Location/Qualifiers
 source 1..1257
 BASE COUNT 485 a 154 c 225 g 393 t
 ORIGIN

Query Match 68.3%; Score 876.2; DB 6; Length 1257;
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DEFINITION	Staphylococcus warneri factor essential for methicillin resistance		
ACCESSION	AF144663		
VERSION	AF144663.1	GI:4929302	

[illegible]

Page 9

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ACCESSION	A97484.1		
VERSION	GI:6780830		
KEYWORDS			
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ORGANISM			
REFERENCE			
AUTHORS	Gala, J. and Vannuffel, P.		
TITLE	GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS		
JOURNAL	Patent: WO 91/6780-A 40 08-APR-1993.		
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QY 1261 aattatgaattacagagtttaa 1283
Db 1281 GAATATGAATTTACAGAGTTAA 1303

RESULT 11
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LOCUS      A97496      1343 bp      DNA      linear      PAT 26-JAN-2000
DEFINITION Sequence 52 from Patent WO9916780.
ACCESSION  A97496
VERSION    A97496.1  GI:6780842
KEYWORDS   Staphylococcus hominis.
SOURCE      Staphylococcus hominis.
ORGANISM   Staphylococcus hominis
            Bacteria; Firmicutes; Bacillus/Clostridium group;
            Bacillus/Staphylococcus group; Staphylococcus.
REFERENCE   1 (bases 1 to 1343)
            Gala, J. and Vannuffel, P.
            GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND
            DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS
            Patent: WO 9916780-A 52 08-APR-1999;
            GALA JEAN LUC (BE); UNIV LOUVAIN (BE)
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Page 11

BASE COUNT 544 a 161 c 218 g 420 t
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Query Match 63.1%; Score 809.6; DB 6; Length 1343;
Best Local Similarity 78.6%; Pred. No. 5e-118;
Matches 968; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

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61 gaaggttaattgaactaaagttgaggaaggaaggaaggaaggaaggaaggaag 201
142 ACTGAAATTTATGAGTTAAAGTTGCTGAGAAAAGTGAACATTTTATGAGAAATTT 201
121 aataatgacacacagatgagcagcagcagcagcagcagcagcagcagcagcag 180
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181 tttaaatatttttactcaaatcgcgagcagcagcagcagcagcagcagcagcag 240
262 TTTAAATATTTTTCATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 321
241 cactttcttcttaagtaataatgtaataatgtaataatgtaataatgtaataat 300
322 CACTTTTCTTAAAGAAATTAATGTAATTAATTAATTAATTAATTAATTAATTAAT 361
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382 ATAGACCTTATTTGCTTATCATATTCATATTCATATTCATATTCATATTCATAT 441
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442 GGGAAATGATGCTTCTGATTAATTAATTAATTAATTAATTAATTAATTAATTA 501
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622 CAAAAAATGCTGTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 681
601 tttaatgaagaatcactcagaagaagaagaagaagaagaagaagaagaagaaga 660
682 TTTATGAGAAATGATCATCAGAGATGATTAATTAATTAATTAATTAATTAATTA 741
661 aatcgactaaatcctttaaagaatgagatgagatgagatgagatgagatgagat 720
742 AATCGATTTGATCATTTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 801
721 gagtatattgagaagaatccttaagaagaagaagaagaagaagaagaagaaga 780
802 GAATATCTTGAGAGACTTCAATGCAAGCTGCAAGCTTAAATTAATTAATTAATTA 861
781 ctcaagaatattgagaagaagaagaagaagaagaagaagaagaagaagaagaaga 840
862 CTAAAGATTTGAGAAAAAGCAGATTAATTAATTAATTAATTAATTAATTAATTA 921
841 caacaagaatattgagaagaagaagaagaagaagaagaagaagaagaagaagaaga 900
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1162 ACTGCTATTTTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1221
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1222 AATGAGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1281
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1282 TCACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1313

RESULT 12
SAFEPA 3446 bp DNA linear BCT 19-JUL-1995
LOCUS S. aureus factor essential for expression of methicillin resistance
DEFINITION (fema) gene, complete cds, and trpA gene, 3' end.
ACCESSION X17688 M23918
VERSION X17688.1 GI:46579
KEYWORDS femA protein.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus.
REFERENCE 1 (bases 1 to 3446)
AUTHORS Berger-Baechli, B., Barberis-Maino, L., Straessle, A. and Kayser, F. H.
JOURNAL Unpublished
COMMENT 2 (bases 1 to 3446)
AUTHORS Berger-Baechli, B., Barberis-Maino, L., Straessle, A. and Kayser, F. H.
TITLE femA, a host-mediated factor essential for methicillin resistance
JOURNAL Mol. Gen. Genet. 219 (1-2), 263-269 (1989)
MEDLINE Draft entry and computer-readable sequence for [1] kindly provided
COMMENT by B. Berger-Baechli, 11-Apr-1989.
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JOURNAL Lancet 357 (9264), 1225-1240 (2001)
 MEDLINE 21311952
 REFERENCE 2 (bases 1 to 346900)
 AUTHORS Ohta,T.
 JOURNAL Direct Submission
 Submitted (28-FEB-2001) Toshiko Ohta, University of Tsukuba College
 of Medical Technology and Nursing, Department of Medical
 Technology, 1-1-1 Ten-noda, Tsukuba, Ibaraki 305-8577, Japan
 (E-mail: tohtasakura.cc.tsukuba.ac.jp, Tel:81-298-53-3454,
 Fax:81-298-53-3454)
 On May 29, 2001 this sequence version replaced gi:13875626.

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 QY 121 aataatgacaaccaagtgatgacgcatgtttattacgtctgacgtgtaagtaaat 180
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 Db 67730 AACATGAATTTTACAGAGTTAA 67752

RESULT 15
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 LOCUS Staphylococcus haemolyticus factor essential for methicillin
 DEFINITION resistance FEMA (fema) gene, complete cds.
 ACCESSION AF099962
 VERSION AF099962.1 GI:3820623
 SOURCE Staphylococcus haemolyticus.
 ORGANISM Staphylococcus haemolyticus
 Bacteria; Firmicutes; Bacillus/Clostridium group;
 Bacillus/Staphylococcus group; Staphylococcus.
 REFERENCE 1 (bases 1 to 1263)
 AUTHORS vannuffel, P.; Heusterspreute, M.; Bouyer, M.; Philippe, M. and Gala
 J.-L.
 TITLE Molecular characterization of femA from Staphylococcus hominis,
 Staphylococcus saprophyticus and Staphylococcus haemolyticus and
 femA-based discrimination of staphylococcal species
 JOURNAL Res. Microbiol. (1998) In press

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REFERENCE 2 (bases 1 to 1263)
AUTHORS Vannuffel, P., Heusterspreute, M. and Gala, J.-L.
TITLE Direct Submission
JOURNALS Submitted (21-OCT-1998) LBCH, UCL, Clos Chapelle-aux Champs
30/3046, Bruxelles 1200, Belgium
Location/Qualifiers
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BASE COUNT 493 a 162 c 212 g 396 t
ORIGIN

Query Match 62.1%; Score 797; DB 1; Length 1263;
Best Local Similarity 77.5%; Pred. No. 4,8e-116;
Matches 965; Conservative 0; Mismatches 280; Indels 0; Gaps 0;

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DB 139 AATAAGATTAATGAGTTATGACGCTGCATGTTGACAGCATACAGATCATGAATTT 198
QY 181 tttaaatatttactcaaatcgcggaagtgatgattatataaagaagcgtt 240
DB 199 TTTAAGTACTTTTATCTAACGAGACCTGTAATGATTAATGATTAATGAGACT 258
QY 241 cacttttcttaagaatgaatgaatgaatgaatgaatgaatgaatgaatgaat 300
DB 259 CACTTTTCTTTAATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 318
QY 301 gtgacctatcttccatcaacttaacttaactgaagcgtgaatatttgaaagct 360
DB 319 GTTACACCTTATTCATATCATATTAATTAATTAATTAATTAATTAATTAAT 378
QY 361 ggcagatggttttcaataagaatgaatgaatgaatgaatgaatgaatgaat 420
DB 379 GGTATGATGTTGTTGATGATGATGATGATGATGATGATGATGATGATGAT 438
QY 421 aaagctcatcctatctcaagtaagataatcattcagtttaagatttaagaat 480
DB 439 AAAGCTTTCATCGATTAACCAATTCGATTCGATTCGATTCGATTCGATTCGAT 498
QY 481 aagctaaagatgactcaagaagatgatttaagaagacgtaatacgaagaagta 540

DB 499 ACATCTAAGATTAATTAATGATGATGATGATGATGATGATGATGATGATGAT 558
QY 541 caaaaaatggtgcaagtcgttccatccgaagaatgaatgaatgaatgaatgaat 600
DB 559 CAAAAAATGCTGTGAAGTTAAGTTCTTTCAGAGAGAACTCCATCCTCGTTCA 618
QY 601 ttatgaagatctcagaaacgaagtcgcgaatgaatgaatgaatgaatgaatgaat 660
DB 619 TTTATGAGATTAATTAATGATGATGATGATGATGATGATGATGATGATGAT 678
QY 661 aatcgttaataacttaagaatgaatgaatgaatgaatgaatgaatgaatgaatgaat 720
DB 679 AATCCCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 738
QY 721 gaagatcgaagaacttaataagaagatgcttcaataagaatgaatgaatgaatgaat 780
DB 739 GAGTACATCGAAGATTAATTAATGATGATGATGATGATGATGATGATGATGAT 798
QY 781 ctcaagaatggaagacgctgataagaagaagcctatacaaaagaagataact 840
DB 799 TTTAAGATTAATTAATGATGATGATGATGATGATGATGATGATGATGAT 858
QY 841 caacaaactatgataacacaaatgaatgaatgaatgaatgaatgaatgaatgaat 900
DB 859 GAAAAACATTTAGATGATGATGATGATGATGATGATGATGATGATGATGAT 918
QY 901 catgtaagatcctcattccatccatccatccatccatccatccatccatccatccat 960
DB 919 CATGTAATGATTAATTAATGATGATGATGATGATGATGATGATGATGATGAT 978
QY 961 tattaagcagtgagacatcgatcgatcgatcgatcgatcgatcgatcgatcgatcgat 1020
DB 979 TATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1038
QY 1021 tgaagaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaat 1080
DB 1039 TCGACAAATGATTAATTAATGATGATGATGATGATGATGATGATGATGATGAT 1098
QY 1081 aatggtgagcttgaagaagcgtgaagatgtaggaatgaatgaatgaatgaatgaat 1140
DB 1159 AATGACAGATTAATTAATGATGATGATGATGATGATGATGATGATGATGAT 1218
QY 1201 gcaatcctaagcgaacttaagaatgaatgaatgaatgaatgaatgaatgaatgaat 1245
DB 1219 TCAGGTATTAATTAATGATGATGATGATGATGATGATGATGATGATGAT 1263

Search completed: June 20, 2002, 22:12:45
Job time: 36575 sec

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601 ttatggaagatactacagaaacgaagaggttcgcatagagatgatatgtttctattat 660
661 aatcgattaaatacttttaagatagatagatttagtaccattagcatatgttgacttcgat 720
661 aatcgattaaatacttttaagatagatagatttagtaccattagcatatgttgacttcgat 720
721 gagtatatgaagaacttaataatgaagaagatgtttcttaataaagattttaataaaggcg 780
721 gagtatatgaagaacttaataatgaagaagatgtttcttaataaagattttaataaaggcg 780
781 ctcaagatattgaagaagacgctgataataaagaagcttatacaaaaagagataatctt 840
781 ctcaagatattgaagaagacgctgataataaagaagcttatacaaaaagagataatctt 840
841 caacaacattagatgcaatacaacaaataatgatgaagctaaataaacttacaacaagaa 900
841 caacaacattagatgcaatacaacaaataatgatgaagctaaataaacttacaacaagaa 900
901 catggttaatacttatttcgctggtatatttcttatttaataatccgtttgaagttgtt 960
901 catggttaatacttatttcgctggtatatttcttatttaataatccgtttgaagttgtt 960
961 tattacgaggtggacacatcgtaacgtttatcgctacatgacggaagttagcaattcaa 1020
961 tattacgaggtggacacatcgtaacgtttatcgctacatgacggaagttagcaattcaa 1020
1021 tggaaatgataaactatctttagaacaatggaattaaacgcttataatttttatggagtt 1080
1021 tggaaatgataaactatctttagaacaatggaattaaacgcttataatttttatggagtt 1080
1081 agtgggacttcagtggaagcgtgaagatgtaggagtaatttaagttcaaaaaggctat 1140
1081 agtgggacttcagtggaagcgtgaagatgtaggagtaatttaagttcaaaaaggctat 1140
1141 aatgctgattgtattgaatgtaggtgattttatcaagcacaataaaccctatgat 1200
1141 aatgctgattgtattgaatgtaggtgattttatcaagcacaataaaccctatgat 1200
1201 gaaactataacgacacttaaaagtttaagaataatgattttttaccacccaattatct 1260
1201 gaaactataacgacacttaaaagtttaagaataatgattttttaccacccaattatct 1260
1261 aattatgaatttaccagagttaa 1283
1261 aattatgaatttaccagagttaa 1283

RESULT 2
AAH54373
ID AAH54373 standard; DNA: 4434 BP.
XX AC AAH54373;
XX AC
XX DT 03-SEP-2001 (first entry)
XX DE
XX DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3737.
XX KW Staphylococcus epidermidis S81 strain; infection; diagnosis;
XX KW vaccination; endocarditis; ds.
XX OS Staphylococcus epidermidis.
XX OS
XX PN WO200134809-A2.
XX PD
XX PD 17-MAY-2001.
XX PF 09-NOV-2000; 2000WO-US30782.
XX PR 09-NOV-1999; 99US-0164258.
XX PR
XX PA (GLAX) GLAXO GROUP LTD.
XX PI
PI Kimmerly WJ;

PI Gala J, Vannuffel P;
XX WPI; 1999-287521/24.
DR P-PSDB; AAY08218.
XX
PT New Staphylococcus-specific oligonucleotides
XX
XX Claim 21; Fig 9a-b; 48pp; English.
XX
XX This invention describes novel Staphylococcus-specific oligonucleotides
CC based on the consensus femA nucleotide sequence which are used to
CC develop products for the identification, detection and therapy of
CC infections. The oligonucleotides can be used for the genetic
CC amplification, the identification and/or quantification of various femA
CC sequences which are specific to known or unknown Staphylococci species.
CC Since the femA sequence is similar to the femB sequence, the
CC oligonucleotides can also be used for the molecular genotyping of femB
CC genes of different Staphylococci species or other gram-positive bacteria.
CC The femA nucleic acids can also be used in therapeutic applications.
CC They can also be used to identify inhibitors, e.g. antibodies or
CC antisense oligonucleotides, for blocking expression of the femA
CC nucleotide sequences. They can also be used for producing vaccines
CC against Staphylococci infections.
XX
SQ Sequence 1283 BP; 484 A; 170 C; 224 G; 405 T; 0 other;

Query Match 100.0%; Score 1283; DB 20; Length 1283;
Best Local Similarity 100.0%; Pred. No. 3.7e-242;
Matches 1283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 acagctaaagatttagtacttactgacataatgcttactatagccattttactcagatg 60
Db 1 acagctaaagatttagtacttactgacataatgcttactatagccattttactcagatg 60

QY 61 gaaggttaattgaactaaagtgtcgaagtcacgacatcacatctcgtagaataaa 120
Db 61 gaaggttaattgaactaaagtgtcgaagtcacgacatcacatctcgtagaataaa 120

QY 121 aataatgacacaaagtgatgacgatttttatttaactgctgacatgtaagtaaaatt 180
Db 121 aataatgacacaaagtgatgacgatttttatttaactgctgacatgtaagtaaaatt 180

QY 181 tttaaatattttactcaaatcgggagcagtgattgattatgataataaagagctttgt 240
Db 181 tttaaatattttactcaaatcgggagcagtgattgattatgataataaagagctttgt 240

QY 241 cacttttttttactaaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaat 300
Db 241 cacttttttttactaaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaat 300

QY 301 gttgacccctattctccttactcaatacttaataatgacggtgaaatttggaaatgct 360
Db 301 gttgacccctattctccttactcaatacttaataatgacggtgaaatttggaaatgct 360

QY 361 ggcctgattggttttcaataagatggaagattgattgaaatgaagctttcat 420
Db 361 ggcctgattggttttcaataagatggaagattgattgaaatgaagctttcat 420

QY 421 aaaggttcctactctatttcaagaatgaatgataatcattcagtttttagatttaaaagataa 480
Db 421 aaaggttcctactctatttcaagaatgaatgataatcattcagtttttagatttaaaagataa 480

QY 481 acgggttaagatgactcaaggaatggaatgatttaagaagcgttaataactaagaagata 540
Db 481 acgggttaagatgactcaaggaatggaatgatttaagaagcgttaataactaagaagata 540

QY 541 caaaaaaattggttcaagtcggtttctctatccgaagatgaattaccctatttttagatca 600
Db 541 caaaaaaattggttcaagtcggtttctctatccgaagatgaattaccctatttttagatca 600

QY 601 ttatggaagatactacagaaacgaaggttcgcatagagatgatatgtttctattat 660

XX
XX WPI: 2001-316495/33.
XX Nucleic acids encoding polypeptides from *Staphylococcus epidermidis*,
PT useful for vaccinating against infections, e.g. endocarditis -
XX
XX
PS Claim 8; Page 1358-1360; 2188bp; English.
XX
XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
CC (II), given in AAH81454 to AAH83120, from *Staphylococcus epidermidis*.
CC (I) and (II) can have antibacterial activity and therefore can be used
CC in vaccination. The nucleic acids (I) may be used to produce the
CC S. epidermidis polypeptides (II) via the production of vectors
CC containing them which are used to produce host cells which express the
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
CC used to vaccinate subjects and to raise antibodies against the bacteria.
CC The polypeptides may also be used to assay for other inhibitors of their
CC activity and therefore identify compounds that may be used for the
CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
CC AAH55090 represent specifically claimed S. epidermidis genomic DNA
CC polynucleotide sequences from the present invention. AAH55091 to
CC AAH55098 represent oligonucleotide sequences and primers which are used
CC in the exemplification of the present invention.
CC N.B. The present invention specifically claims all the polynucleotide
CC sequences given in the sequence listing of the present specification,
CC however the sequence listing only goes up to SEQ ID NO:4454 so even
CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
CC no sequences are present for SEQ ID NO:4455 to 4464.
XX
XX Sequence 4434 BP; 1676 A; 554 C; 819 G; 1385 T; 0 other;
SQ

Query Match 70.3%; Score 902.2; DB 22; Length 4434;
Best Local Similarity 82.0%; Pred. No. 1.5e-167;
Matches 1052; Conservative 0; Mismatches 228; Indels 3; Gaps 1;

QY 1 acagcctaagaatttagtacttctcgtatcaaatgcttattcgcatttcctagatg 60
DB 2885 aagcctaagaatttagtacttctcgtatcaaatgcttattcgcatttcctagatg 2944
QY 61 gaaggaatttagtacttctcgtatcaaatgcttattcgcatttcctagatg 120
DB 2945 gaaggaatttagtacttctcgtatcaaatgcttattcgcatttcctagatg 3004
QY 121 aataatgaacacgaagtgatgacgaatgttatttaactgcgtacattgaatgaatt 180
DB 3005 aataatgaacacgaagtgatgacgaatgttatttaactgcgtacattgaatgaatt 3064
QY 181 tttaaatattttctcaaatcgcggccgaagtgatgacgaatgttatttaactgcgtac 240
DB 3065 tttaaatattttctcaaatcgcggccgaagtgatgacgaatgttatttaactgcgtac 3124
QY 241 cacttttctttaaagtaataatgaataatgaataatgaataatgaataatgaataatga 300
DB 3125 cacttttctttaaagtaataatgaataatgaataatgaataatgaataatgaataatga 3184
QY 301 gtgaccttactctccttaactaactaactaactaactaactaactaactaactaactaacta 360
DB 3185 gtgaccttactctccttaactaactaactaactaactaactaactaactaactaactaacta 3244
QY 361 ggcacatgattgttttcaataagatgagaagaattaggaattgacgtgaagctttct 420
DB 3245 ggcacatgattgttttcaataagatgagaagaattaggaattgacgtgaagctttct 3304
QY 421 aaagcttcacatccatcttacaagaatgaatgaatgaatgaatgaatgaatgaatgaatga 480
DB 3305 aaagcttcacatccatcttacaagaatgaatgaatgaatgaatgaatgaatgaatgaatga 3364
QY 481 agcgctaaagatgatacgaagaatgagatgtttaaagaacgcttaataactaagaagaa 540
DB 3365 agcgctaaagatgatacgaagaatgagatgtttaaagaacgcttaataactaagaagaa 3424
QY 541 caaaaaaatggtcgaagaatgctttcctacacgaagaatgaatgaatgaatgaatgaatga 600

DB 3425 aagaaaaatgagtgataagtcgcttttattctcgtagaagaagttaccattattagatga 3484
QY 601 ttatagaagatactacagaagaagatgcgcgtatgaagtgatgttattctatt 660
DB 3485 ttatagaagatactcctcgaactcaagaagatttgaagaatgaagaatgtttattac 3544
QY 661 aatcgtttaaatattcttaagaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 720
DB 3545 aacgaattccaataatcaagaacgctgttttgaaccacgaactatattacttatt 3604
QY 721 gattatgaagaacttaataatgaagaagatgttcttaataagaatttaataagcg 780
DB 3605 gattatgaagaacttaataatgaagaagatgttcttaataagaatttaataagcg 3664
QY 781 ctcaagaatattgaagaagacgtgataatgaagaagctttatacaaaaagataatct 840
DB 3665 tttaagaacattgagaagaacgtccagagaataaaaaagcacatacaaaaagataat 3724
QY 841 caacaacatttagatgaatcaatacaaaaattgatagaagcttaaaacttaacaaga 900
DB 3725 gaacaacaactgattgcaaatcaagaataaaattgaagcttaaaacttaacaaga 3784
QY 901 catgtatgaattattcattcttcacgtgattcttctcattacatccgtttgaagttg 960
DB 3785 catgtatgaattattcattcttcacgtgattcttctcattacatccgtttgaagttg 3844
QY 961 tattacgaagtgagacacgaatcgtatcgtacatcgtccgaagtgatgaatca 1020
DB 3845 tattacgaagtgagacacgaatcgtatcgtacatcgtccgaagtgatgaatca 3904
QY 1021 tggaaatgataaactatgctttagaagaatgaatgaatgaatgaatgaatgaatgaatga 1080
DB 3905 tggaaatgataaactatgctttagaagaatgaatgaatgaatgaatgaatgaatgaatga 3964
QY 1081 agtggagactcagtgagaacgctgaagaatgtagaggaatgaatgaatgaatgaatgaatga 1140
DB 3965 agtggagactcagtgagaacgctgaagaatgtagaggaatgaatgaatgaatgaatgaatga 4024
QY 1201 gcaatcctaacgaacttaaaaagttaagaagaatgaatgaatgaatgaatgaatgaatga 1260
DB 4085 aacattcttagaagaacttaaaaactaagaataga---tttaagaagggaattatct 4141
QY 1261 aattatgaattacagattaa 1283
DB 4142 aattatgaattacagattaa 4164

RESULT 3
AAO78141
ID AAO78141 standard; DNA; 1257 BP.
XX
XX AAO78141;
XX 19-JUL-1995 (first entry)
XX
XX Staphylococcus epidermidis fema gene.
DE fema protein; fema gene; methicillin-resistant bacteria; ds.
KM
XX
XX Staphylococcus epidermidis.
OS
XX
XX Key Location/Qualifiers
FH mat_peptide 1..1257
FT
XX
XX EP625575-A.
PN
XX
XX 23-NOV-1994.
PD

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XX PF 25-APR-1994; 94EP-0302950.
 XX PR 30-APR-1993; 93US-0057163.
 XX PA (ELIL) LILLY & CO ELI.
 XX PI Alborn WE, Hoskins JA, Skatrud PL, Unal S, Uenal S;
 XX DR WPI: 1994-359748/45.
 XX DR P-PSDB; AAR63440.
 XX PT Isolated femA gene of *Staphylococcus epidermidis* - used to
 PT develop agents for inhibiting femA protein for use in treating
 PT methicillin-resistant bacteria
 XX Claim 2; Page 15; 23pp; English.
 XX PS AA078141 encodes AAR63440 the femA protein from *Staphylococcus*
 CC *epidermidis* (SE), AAQ78141 can be used in disruption studies in
 CC SE. These studies can be used to generate an assay for agents
 CC which inhibit the femA protein, and are therefore useful in
 CC combination with antibiotics to treat methicillin-resistant
 CC bacteria.
 XX CC
 XX SQ Sequence 1257 BP; 485 A; 154 C; 225 G; 393 T; 0 other;
 Query Match 68.3%; Score 876.2; DB 15; Length 1257;
 Best Local Similarity 81.9%; Pred. No. 1.5e-162;
 Matches 1010; Conservative 0; Mismatches 223; Indels 0; Gaps 0;

QY 1 acagctaaagaatttagtgacttactgacaaatgcttactagcatttactagatg 60
 DB 25 acagctaaagaatttagtgacttactgacaaatgcttactagcatttactagatg 84
 QY 61 gaagctaaatgaactaaagtgctgaaggtacggattacacatttactagatgaa 120
 DB 85 gaagctaaatgaactaaagtgctgaaggtacggattacacatttactagatgaa 144
 QY 121 aataatgacacacgaagtgatgacgatttacttactgacgatttactgacgatt 180
 DB 145 aataatgacacacgaagtgatgacgatttacttactgacgatttactgacgatt 204
 QY 181 ttaataatatttttactcaaatcgccgagtgattgattgattgattgattgattgatt 240
 DB 205 ttaataatatttttactcaaatcgccgagtgattgattgattgattgattgattgatt 264
 QY 241 cacttttttactcaaatcgccgagtgattgattgattgattgattgattgattgatt 300
 DB 265 cacttttttactcaaatcgccgagtgattgattgattgattgattgattgattgatt 324
 QY 301 gttgaccttacttcttactcaaatcgccgagtgattgattgattgattgattgattgatt 360
 DB 325 gttgaccttacttcttactcaaatcgccgagtgattgattgattgattgattgattgatt 384
 QY 361 gttgaccttacttcttactcaaatcgccgagtgattgattgattgattgattgattgatt 420
 DB 385 gttgaccttacttcttactcaaatcgccgagtgattgattgattgattgattgattgatt 444
 QY 421 aaaggggttccatcttactcaaatcgccgagtgattgattgattgattgattgattgatt 480
 DB 445 aaaggggttccatcttactcaaatcgccgagtgattgattgattgattgattgattgatt 504
 QY 481 acggtcaagaatgactcaaatcgccgagtgattgattgattgattgattgattgattgatt 540
 DB 505 agtgctaaagtgatttcaaatcgccgagtgattgattgattgattgattgattgattgatt 564
 QY 541 caaaaaaagtgctcaaatcgccgagtgattgattgattgattgattgattgattgattgatt 600
 DB 565 aaaaaaagtgctcaaatcgccgagtgattgattgattgattgattgattgattgattgatt 624
 QY 601 ttttgaagaatactactcaagaacgaagtgctgacgattgacgattgattgattgattgatt 660

DB 625 tttatgaggatcacctctgaaactaaagatttgcagatagagaagatagttttattac 684
 QY 661 aatcgattaaataactttaagatagattagttaccattagcattagcattagttgactgag 720
 DB 685 aacagattcaaacattatacaagacgtgttttagtaccactagcctattataactttgat 744
 QY 721 agttatattgaagacttaataatgaagagatttcttaataaagatttaataaagcg 780
 DB 745 gattatagaggaaactaaataatgaagaaatgcttataaagattataataaagct 804
 QY 781 ctcaaaatattgagaagacgtgataataaagaagcttatacaaaaagagataatct 840
 DB 805 ttaaagacattgagaacgttccagagaataaaaaagcacatacaaaaaggaaattta 864
 QY 841 caacacaaatagatgcaaatcaacaaaaaatgatgaagctaaacacttacaacaagaa 900
 DB 865 gaacacaaactcgatgcaaatcagcaaaaaataatgaagctaaacacttacaacaagaa 924
 QY 901 catggttaataatcacctatttccagctgatttcttcaataatccgtttgaagttgtt 960
 DB 925 catggaatgaattaccattctctgctgcttcttataataatccgtttgaagttgtt 984
 QY 961 tattacgaggtgacacatcgatcgttactgacattcgtcgtgagttatgcattca 1020
 DB 985 tactacgctggtggaacttcaaatcgttccatcgttccatcgttccatcgttccatcgtt 1044
 QY 1021 tggaaaatgataaactgattttagaacatggaatgaatgaatgaatgaatgaatgaat 1080
 DB 1045 tggaaatgataaactgattttagaacatggaatgaatgaatgaatgaatgaatgaat 1104
 QY 1081 agtgggacactcagtggaagcgtggaagatgtaggagtaataaagttcaaaaaggctat 1140
 DB 1105 agtgggacactcagtggaagcgtggaagatgtaggagtaataaagttcaaaaaggctat 1164
 QY 1141 aatgctgattgattgattgattgattgattgattgattgattgattgattgattgatt 1200
 DB 1165 gatcgctgattgattgattgattgattgattgattgattgattgattgattgattgatt 1224
 QY 1201 gaacttataacgacttataaagtttaaaagaa 1233
 DB 1225 aacattatagaacacttataaagtttaaaagaa 1257

RESULT 4
 AAH52400
 ID AAH52400 standard; DNA; 1179 BP.
 XX AC AAH52400;
 XX DT 03-SEP-2001 (first entry)
 XX DE S. epidermidis open reading frame nucleotide sequence SEQ ID NO:193.
 XX KW *Staphylococcus epidermidis* SRI strain; infection; diagnosis;
 XX OS Staphylococcus epidermidis.
 XX OS WO200134809-A2.
 XX PD 17-MAY-2001.
 XX PF 09-NOV-2000; 2000WO-US30782.
 XX PR 09-NOV-1999; 99US-0164258.
 XX PA (GLAX) GLAXO GROUP LTD.
 XX PI Kimerly WJ;
 XX DR WPI: 2001-316495/33.
 XX DR P-PSDB; AAG81550.

PI Gala J, Vannuffel P;

XX WPI: 1999-287521/24.

DR P-PSDB; AY08215.

XX New Staphylococcus-specific oligonucleotides

PS Claim 15; Fig 6a-b; 48pp; English.

XX This invention describes novel Staphylococcus-specific oligonucleotides
CC based on the consensus femA nucleotide sequence which are used to
CC develop products for the identification, detection and therapy of
CC infections. The oligonucleotides can be used for the genetic
CC amplification, the identification and/or quantification of various femA
CC sequences which are specific to known or unknown Staphylococci species.
CC Since the femA sequence is similar to the femB sequence, the
CC oligonucleotides can also be used for the molecular genotyping of femB
CC genes of different Staphylococci species or other gram-positive bacteria.
CC The femA nucleic acids can also be used in therapeutic applications.
CC They can also be used to identify inhibitors, e.g. antibodies or
CC antisense oligonucleotides, for blocking expression of the femA
CC nucleotide sequences. They can also be used for producing vaccines
CC against Staphylococci infections.

XX Sequence 1305 BP; 513 A; 165 C; 222 G; 405 T; 0 other;

Query Match 53.1%; Score 810.2; DB 20; Length 1305;
Best Local Similarity 77.5%; Pred. No. 1.2e-149;

Matches 994; Conservative 0; Mismatches 288; Indels 1; Gaps 1;

Qy 1 acagtaagaatttagcttactgatacaaatcccttactgacatttactcagatg 60
Db 22 acagtcacagaggttggcaattatcacagataagatgccatagctattccacaaag 81
Qy 61 gaaggtaattatgaactaaagtctgaaggtgacgattccatctcgtggaattaaa 120
Db 82 actgaaaaactatgagtgaaagttgcataaaacagaacactcactttagtgataaaa 141
Qy 121 aataagcaaacacagagtgatgagcagctgttttataactgctgtaactgtaataaatt 180
Db 142 aataagataatgaggttattgagcctgctgctgctgctgctgctgctgctgctgct 201
Qy 181 tttaaatatttttactcaaatcgcggcgagctgattgattatgataataaagagctgttt 240
Db 202 tttaagtactttttactcaacgagcctgtaattgattgattgattgattgattgattgatt 261
Qy 241 cactttttttaaataagtaataatgataataataataataataataataataataata 300
Db 262 cactttttttaaataagtaataatgataataataataataataataataataataata 321
Qy 301 attgaccttattcttcttactcaatacttaataatcattgacggtgaaattattgaaatgct 360
Db 322 gttgaccttatttaccataatcaataatttaataatcattgacggtgaaattattgaaatgct 381
Qy 361 ggcctatgattggttttcaataagatgagaattagattgacatgaagcgttttcaat 420
Db 382 ggtaaatgattggttttcaataagatgagaattagattgacatgaagcgttttcaat 441
Qy 421 aaaggcttccatcttcttactcaataatgataataataataataataataataataata 480
Db 442 aaaggcttccatcttcttactcaataatgataataataataataataataataataata 501
Qy 481 acggcttaagatgactcaaaagatgagattgattgaaagcgttaactaagaagata 540
Db 502 acatctaaagatatataatggaatgagtagtgcgttaacgcttaactcaaaagatt 561
Qy 541 caaaaaatggttcaagtcgttccctacccgaagatgaattaccctattcttagatca 600
Db 562 caaaaaatggttgaagtagtcttcttactcagaagaagacattccattctcgttca 621
Qy 601 ttatggaagatcactacagaacgaagaggttcgcgatagagatgattcttattat 660

Db 622 ttatggaagatcacaccgaaacgaagaattcccaagatagatgatagttcttattat 681
Qy 661 aatcgattaaaatactttaagatagatgatttagtaccattagcatatgttacttgat 720
Db 682 aatcgctatagacatttcaaaagatcagtgctgttaccactagctattatgaattgat 741
Qy 721 gagtattgaaagacttaataatgaagagatgttcttataaagaatttaataaagcgt 780
Db 742 gagtacatcgaagaattacaaaatgaacgtgaaactttaataaagaatttaataaagct 801
Qy 781 ctcaagatattgaaagacgtgataataaagaagctttaatacaaaaagataatctt 840
Db 802 ttaaaagattatgaaagacgaccagacataaaagagcatttaataaaaaaagaaatctt 861
Qy 841 caacaacaatttagatgcgaatacaaaaaaattgataagctcaaaaacttcaacaagaa 900
Db 862 gaaaaacaatttagatcccaattcaaaaaaattagagcgtcaaaaaattcaacgcgaa 921
Qy 901 catggttaataatgaatttacttccagctggtattttcttattatccattggaattgtt 960
Db 922 catggttaataatgaatttacttccagcaggtttcttattatccattggaattgtt 981
Qy 961 tattacgcaggtgacatcgaaatcggttattcgctactatgcgcggaagttatgcaattcaa 1020
Db 982 tattatgcaggtgaaacttctataataatagacattttgcaggcagttatgctattcaa 1041
Qy 1021 tggaataatgaataactatgctttagaacaattgaaatgaacogttataatttttggagtt 1080
Db 1042 tggacaattgataactatgcaattgattcatggttattgataagatacaattttctatgtatt 1101
Qy 1081 agtggggacttcagtgagacgtgagatgtagtagtagtagtagtagtagtagtagtagtag 1140
Db 1102 agcggtaattttgagagacgtgagatgtagtagtagtagtagtagtagtagtagtagtag 1161
Qy 1141 aatgctgattgattgattgattgattgattgattgattgattgattgattgattgattgatt 1200
Db 1162 aatgcagacgttaattgattgattgattgattgattgattgattgattgattgattgatt 1221
Qy 1201 gcaatctataacgcacttaaaagtttaaaagataagatttttttaccacccaattatct 1260
Db 1222 tcagtgtataagacactcaaaaagattaa-aaaaagatttaataaagaggggaatagac 1280
Qy 1261 aattatgaaatttacagagattaa 1283
Db 1281 gaatatgaaatttacagagattaa 1303
RESULT 6
AA37804
ID AAX37804 standard; DNA; 1342 BP.
XX AAX37804;
AC AAX37804;
XX 09-JUL-1999 (first entry)
DT Staphylococcus hominis femA DNA.
DE Staphylococcus hominis.
XX femA: identification; detection; therapy; infection; femB;
XX amplification; genotyping; gram-positive bacteria; vaccine; ss.
OS Staphylococcus hominis.
XX Key Location/Qualifiers
XX CDS 64..1327
XX FT /*tag= a
XX FT /product= "femA"
XX PN WO9916780-A2.
XX PD 08-APR-1999.
XX PF 28-SEP-1998; 98WO-BE00141.
XX XX

PR 26-SEP-1997; 97EP-0870146.
 XX (BENA-) BELGIAN MIN NAT DEFENCE.
 PA (UYLO-) UNIV CATHOLIQUE LOUVAIN.
 XX
 XX Gala J, Vannuffel P;
 XX WPI: 1999-287521/24.
 DR P-PSDB: AAY08221.
 XX
 PT New Staphylococcus-specific oligonucleotides
 PS
 PS Claim 27, Fig 12, 48pp; English.
 XX
 XX This invention describes novel Staphylococcus-specific oligonucleotides
 CC based on the consensus fema nucleotide sequence which are used to
 CC develop products for the identification, detection and therapy of
 CC infections. The oligonucleotides can be used for the genetic
 CC amplification, the identification and/or quantification of various fema
 CC sequences which are specific to known or unknown Staphylococci species.
 CC Since the fema sequence is similar to the molecular genotyping of fema
 CC oligonucleotides can also be used for the molecular genotyping of fema
 CC genes of different Staphylococci species or other gram-positive bacteria.
 CC The fema nucleic acids can also be used in therapeutic applications.
 CC They can also be used to identify inhibitors, e.g. antibodies or
 CC antisense oligonucleotides, for blocking expression of the fema
 CC nucleotide sequences. They can also be used for producing vaccines
 CC against Staphylococci infections.
 XX
 SQ Sequence 1342 BP; 544 A; 161 C; 217 G; 420 T; 0 other:
 Query Match 62.4%; Score 800.8; DB 20; Length 1342;
 Best Local Similarity 78.7%; Pred. No. 8,6e-148;
 Matches 969; Conservative 0; Mismatches 262; Indels 1; Gaps 1;

DB 621 caaaaaatggttaagtaagattcttacttaagaagaattaccattccagatca 680
 QY 601 ttatggaagatactacgaagaagagttgcgcgataagagatgttctat 660
 DB 681 ttatggaagatactacgaagaagagttgcgcgataagagatgttctat 740
 QY 661 aatgcatttaaaacttaagaagatagatagaccattagcatgttgcctgat 720
 DB 741 aatgcatttgacatttaagaagatagatagaccattagcatgttgcctgat 800
 QY 721 gagtattggaagacttaataatgaagagatgttcttataagatttaagaagcg 780
 DB 801 gaattcttggaagacttcatgcaagacgtcagacattataaagacttaacaagct 860
 QY 781 ctcaagatattggaagagacgtcgttaataagaagacttatacaagaagatatt 840
 DB 861 ctcaagatattggaagagacgtcgttaataagaagacttatacaagaagatatt 920
 QY 841 caacacaaattagatgcaatcaacaacaaattgattgaagcttaaaacttaacaaga 900
 DB 921 gaacagcaattaaagcaaatgcaaaatgattgtagcaacacacacttaagaa 980
 QY 901 catggaatgaattacatttcaagcttggaattcttcaattacccgtttgaattgt 960
 DB 981 catggaatgaattacatttcaagcttggaattcttcaattacccgtttgaattgt 1040
 QY 961 tathacagagtgagacatcgatccgttatcgtaactctggcgaagattcaactaa 1020
 DB 1041 tattatgcaggtggaagcgtcaataataatagacacttcgcgtgaagattatcgatt 1100
 QY 1021 tggaaatgataaactatgcttagaacatgataacgcttaattttattgagatt 1080
 DB 1101 tggactatgatttaattatgacatgacatgacatgacatgacatgacatgacat 1160
 QY 1081 agtggagactcagtgagacgctggaagatgtaggaatttaagttcaaaaagctat 1140
 DB 1161 agtggactcagtgagacgctggaagatgtaggaatttaagttcaaaaagctat 1220
 QY 1141 aatgcatttcttgaataatgtaggtatttataacacatcaataacattgatt 1200
 DB 1221 aatgcatttcttgaataatgtaggtatttataacacatcaataacattgatt 1280
 QY 1201 gcaactataacgacttaaaaagttaagaa 1232
 DB 1281 tcaactataacacacttaaaaatttaaaa 1312

RESULT 7
 AAX37800
 ID AAX37800 standard; DNM; 1295 BP.
 XX
 AC AAX37800;
 XX
 DT 09-JUL-1999 (first entry)
 XX
 XX Staphylococcus xylosus fema DNA.
 DE
 XX fema; identification; detection; therapy; infection; fema;
 XX amplification; genotyping; gram-positive bacteria; vaccine; ss.
 KW
 XX Staphylococcus xylosus.
 OS
 XX
 XX Key Location/Qualifiers
 FH 1.1295
 FT CDS
 FT /product= "fema"
 FT /note= "partial sequence, no start or stop codon"
 XX
 PN W09916780-A2.
 XX
 PD 08-APR-1999.

XX MO9916780-A2.
 XX 08-APR-1999.
 XX 28-SEP-1998; 98WO-BE00141.
 XX 26-SEP-1997; 97EP-0870146.
 XX (BENA-) BELGIAN MIN NAT DEFENCE.
 XX (UTLO-) UNIV CATHOLIQUE LOUVAIN.
 XX Gala J, Vannuffel P;
 XX MPI: 1999-287521/24.
 XX P-PSDB: AAY08222.
 XX New Staphylococcus-specific oligonucleotides
 XX Claim 29; Fig 13; 48pp; English.
 XX This invention describes novel Staphylococcus-specific oligonucleotides
 XX based on the consensus fema nucleotide sequence which are used to
 XX develop products for the identification, detection and therapy of
 XX infections. The oligonucleotides can be used for the genetic
 XX amplification, the identification and/or quantification of various fema
 XX sequences which are specific to known or unknown Staphylococci species.
 XX Since the fema sequence is similar to the femB sequence, the
 XX oligonucleotides can also be used for the molecular genotyping of femB
 XX genes of different Staphylococci species or other gram-positive bacteria.
 XX The fema nucleic acids can also be used in therapeutic applications.
 XX They can also be used to identify inhibitors, e.g. antibodies or
 XX antisense oligonucleotides, for blocking expression of the fema
 XX nucleotide sequences. They can also be used for producing vaccines
 XX against Staphylococci infections.
 XX Sequence 1371 BP; 545 A; 155 C; 248 G; 423 T; 0 other:
 SQ
 Query Match 57.8%; Score 741.2; DB 20; Length 1371;
 Best Local Similarity 73.6%; Pred. No. 4e-136;
 Matches 944; Conservative 0; Mismatches 338; Indels 0; Gaps 0;

Db 502 actggtttaccaccaacttcaataagattccattcgttttagattagctgggaaa 561
 Qy 481 acggtcaaaagatgtactcaaaaggatgatttaagaagcgtaactaagaagaa 540
 Db 562 actgtcaaaagcgtaacttaattgattgattgatttgcgttaacgaatacaaaagaa 621
 Qy 541 caaaaaatggtgtcaaaagtcggtttccatcgcgaagatgaattaccattcttagaa 600
 Db 622 cagaataaattggttgaagatgaattcttaaggtagaagatggttcgaattccgtcaa 681
 Qy 601 ttatagagaatactacagaacgaagaagtcgcgagatagatagatgattctattat 660
 Db 682 ttcaagagaagatcttctgaagaagaagatttgacagatagatgacgattttattat 741
 Qy 661 aatcattataaatacttcaaaagatagatctatctaccattagcattggtactcgt 720
 Db 742 aataggttaagaatatataagaatcgtgtgtccattagcttattatgatttggat 801
 Qy 721 gagtatatgaagaacttaataatgaagaagatgttcttaataaagatttaagaagcg 780
 Db 802 gaatatataacagaaattaaagcgtggaacggaagtatttaagaatgaataaaga 861
 Qy 781 ctcaagaatattgaagaagacgtgataataagaagcttatacaaaagataactc 840
 Db 862 gtcaagaatatagaaaaaagacagaataataaagaagctatataaagaataaattta 921
 Qy 841 caacacaaattagatgcaaaatcaacaaaattgtgtgaagtgtaaaaaacttaacaaga 900
 Db 922 gaacacaaactgattgcaaaacacaaaataagatgaagccactgcgttaacaagaag 981
 Qy 901 catgttaagatctccatttcaatgctgtgattttcttcaattacggtttgattgt 960
 Db 982 catgttaagatctccatttcaatgctgtgattttcttcaattacggtttgattgt 1041
 Qy 961 tattacagagtgagacacacgtacgttgcgttgcgttgcgttgcgttgcgttgcgttgc 1020
 Db 1042 tactacagagtgagacacacgtacgttgcgttgcgttgcgttgcgttgcgttgcgttgc 1101
 Qy 1021 tggaaaatgataaactatgctttagaacaatgaaatcaacgtttatttttttagtgatt 1080
 Db 1102 tggagaatgatttaattatgcatagacataatagatagatagatattttttagtgatt 1161
 Qy 1081 agtgggagcttcagtgagaagacgtgagatgtagatgaatttaacaaagagctat 1140
 Db 1162 agtgggagcttcagtgagaagacgtgagatgtagatgaatttaacaaagagctat 1221
 Qy 1141 aatgtgatgttttcaatagatgattttatcaagcgaatcaatcaatcaatcaatcaat 1200
 Db 1222 aatgcagatgtatgaataatgattgttgatttttcaacgatttaagcgaatgattac 1281
 Qy 1201 gaaatcataacgcacttaaaagttaagaagaatgatttttttcaacccaattatct 1260
 Db 1282 aaattcttaagcaattgaaaaaattaaagatatanaaagaatacaataaagaagg 1341
 Qy 1261 aattatgaatttaccaggtta 1282
 Db 1342 aactaagatgaatgaattta 1363

RESULT 9
 AAX37799 standard; DNA; 1280 BP.
 ID AAX37799
 XX AAX37799;
 AC
 XX 09-JUL-1999 (first entry)
 DE
 XX Staphylococcus lugdunensis Fema DNA.
 XX Fema; identification; detection; therapy; infection; femB;
 XX amplification; genotyping; gram-positive bacteria; vaccine; ss.
 OS Staphylococcus lugdunensis.

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XX	Key	Location/Qualifiers	
FT	CDS	1..1280	
FT		/tag= a	
FT		/product= "FemA"	
FT		/note= "partial sequence, no start or stop codon"	
XX	XX	WO916780-A2.	
XX	XX	08-APR-1999.	
XX	XX	28-SEP-1998; 98WO-BE00141.	
XX	XX	26-SEP-1997; 97EP-0870146.	
XX	XX	(BENA-) BELGIAN MIN NAT DEFENCE.	
PA	PA	(UYLO-) UNIV CATHOLIQUE LOUVAIN.	
XX	PI	Gala J, Vannuffel P;	
XX	XX	WPI: 1999-287521/24.	
DR	DR	P-PSDB; AA108216.	
XX	XX	New Staphylococcus-specific oligonucleotides	
XX	PS	Claim 17; Fig 7a-b; 48pp; English.	
XX	CC	This invention describes novel staphylococcus-specific oligonucleotides	
CC	CC	based on the consensus femA nucleotide sequence which are used to	
CC	CC	develop products for the identification, detection and therapy of	
CC	CC	infections. The oligonucleotides can be used for the genetic	
CC	CC	amplification, the identification and/or quantification of various femA	
CC	CC	sequences which are specific to known or unknown Staphylococci species.	
CC	CC	Since the femA sequence is similar to the femB sequence, the	
CC	CC	oligonucleotides can also be used for the molecular genotyping of femB	
CC	CC	genes of different Staphylococci species or other gram-positive bacteria.	
CC	CC	The femA nucleic acids can also be used in therapeutic applications.	
CC	CC	They can also be used to identify inhibitors, e.g. antibodies or	
CC	CC	antisense oligonucleotides, for blocking expression of the femA	
CC	CC	nucleotide sequences. They can also be used for producing vaccines	
CC	CC	against Staphylococci infections.	
XX	XX	Sequence 1280 BP; 484 A; 197 C; 221 G; 378 T; 0 other;	
SQ			
Query Watch	57.4%;	Score 736.6; DB 20; Length 1280;	
Best Local Similarity	74.0%;	Pred. No. 3.1e-135;	
Matches 949; Conservative	0;	Mismatches 329; Indels 5; Gaps 1;	
Qy	1	acagtaagaatttgtagcttactgacataatgccttatagcattttactcagatg 60	
Db	1	acagcaaatgaattcggtagttacacagatacaatgccatatagtcattttactcaatg 60	
Qy	61	gaagtaattatgaactaaagtgtgtaaggtacggtacgattccacatcgtcgtggaataaa 120	
Db	61	acaggtactactaatttaaaagtgtcccaaaaacagacacattttgtgtgtaaa 120	
Qy	121	aataatgacaaccaagtgtgagcagatgtttatttaactgtcgtacgttaataaatt 180	
Db	121	aataataacaagaatttgagcagatgtttatttgacgtgtcaccagtcagatgaattt 180	
Qy	181	tttaataatttttactcaatcggcggtgattgtattatgataataaagctgtgtt 240	
Db	181	tttaataatttttactcagcaatagagccagttatagattatgctaaccacaactgta 240	
Qy	241	cacttttttttaagttaattgaattatgataataaagcataattgtttattataaga 300	
Db	241	catttttttttaagagcagtaactaaatttttaaaagataactgctctctatgcgc 300	
Qy	301	gttgaccttattctcttactcaactaaatcatgacgtggaattattgtggaatgct 360	
Db	301	atagatccactactcttatcaatatagagaccatgacgtgtaataataacggcgaatgct 360	
Qy	361	ggccatgattggtttttcaataaagatggaagaattaggtttgaacatgagggtttcat 420	
Db	361	ggcaatgattggtttttcaataaagatggaacaactcggataccatcatgatgggtttaca 420	

RESULT 10
 AAX37797
 ID AAX37797 standard; DNA; 1328 BP.
 XX
 AC AAX37797;
 XX 09-JUL-1999 (first entry)
 DT
 XX

00-TTT-1999 (first entry)

DT 09-JUL-1999 (first entry)

Db	250	tttaagaactttccaaaataatgtaagaataatcacgcattgtattgtgagtagtagccctt	309
Qy	310	tattcttcctttaacaactactaaatcatgacggtgaaattattggaaatgctggccatgat	369
Db	310	tatttccaatgttaagcgaaaccattggtggaagtgtgaagatacggcagtgac	369
Qy	370	tggttttcaataagatggaagaattagatttgaacatgaagccttcaataaaggcttc	429
Db	370	tggtttttgataaaatgctgaattaaactttgaacatgaagtttccaacctgggttt	429
Qy	430	catcctactcttaacagtaagatatacttcagtttttagatttaaaagataaaacgcgtcaa	489
Db	430	gatacaataaggcaaatctgttttcattctgtcgtgattgaaataaaaacatcaaaa	489
Qy	490	gatgtactcaaaagaatgattttaaagaagcgttaatactaagaagatacaaaaaaat	549
Db	490	gacatcttaataccaatgggaacatttgaaggaaaaaatacgaaaaaagtacagaaaat	549
Qy	550	gggtcaaaagtccgtttcctatccgaagatgaattaccotactctttgatcatttatgaa	609
Db	550	ggtgtgaagtcgctatctaagaagatgaattacatatcttcogttcgtttatggaa	609
Qy	610	gatactacagaanaagagtttgcgataagatgattttctattataatcogatta	669
Db	610	gatacatctgaacaaaagatttggacagagatgcgatttttattcatcgtatg	669
Qy	670	aaatccttaagaatagatttagtaccattagcatatgttgactcgtatgatatatt	729
Db	670	aaatactataagatcgtgtccggtaccactagctatattgattttaatgcataatta	729
Qy	730	gaagaacttaataatgaagagatgtcttaataaagatttaataaggcgtccaaagt	789
Db	730	gcagagctcaacactgaagcgaacacttataaagaagaattcgaaagcagataaagc	789
Qy	790	attgaagaagacctgataataagaagaccttataacaaaagagataatcttccaacaaa	849
Db	790	atcgacaagcctctgaaaaatcagaagccataaataaaaagaaaaatttagagcaaca	849
Qy	850	ttagatgcaaatcaacaaaaaattgatgaactaaaaactcaacaagaacatggtaat	909
Db	850	ctagaagcgaatcaagcttaaaaataaaagaagcagacactgcaacttaaacacgtgac	909
Qy	910	gaattaccatttcagctggatattcttcatttaactccgtttgaagttgtttatacga	969
Db	910	acattaccgatttcggtcggtattcttatttaataccatttgagggtgtttatcgca	969
Qy	970	ggtggcacatcgaatcgtttatcgtactatgccgggaagtatgcaattcaatggaaaatg	1029
Db	970	ggcggcacagcaaacgaatttcgtctatttggcgtgacgcagcagcgaatgggaaatg	1029
Qy	1030	ataaactatcgttttagacatggaataacccgttataatttttatggagtttagtggggac	1089
Db	1030	atttaattatcgattgattatacaaatccaagatataaacttttattggcattagtgat	1089
Qy	1090	ttcagtgaaagcgtgaaagatgtaggagtaatttaagtccaacaaaggctcataatgctgat	1149
Db	1090	ttttcagaagatcgagaagatcgagggtgtgataaatttataaaaaggctcataatgcgaa	1149
Qy	1150	gttatgaatatgattgattttatcaagccaactcaataaacctatgtatgcattcat	1209
Db	1150	gtaataagatatcgtgtgtatttttaaacctataaaccataaaccctgcctatacagtctac	1209
Qy	1210	aacgcacttaaaaagttaagaanaatgat	1238
Db	1210	ataaattatagcgaattataaacaagaat	1238

RESULT 12
AAX37803
ID AAX37803 standard; DNA; 1284 BP.
XX
AC AAX37803;

	X	Staphylococcus schleiferi FemA DNA.
DE	FEM	FemA; identification; detection; therapy; infection; femB;
KW	AMPLIF	amplification; genotyping; gram-positive bacteria; vaccine; ss.
XX	SCHL	Staphylococcus schleiferi.
CS	Key	Location/Qualifiers
FEH	CDS	1..1297 a
PFT	/tag=	"FemA"
FFT	/prod=	"partial sequence, no start or stop codon"
FFT	/note=	"partial sequence, no start or stop codon"
FX	WP9916780-A2.	
PN	08-APR-1999.	
PD	28-SEP-1998;	98WO-BE00141.
PF	26-SEP-1997;	97EP-0870146.
PR	(BENA-) BELGIAN MIN NAT DEFENCE.	
XX	(UYLO-) UNIV CATHOLIQUE LOUVAIN.	
PA	Gala J, Vannuffel P;	
PI	WPI: 1999-287521/24.	
DR	P-PDSB; AAY08219.	
DN	New Staphylococcus-specific oligonucleotides	
PT	Claim 23; Fig 10a-b; 48pp; English.	
PS	This invention describes novel Staphylococcus-specific oligonucleotides based on the consensus femA nucleotide sequence which are used to develop products for the identification, detection and therapy of infections. The oligonucleotides can be used for the genetic amplification, the identification and/or quantitation of various femA sequences which are specific to known or unknown Staphylococci species. Since the femA sequence is similar to the femB sequence, the oligonucleotides can also be used for the molecular genotyping of femB genes of different Staphylococci species or other gram-positive bacteria. The femA nucleic acids can also be used in therapeutic applications. They can also be used to identify inhibitors, e.g., antibodies or antisense oligonucleotides, for blocking expression of the femA nucleotide sequences. They can also be used for producing vaccines against Staphylococci infections.	
XX	Sequence 1297 BP:	495 A; 184 C; 249 G; 369 T; 0 other;
SQ	Query Match	52.3%; Score 670.6; DB 20; Length 1297;
	Best Local Similarity	71.6%; Pred. No. 2.6e-122;
	Matches	880; Conservative Indels 0; Gaps 0;
QY	10 gaattagtcacttaatgatcaaatgccttataggccatttacctcagtgaaggtgaaac	69
Db	10 gaattgggttgcttacgatcatcaaatgccatataggcattaccgacaatgtaggggaac	69
QY	70 tatgaactaaaagtttgtgaagtcagcattcacatactcgtagagaattaaataatgac	129
Db	70 tatgaattaagaagtttgtgaagttgttgaaacacacattctgcgcattaaagataaacac	129
QY	130 aaaccaagtgattgysogaogattttaataactctgtacctgaatgaaaaatttttaaataat	189
Db	130 ataagctaactagcagcatgtttactgacagcagtcgacagtcgaatgaatttttttaaatat	189
QY	190 tttaactcaaatcgsgccagtgattgattatgatataataaagagttgttcactttttc	249
Db	190 tttttatcaaacccggsaccagtcagtgactacgaaaaataaagagctgcgtcattctttt	249
QY	250 tttaatgaattaaagtaaatatgttaaaaagcataattgtctttatctaagttgacocc	309

OY	250	tttaattgattaaagtaataatgtaaaagaacataattgtctttatcttaagaagtgtccct	309
Db	247	tttaagaagaatcgtgagcattttaaaagaatttaaaagatttcttctttaagaacgtacc	306
OY	310	tattcttccttaactacttaataatgaacgtggaattatttggaaatgctgtgcccattg	369
Db	307	tactgtccattctcactaagaagatcatgacatgagcaattatataaaatcattcaacgttg	366
OY	370	tgtgttttcaataagatgaggaattgaatttgaacatgaaagcgttcataaagcttc	429
Db	367	ggttttaattaaacatttgaatcatgattgaatgaacaacaagcttcacaactgttttc	426
OY	430	catcctattcttaacagtaagaatacatccagttttgattttaaagaataaagcgtctaa	489
Db	427	caccctaatacctaataattagatgtcattctgtacttatttgaagaagtatgacgaaag	486
OY	490	gattgtcttaagaagaatggttagtttaagaagaagctaaactaagaagaatgtaaaaaaat	549
Db	487	acgctcatcaagaacatgagcaatgtaaaagaataactcaaaaaagttcaaaaaaat	546
OY	550	ggtgtcaaaagtcggtttccctaccggaatggaattactatctttagatcatattgaa	609
Db	547	ggtgtcaaaagtcgtttctatctataagaatggaatgccaattccgttcaatttatgaa	606
OY	610	gatactacagaaacgaagaagtcgcggatagagatgattggtttctattacaacgcta	669
Db	607	gatactacagagaagaagaatttcaacgctcgtggtggaattccctcatcaacatagatta	666
OY	670	aaatacttaagaatagatgatttagacattagataatgttgaactcgatgtagataatt	729
Db	667	aaatacttggaaat--gtaaagattccttagacatatagacttgaacttgaacttaact	723
OY	730	gaagaacttaataatgaagaagatggttcttaataaagaatttaataagcgtccaagat	789
Db	724	ccaacaattgaaagaagaacatgaaacatgaaacatacaagaagatttcgaagaactgaa	783
OY	790	atgagaagaagcctgataataaagaagctttaaacaagaagatattccttaacaaca	849
Db	784	ttagaagaagaacacggataatacaaaaaacgatttaataaaataagcaacttaaaacaa	843
OY	850	ttagatgcaaatcaaaaaaataatgtaagaagctaaaaaacttacaacaagaacgtgaat	909
Db	844	agagaagaagaatgaactaaattgaagaagaacgttcaactacaacaagaacatggtat	903
OY	910	gaataactatttcagctggaatcttccatctaataatcgtttgaagtgtttatagca	969
Db	904	acattacaacatagcagctggtttcttattatataacatcttgaagttgataattgca	963
OY	970	ggtgacacatcgaaatcgttatgtgtactatgacgaggaagtatgcaattcaatgaaatg	1029
Db	964	ggtgttcatcgaatgaatcatctgtcaacttcgcggatgattgcaatcctgaatg	1023
OY	1030	ataaacctgtcttagagacatgaaatgaactaaccgttatataattttatggaatgtggac	1089
Db	1024	atthaatcgggttagatccaacaacttgaacggttataacttctatgatacgcggaagac	1083
OY	1090	ttaactgaagaagcgtggaagtgtgaggaatgaatttaaaaaaaggtataatgctgtat	1149
Db	1084	tctcagaagaatgcaactgattgtgtgtatttaaaatttaaaaaaggttcaaatgcaat	1143
OY	1150	gttaattgaattgtaggtgttttttcaagccaatacaataaaccctatagcatcat	1209
Db	1144	gtttatgataatattgtgtttcgttcaacccaataataaacccgctgaacgaatcat	1203
OY	1210	aaagcacttaaaagtt-----aaagaaatagatttttttcaacccaattatctaa	1263
Db	1204	acaacccataaaaagctataaaaaaatgaatggttttcgtaagaaggaatttagata	1265
OY	1263	ttatgaatttcaagattttaa 1283	
Db	1264	ataagaatttcaagattttaa 1284	

Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;
Rosen CA;
WPI; 1997-374922/35.
Polynucleotide(s) and proteins derived from *Staphylococcus aureus*
stored on computer readable medium and used in the production of
anti-S.aureus vaccines
Claim 1: Page 1339-1340: 3271pp; English.

Search completed: June 20, 2002, 14:46:22
Job time: 18772 sec

This sequence represents one of 5191 *Staphylococcus aureus* DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the *S. aureus* DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against *S. aureus* infection. The polypeptides can also be used in a kit for the immunodetection of *S. aureus* in a sample. *S. aureus* is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the *S. aureus* DNA sequences contained on the computer readable medium.

Sequence 3271 BP: 948 A: 625 C: 461 G: 1168 T: 69 other;

Query Match 25.4%; Score 326; DB 18; Length 3271;
Best Local Similarity 75.5%; Pred. No. 8, 2e-55;
Matches 429; Conservative 0; Mismatches 137; Indels 2; Gaps 2;

1	QY	acagctaaagaattadgaacttactgatcaaaatgccttatagccattttactcagcg	60
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61	QY	gaaggtaatatgaacttaaaattgctcaaggtacgaggtacacatctcgtaggaataaa	120
511	Db	GTTGGCCACTATGATTTAAAGCTTGCTGAAGGTTATGAACACATTTAGTGGGAAATAAA	452
121	QY	ataatgacacaacaagtgattgcagcatgtttattaactctgctgacotgtaataagaatt	180
451	Db	AACAAATAAAGCAGGTCNTGCGCTTGCTTACTTACTGCTGTAACCTGTTATGAAAGTG	392
181	QY	tttaaatatttttactcaaaatcgcggccagtgattgattatgatataaagaagcttggt	240
391	Db	TTCAAGTATTTTATTCAAATCGCGGTCCAGTGAATTGATTTATGAAAATCAAGAAGCTCGTA	332
241	QY	cacttttttcttaatgaattaagttaaataatgtataaagaagataaattgctttatctcaaga	300
331	Db	CACTTTTTCTTAAATGAATATCAAAATATGTAAAAAACAATCGTTGTCTATACCTACAT	272
301	QY	gtgacccttatcttccttatcaacttaactaaatcatcagcgtgaaatatttggaaatgct	360
271	Db	ATCGATCCATATTTACCATATCAATACTTTGAATCATGATGCGAGATTACAGGTAAATGCT	212
361	QY	ggccatgattggttttccaataagatggaaagttaggatttgaacatgaaggctttcat	420
211	Db	GGTAATGATTGGTGTCTTTGATTAATATGAGTAGTACTTTAGGATTTGAACATATGGATTCCAT	152
421	QY	aaaggcttcactctatcttacaagtaagaatcatcattcagtttagattttaaagaataaa	480
151	Db	AAAGGATTGNTCCTGTGCTACAAATTCGKTATCACTCAGTGTGTAGATTTTAAAGATAAA	92
481	QY	acgcyctaaagatgtactcaagggaatggatag-tttaagaagaagcgttaatactcaagaag-	538
91	Db	ACACGAGATGACATCATTTAAAAATATGGATGGACCTTAAGNAAGAAACACAAAGAAAGT	32

Fri Jun 21 08:38:19 2002

us-09-509-234c-46.rng

Page 17

Fri Jun 21 08:38:19 2002

us-09-509-234c-46.rml

GenCore version 4.5
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OK nucleic - nucleic search, using sw model

Run on: June 20, 2002, 12:03:54 ; Search time 208.59 Seconds
(without alignments)
1510.848 Million cell updates/sec

Title: US-09-509-234c-46
Perfect score: 1283
Sequence: 1 acagctaaagaattacgtga.....tatgaattacagagttaa 1283
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues
Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, NA:*
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3: /cgn2_6/pdata/2/1na/6A.COMB.seq:*
4: /cgn2_6/pdata/2/1na/6B.COMB.seq:*
5: /cgn2_6/pdata/2/1na/PCUS.COMB.seq:*
6: /cgn2_6/pdata/2/1na/backfillseq1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	876.2	68.3	1257	1	US-08-330-154-1 Sequence 1, Appl
2	277.2	21.6	453	3	US-09-714-918-9 Sequence 9, Appl
3	277.2	21.6	453	4	US-09-265-315-9 Sequence 9, Appl
4	277.2	21.6	453	4	US-09-265-315-9 Sequence 9, Appl
5	277.2	21.6	453	4	US-09-266-417-9 Sequence 9, Appl
6	256	20.0	410	3	US-08-714-918-6 Sequence 6, Appl
7	256	20.0	410	4	US-09-265-315-6 Sequence 6, Appl
8	256	20.0	410	4	US-09-266-417-6 Sequence 6, Appl
9	256	20.0	410	4	US-08-714-918-4 Sequence 4, Appl
10	221.2	17.2	400	3	US-09-265-315-4 Sequence 4, Appl
11	221.2	17.2	400	4	US-09-265-315-4 Sequence 4, Appl
12	221.2	17.2	400	4	US-09-266-417-4 Sequence 4, Appl
13	221.2	17.2	400	4	US-08-714-918-19 Sequence 19, Appl
14	97.6	7.6	5253	3	US-08-265-315-19 Sequence 19, Appl
15	97.6	7.6	5253	4	US-09-265-315-19 Sequence 19, Appl
16	97.6	7.6	5253	4	US-09-266-417-19 Sequence 19, Appl
17	97.6	7.6	5253	4	US-08-714-918-14 Sequence 14, Appl
18	56.2	4.4	8920	2	US-08-446-855A-1 Sequence 1, Appl
19	56.2	4.4	8920	4	US-08-936-165A-1 Sequence 1, Appl
20	56.2	4.4	8920	4	US-08-936-165A-74 Sequence 74, Appl
21	55.6	4.3	950	4	US-08-998-416-595 Sequence 186, App
22	55.6	4.3	950	4	US-08-998-416-186 Sequence 2, Appl
23	51.8	4.0	615	4	US-08-973-462-2 Sequence 1, Appl
24	51.8	4.0	615	4	US-08-973-462-1 Sequence 2, Appl
25	51.8	4.0	615	4	US-09-316-083-2 Sequence 13, Appl
26	51	4.0	19124	2	US-08-487-826B-13 Sequence 13, Appl
27	51	4.0	19124	2	US-08-487-826B-13 Sequence 13, Appl

c	28	51	4.0	19124	2	US-08-487-826B-13	Sequence 13, Appl
c	29	48.6	3.8	837	4	US-08-998-416-288	Sequence 288, App
c	30	48.4	3.8	7101	1	US-08-480-604A-9	Sequence 9, Appl
c	31	48.4	3.8	7101	2	US-08-405-496A-9	Sequence 9, Appl
c	32	48.4	3.8	7101	4	US-08-915-136-9	Sequence 9, Appl
c	33	48	3.7	3095	6	5231168-1	Patent No. 5231168
c	34	47.8	3.7	636	4	US-08-998-416-1137	Sequence 1137, Ap
c	35	47.2	3.7	837	4	US-08-998-416-288	Sequence 288, App
c	36	47.2	3.7	4766	5	PCT-US93-07261-10	Sequence 10, Appl
c	37	45.4	3.5	9636	1	US-08-323-170B-1	Sequence 1, Appl
c	38	45.4	3.5	9636	1	US-08-954-441-1	Sequence 1137, Ap
c	39	44	3.4	636	4	US-08-998-416-1137	Sequence 1, Appl
c	40	44	3.4	1956	4	US-08-998-416-186	Sequence 186, App
c	41	43.8	3.4	615	4	US-08-998-416-186	Sequence 1, Appl
c	42	43.6	3.4	6243	2	US-09-056-075-1	Sequence 1, Appl
c	43	43.6	3.4	634	1	US-08-450-065-1	Sequence 1137, Ap
c	44	43.6	3.4	634	1	US-08-450-065-1	Sequence 1, Appl
c	45	43.4	3.4	724	4	US-08-998-416-683	Sequence 683, App

ALIGNMENTS

RESULT 1
US-08-330-154-1
Sequence 1, Application US/08330154
Patent No. 5587307
GENERAL INFORMATION:
APPLICANT: Alborn Jr., William E
APPLICANT: Hoskins, Joan
APPLICANT: Skatrud, Paul L
TITLE OF INVENTION: FEMA GENE OF STAPHYLOCOCCUS EPIDERMIDIS.
TITLE OF INVENTION: FEMA PROTEIN, AND VECTORS AND MICROORGANISMS COMPRISING
TITLE OF INVENTION: THE FEMA GENE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Division/ARH
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,154
FILING DATE: 27-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/208,925
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US/08/057,163
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hamilton, Amy E
REGISTRATION NUMBER: 33,894
REFERENCE/DOCKET NUMBER: X-8894
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3169
TELEFAX: 317-276-1284
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1257 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS

Query Match 21.6%; Score 277.2; DB 3; Length 453;
 Best Local Similarity 74.3%; Pred. No. 1.7e-54;
 Matches 336; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 667 ttaaaactcttaaaagatagatattagaccattagcatatgctgactcgatgagat 726
 DB 2 TTAATAATATACAAAGACCGTGTGNAGTACCTNAGCGATATCACTTAATGAATAT 61
 QY 727 atgaagaacttaataaagaagatgcttcaataaagaattcaaaagcgctcaa 786
 DB 62 ATTAAGAACTAAACGAAGCGGTGATTTTAAATAAAGATTAAAGCGCTTAAAG 121
 QY 787 gatctgagaagagactgataataaagaagcttatataaagaagataacttcaaca 846
 DB 122 GATATTGAAAAAGCTCTGTAATAAAGACATACACGAGATACCTTACAAACNA 181
 QY 847 caattagatgcaaatcaaaaaaattgatgaagctaaactcaacaagaacatggt 906
 DB 182 CAACCTTATCAAAATGAGCAAAAGATTGANGACGTTACAAAGANGANGATGCT 241
 QY 907 aatgaattaccatttcagctgagatattcttcattcaatccgtttgaagttgattac 966
 DB 242 AATGNTTACCTATCTCTCGTTCCTTATCAATCAGTTCGANGTGTATATATAT 301
 QY 967 gcaggtggcacatcgatcgcttactactgacggaagttatgcaattccatgaaa 1026
 DB 302 GCTGTGTGATCAATCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 361
 QY 1027 atgtaaacatctctttagaagaaactgaactgaactgaactgaactgaactga 1086
 DB 362 ATGNTTATTTTGCATTATATATATATATATATATATATATATATATATATAT 421
 QY 1087 gacttcagtgaaagcgtgaagatgtagagt 1118
 DB 422 NAATTNCGNAGGTGCTGAAGATGCTGCTGT 453

RESULT 3
 US-09-265-315-9
 Sequence 9, Application US/09265315
 Patent No. 6187541
 GENERAL INFORMATION:
 APPLICANT: Benton, Bret
 APPLICANT: Lee, Ying J.
 APPLICANT: Malouin, Francois
 APPLICANT: Martin, Patrick K.
 APPLICANT: Schmid, Molly B.
 APPLICANT: Sun, Dongxu
 TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
 TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
 NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/265,315
 FILING DATE: March 9, 1999
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/714,918

FILING DATE: September 13, 1996
 APPLICATION NUMBER: 60/009,102
 FILING DATE: December 22, 1995
 APPLICATION NUMBER: 60/003,798
 FILING DATE: September 15, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 240/247
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 453 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-265-315-9

Query Match 21.6%; Score 277.2; DB 4; Length 453;
 Best Local Similarity 74.3%; Pred. No. 1.7e-54;
 Matches 336; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 667 ttaaaactcttaaaagatagatattagaccattagcatatgctgactcgatgagat 726
 DB 2 TTAATAATATACAAAGACCGTGTGNAGTACCTNAGCGATATCACTTAATGAATAT 61
 QY 727 atgaagaacttaataaagaagatgcttcaataaagaattcaaaagcgctcaa 786
 DB 62 ATTAAGAACTAAACGAAGCGGTGATTTTAAATAAAGATTAAAGCGCTTAAAG 121
 QY 787 gatctgagaagagactgataataaagaagcttatataaagaagataacttcaaca 846
 DB 122 GATATTGAAAAAGCTCTGTAATAAAGACATACACGAGATACCTTACAAACNA 181
 QY 847 caattagatgcaaatcaaaaaaattgatgaagctaaactcaacaagaacatggt 906
 DB 182 CAACCTTATCAAAATGAGCAAAAGATTGANGACGTTACAAAGANGANGATGCT 241
 QY 907 aatgaattaccatttcagctgagatattcttcattcaatccgtttgaagttgattac 966
 DB 242 AATGNTTACCTATCTCTCGTTCCTTATCAATCAGTTCGANGTGTATATATAT 301
 QY 967 gcaggtggcacatcgatcgcttactactgacggaagttatgcaattccatgaaa 1026
 DB 302 GCTGTGTGATCAATCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 361
 QY 1027 atgtaaacatctctttagaagaaactgaactgaactgaactgaactgaactga 1086
 DB 362 ATGNTTATTTTGCATTATATATATATATATATATATATATATATATATATAT 421
 QY 1087 gacttcagtgaaagcgtgaagatgtagagt 1118
 DB 422 NAATTNCGNAGGTGCTGAAGATGCTGCTGT 453

RESULT 4
 US-09-265-315-9
 Sequence 9, Application US/09265315
 Patent No. 6187541
 GENERAL INFORMATION:
 APPLICANT: Benton, Bret
 APPLICANT: Lee, Ying J.
 APPLICANT: Malouin, Francois
 APPLICANT: Martin, Patrick K.
 APPLICANT: Schmid, Molly B.
 APPLICANT: Sun, Dongxu
 TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
 TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
 NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/265,315
 FILING DATE: March 9, 1999
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/714,918

Query Match	21.6%;	Score	277.2;	DB	4;	Length	453;
Best Local Similarity	74.3%;	Pred. No.	1.7e-54;				
Matches	336;	Conservative	0;	Mismatches	116;	Indels	0;
Gaps	0;						

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QY	727	atggaagaacttaataatgaagagatcttcttaataagaatttaataaagcgctcaaa	786
DB	62	ATTAAGAATCACTTAACGAAGAGCGTGATATTTAAATAAAGATTTAAATAACGGTTAAAG	121
QY	787	gatatggagaagagacctgataataagaagccttaatacaaaagagataaatcttccaaa	846
DB	122	GATATTGAAAACGCTCTGTAATTAATAAANACACATAACAACGGAGATAACTTACAACAA	181
QY	847	caattagatgcaaatcaacaaaaattgatgaagcttaaaaaacttacacaagaacatggt	906
DB	182	CAACTTGTATGCAANTAGCAAAAGATTGANGACGGTAAACGGCTACAGAAGANGANTGGT	241
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DB	242	AATGNTTTAACCATTATCTCCTGGTCTCTCTTTATCAATTCNTTTGANGTGTGTTATAT	301
QY	967	gcaggtggcacatcgaaatcgattatcgctcaactatccggaagttatgcaattcaatgaaa	1026
DB	302	GCTGGTGGTACATCAAAATGCNTTCCGTCATTTTCCGGANGTTATGCTGNGTGCATGGGAA	361
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Query Match      21.6%; Score 277.2; DB 4; Length 453;
Best Local Similarity 74.3%; pred. No. 1.7e-54;
Matches 336; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 667 ttataataactttaaagatagagtattagtsaccattagcatgttgtagcttcgatgatat 726
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2 TTTAAATATTACAAAGACCGTGTGTGAGTACCTTNAGCGTATATCACTTAAATGAATAT 61

QY 727 attgaagaactttaataatgaagagagatgtctcttaataaagaatttaaataggcgctcaaa 786

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DB 62 ATTAAGAACTAAAGAGAGCGTGATATTTTAAATAAGATTAAAGCGTTAAAG 121
QY 787 gatattgagaagaagcctgataaagaagccttaacaaagaagatactctcaaaa 846
DB 122 GATATTGAAAAACGTCTGAAAAATMAAAAGCACATMAAGCCGAGTAACCTTACACAA 181
QY 847 caattagatgacaacacaaataatgtagaagcctaataactacacaagaacatggt 906
DB 182 CAAGTGAATGCAATGACCAAAAGATTGAGAGCGTAACGCTACAAAGNAGNCATGGT 241
QY 907 aatgaataaccatttcagctgatacttctcattcaatcgtttgaagttgattac 966
DB 242 AATGNTTACCTATCTCTCGGTTTCTCTTATCAATCCNTTGAAGTTGTTATTA 301
QY 967 gcaagtggagacatcgatcgttactcgtcactatgcgggaagtatgcaatcgaaga 1026
DB 302 GCGTGGTGAATCAAAATGCMTCGTCATTTTCCGAGNCTTATGCGTCAATGGGAA 361
QY 1027 atgataactatgctttagaacaatggaatgaacgttataatcttatgagttagtg 1086
DB 362 ATGTTAATTTTGCATTAAATGATGCGATTGCGTTATTAATNCTATGCTTAGTGT 421
QY 1087 gacttcagtgagaagcgtcgaagatgtagagt 1118
DB 422 NAATTTNCAGNAGTGTCTGAGAGATGCTGTGT 453

RESULT 6
US-08-714-918-6
Sequence 6, Application US/08714918
Patent No. 6037123
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Ving
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714, 918
FILING DATE: September 13, 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Wardburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 222/005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-714-918-6

Query Match 20.0%; Score 256; DB 3; Length 410;
Best Local Similarity 76.2%; Pred. No. 1.1e-49;
Matches 310; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

DB 64 atgatagttctataatcgtatgaataaacttaaatgagatgattgattaccattag 703
QY 4 ATGACAATNTAATCTACATGCTTAAATATTACAAAGACCGTGTGTAACCTTTAG 63
DB 704 catatgtgacttcgattgattatgagaacttaataatgaaagatgttcttaata 763
QY 64 CGTATATCACTTTAATGATATATTTAAAGACTAAACGAGCGTATTTTAAAT 123
DB 764 aagatttaataagcgctcaagatatgagaagacgtgataataagaagcttata 823
QY 124 AAGATTTAAATTAAGCGTTAAAGATATGTAAGAAAGCTCTGAAATAAAGACACATA 183
DB 824 acaaaagagataactctcaacacaataatgtagaactcaacaaaaattgataagcta 883
QY 184 ACAAGCGATFAACTTACACACACACTGATGCAATGACAAAGATTGAAGAGATG 243
DB 884 aaaaactacaagaacatggttaattgataatcttctcgttgcgtgattcttcatta 943
QY 244 AACGCTACAAAGANGAATGATGATTAATCTATCTCTGCTGCTTCTTCTTATCA 303
DB 944 atcgcttgaagtgtttatttagcagggtgacatgcatgcatgcttgcatactgca 1003
QY 304 ATCCATTTGANGTGTGTTATATATGCTGCTGATGATCAATTAATGATTCGCTCATTTTCCG 363
DB 1004 gaagatgacatcaatggaataatgataaactatgctttagaagat 1050
DB 364 GAAGTTATGCGTGCATGGAATGGAATTAATTAATGATTAATCAAT 410

RESULT 7
US-09-265-315-6
Sequence 6, Application US/09265315
Patent No. 6187541
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Ving J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265, 315

Fri Jun 21 08:38:19 2002

FILING DATE: March 9, 1999
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/714,918
 FILING DATE: September 13, 1996
 APPLICATION NUMBER: 60/009,102
 FILING DATE: December 22, 1995
 APPLICATION NUMBER: 60/003,798
 FILING DATE: September 15, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 240/247
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 410 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-265-315-6

Query Match 20.0%; Score 256; DB 4; Length 410;
 Best Local Similarity 76.2%; Pred. No. 1.1e-49;
 Matches 310; Conservative 0; Mismatches 97; Indels 0; Gaps 0;
 QY 644 atgagttcttattataatcgtatgaagaacttaataatgaagaagatgtagtaccattag 703
 Db 4 ATGACAAATNTAACTACATCGCTTAAATATATACAAAGACCGTGTGTTAGTACCTTTAG 63
 QY 704 catatgttgaacttcgtatgaagaacttaataatgaagaagatgtagtaccattag 763
 Db 64 CGTATATCACTTTAATGAATATATTAAGAACTAAACGAAGAGCGTGATATTTTAAATA 123
 QY 764 aagatttaataaagcgctcaagatattgagaagacgtgataaagaagcttata 823
 Db 124 AAGATTAAATAAAGCGTTAAGGATATTGAAACGCTCTGAAATAAATAAAGACACATA 183
 QY 824 acaaaagagataatcttcaacaataattagatgcaaatcaaaaaaattgatgaagcta 883
 Db 184 ACAAGCGAGTAACTTACACACACACTTTGATGCAAAATGAGCAAAAGATTGAAGAAGGTA 243
 QY 884 aaacttaacaagaacatggttaagtaattcctatttcagctggtgattcttcatta 943
 Db 244 AACGCTACAAGAACATCGTAAATGAAATACCTATCTCTCTGTTCTTCTGTTTATCA 303
 QY 944 atccgttgaagttgtttattacagcagtgacacatcgtaacgttattcgtcactatgcg 1003
 Db 304 ATCCATTGANGTTGTTTATTATCTGCTGGTGATCAATCAATGCAATTCGGTCATTTCG 363
 QY 1004 gaagttatgaattcaatggaaaatgataaactatgcttttagaacat 1050
 Db 364 GAAGTTATGCGATGCAATGGGAATGATTAATTTGCAATTAATCAT 410

RESULT 8
 US-09-265-315-6
 ; Sequence 6, Application US/09265315
 ; Patent No. 6187541
 ; GENERAL INFORMATION:
 ; APPLICANT: Benton, Bret
 ; APPLICANT: Lee, Wing J.
 ; APPLICANT: Malouin, Francois
 ; APPLICANT: Martin, Patrick K.
 ; APPLICANT: Schmid, Molly B.
 ; APPLICANT: Sun, Dongxu
 ; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
 ; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
 ; TITLE OF INVENTION: TARGET GENES

NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/265,315
 FILING DATE: March 9, 1999
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/714,918
 FILING DATE: September 13, 1996
 APPLICATION NUMBER: 60/009,102
 FILING DATE: December 22, 1995
 APPLICATION NUMBER: 60/003,798
 FILING DATE: September 15, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 240/247
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 410 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-265-315-6

Query Match 20.0%; Score 256; DB 4; Length 410;
 Best Local Similarity 76.2%; Pred. No. 1.1e-49;
 Matches 310; Conservative 0; Mismatches 97; Indels 0; Gaps 0;
 QY 644 atgagttcttattataatcgtatgaagaacttaataatgaagaagatgtagtaccattag 703
 Db 4 ATGACAAATNTAACTACATCGCTTAAATATATACAAAGACCGTGTGTTAGTACCTTTAG 63
 QY 704 catatgttgaacttcgtatgaagaacttaataatgaagaagatgtagtaccattag 763
 Db 64 CGTATATCACTTTAATGAATATATTAAGAACTAAACGAAGAGCGTGATATTTTAAATA 123
 QY 764 aagatttaataaagcgctcaagatattgagaagacgtgataaagaagcttata 823
 Db 124 AAGATTAAATAAAGCGTTAAGGATATTGAAACGCTCTGAAATAAATAAAGACACATA 183
 QY 824 acaaaagagataatcttcaacaataattagatgcaaatcaaaaaaattgatgaagcta 883
 Db 184 ACAAGCGAGTAACTTACACACACACTTTGATGCAAAATGAGCAAAAGATTGAAGAAGGTA 243
 QY 884 aaacttaacaagaacatggttaagtaattcctatttcagctggtgattcttcatta 943
 Db 244 AACGCTACAAGAACATCGTAAATGAAATACCTATCTCTCTGTTCTTCTGTTTATCA 303
 QY 944 atccgttgaagttgtttattacagcagtgacacatcgtaacgttattcgtcactatgcg 1003
 Db 304 ATCCATTGANGTTGTTTATTATCTGCTGGTGATCAATCAATGCAATTCGGTCATTTCG 363
 QY 1004 gaagttatgaattcaatggaaaatgataaactatgcttttagaacat 1050

Db 364 GAAGTTATGCAAGTCATGGAATGATTATTAATGATTAATCAT 410

RESULT 9

US-09-266-417-6

; Sequence 6, Application US/09266417

; Patent No. 6228588

; GENERAL INFORMATION:

; APPLICANT: Benton, Bret

; APPLICANT: Lee, Ving J.

; APPLICANT: Malouin, Francois

; APPLICANT: Martin, Patrick K.

; APPLICANT: Schmid, Molly B.

; APPLICANT: Sun, Dongxu

; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS

; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS

; TITLE OF INVENTION: TARGET GENES

; NUMBER OF SEQUENCES: 111

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/266,417

; FILING DATE: March 9, 1999

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/714,918

; FILING DATE: September 13, 1996

; APPLICATION NUMBER: 60/009,102

; FILING DATE: December 22, 1995

; APPLICATION NUMBER: 60/003,798

; FILING DATE: September 15, 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 240/248

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELETYPE: 67-3510

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 410 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-09-266-417-6

Query Match

Best Local Similarity

Matches 310; Conservative

20.0%; Score 256; DB 4; Length 410;

Pred. No. 1,1e-49;

Mismatches 97; Indels 0; Gaps 0;

Db 644 atgagttctatataatgataaacttaagatagattagaccattag 703

Db 4 ATGACAATWTAACTACATACGCTTAAATTTACAAAGACCGTGTGACCTTTAG 63

Qy 704 catgttgacttgatgataatgagaacttaataatgaagagatgtcttaata 763

Db 64 CGTATATCAACCTTTAATTAATTAATTAAGACATAAGAGGCTATATTTAAATA 123

Qy 764 aagatttaataagcgctcaagatatltgagaagaccctgataataagaagctata 823

Db 124 AAGATTAAATTAAGCGCTTAAGATATTGAAAAACGCTGAAAAATTAAGACACTA 183

Qy 824 acaaaagataatcttcacacaaatagatgacaaatcaacaaaaatgataagcta 883

Db 184 ACAAGGAGATTAACCTTACACAACTGATGCAAAATGAGCAAAAGATTGAAGAAGTA 243

Qy 884 aaacttaacaaagacatgataatgataatcttacttcaagctgatatcttcatta 943

Db 244 AAGCTTACAGANAGACATGTAATGAAATTAATCTATCTCTCTCTCTCTCTTATCA 303

Qy 944 atccgttgagttgttataatgacagtgagacatgacatgacatgacatgacatg 1003

Db 304 ATCCATTGAGCTTCTTTATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 363

Qy 1004 gaagtatgacatgataatgataatgataatgataatgataatgataatgataat 1050

Db 364 GAAGTTATGCAAGTCATGGAATGATTATTAATGATTAATCAT 410

RESULT 10

US-08-714-918-4/C

; Sequence 4, Application US/08714918

; Patent No. 6037123

; GENERAL INFORMATION:

; APPLICANT: Benton, Bret

; APPLICANT: Lee, Ving

; APPLICANT: Malouin, Francois

; APPLICANT: Martin, Patrick K.

; APPLICANT: Schmid, Molly B.

; APPLICANT: Sun, Dongxu

; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL

; TITLE OF INVENTION: TARGET GENES

; NUMBER OF SEQUENCES: 111

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/714,918

; FILING DATE: September 13, 1996

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/009,102

; FILING DATE: December 22, 1995

; APPLICATION NUMBER: 60/003,798

; FILING DATE: September 15, 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 222/005

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELETYPE: 67-3510

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 400 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-714-918-4

us-09-509-234c-46.rni

Fri Jun 21 08:38:19 2002

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Query Match      17.28; Score 221.2; DB 3; Length 400;
Best Local Similarity 72.88; Pred. No. 8.2e-42;
Matches 291; Conservative 0; Mismatches 108; Indels 1; Gaps 1;

QY 205 gggccagtgattgattgataaagaagcgttgcttcaacttttttcttaataatgaattaa 264
Db 400 GTCGCGTGGATTGANTATGAAATCAAGNACTGCTACACTTTTCTTAAATGAATTATCC 341
QY 265 -aaatgtataaagaacataattgttatttcaatgaagtgaccccttatctcttaca 323
Db 340 AAAATATGTTAAATAACATCGTTGCTATACCTACATACATGATCCATTTACCATATCA 281
QY 324 atacttaataatcagcgtgaaatattggaatgctggccatgattggtttttcaataa 383
Db 280 ATACTTGAATCATGATGGCGAGATTACAGGTAATGCTGGTAATGATGGTCTTTGATAA 221
QY 384 gatggaagaattaggattgaacatgaagcgtttcacaagaagcgttaagtgactcaaa 443
Db 160 AATCCGTTATCAGTCAGTGTAGATTAAAGATAAAACAGCAGATGACATCATTTNAAA 101
QY 504 atggtatgatttaagaagcgttaactaagaagaacatacaaaaaaagtggtcacaagtc 563
Db 100 TATGGATGACTTAGAAAAAGAACACACGGAANNAGTTNAAAGAGATGGTGTAAAGTAAG 41
QY 564 ttccctatccgaagtgaaattacattcttctttagatcatt 603
Db 40 ATTTTATCTGAAGGAGNACTACCAATTTTATAGATTATT 1

RESULT 11
US-09-265-315-4/C
; Sequence 4, Application US/09265315
; Patent No. 6187541
; GENERAL INFORMATION:
; APPLICANT: Benton, Bret
; APPLICANT: Lee, Ving J.
; APPLICANT: Malouin, Francois
; APPLICANT: Martin, Patrick K.
; APPLICANT: Schmid, Molly B.
; APPLICANT: Sun, Dongxu
; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
; TITLE OF INVENTION: TARGET GENES
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/265,315
; FILING DATE: March 9, 1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/714,918
; FILING DATE: September 13, 1996
; APPLICATION NUMBER: 60/009,102
; FILING DATE: December 22, 1995
; APPLICATION NUMBER: 60/003,798

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; FILING DATE: September 15, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 240/247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 400 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-265-315-4

Query Match      17.28; Score 221.2; DB 4; Length 400;
Best Local Similarity 72.88; Pred. No. 8.2e-42;
Matches 291; Conservative 0; Mismatches 108; Indels 1; Gaps 1;

QY 205 gggccagtgattgattgataaagaagcgttgcttcaacttttttcttaataatgaattaa 264
Db 400 GTCGCGTGGATTGANTATGAAATCAAGNACTGCTACACTTTTCTTAAATGAATTATCC 341
QY 265 -aaatgtataaagaacataattgttatttcaatgaagtgaccccttatctcttaca 323
Db 340 AAAATATGTTAAATAACATCGTTGCTATACCTACATACATGATCCATTTACCATATCA 281
QY 324 atacttaataatcagcgtgaaatattggaatgctggccatgattggtttttcaataa 383
Db 280 ATACTTGAATCATGATGGCGAGATTACAGGTAATGCTGGTAATGATGGTCTTTGATAA 221
QY 384 gatggaagaattaggattgaacatgaagcgtttcacaagaagcgttaagtgactcaaa 443
Db 220 AATGAGTAACCTTAGGATTGACATACATGATCCATAAAGGATTTGATCCTGTGCTACA 161
QY 444 agtaagatattcattcagtttttagatttaagaagataaaacggcttaagtgactcaaa 503
Db 160 AATCCGTTATCAGTCAGTGTAGATTAAAGATAAAACAGCAGATGACATCATTTNAAA 101
QY 504 atggtatgatttaagaagcgttaactaagaagaacatacaaaaaaagtggtcacaagtc 563
Db 100 TATGGATGACTTAGAAAAAGAACACACGGAANNAGTTNAAAGAGATGGTGTAAAGTAAG 41
QY 564 ttccctatccgaagtgaaattacattcttctttagatcatt 603
Db 40 ATTTTATCTGAAGGAGNACTACCAATTTTATAGATTATT 1

RESULT 12
US-09-265-315-4/C
; Sequence 4, Application US/09265315
; Patent No. 6187541
; GENERAL INFORMATION:
; APPLICANT: Benton, Bret
; APPLICANT: Lee, Ving J.
; APPLICANT: Malouin, Francois
; APPLICANT: Martin, Patrick K.
; APPLICANT: Schmid, Molly B.
; APPLICANT: Sun, Dongxu
; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
; TITLE OF INVENTION: TARGET GENES
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.

```


Fri Jun 21 08:38:19 2002

us-09-509-234c-46.rml

Page 11

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 5253 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-265-315-19

Query Match 7.68; Score 97.6; DB 4; Length 5253;
Best Local Similarity 46.38; Pred. No. 1.7e-13;
Matches 396; Conservative 1; Mismatches 450; Indels 9; Gaps 2;
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DB 2968 ttgcataaattggaaagcgcttggttttaacataaagatttaagagctttatcaca 2909
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DB 2908 agactacatgcacacgacatgactatgattacacaaattgataaataatgatgagtt 2849
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DB 2848 attaaatagtttgaacgacgcaaatcgttcaaaaatgacgcttttaaaacgagttac 2789
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QY 1146 tgaatgattgaatgtagatgatttatacaagcattgaatgaatgaatgaatgaatgaatgaatgaat 1205
DB 2188 atacttaagtaaaagattggaattgattgattgattgattgattgattgattgattgattgatt 2129
QY 1206 ctataagcattaa 1221
DB 2128 aattgacagagttaaa 2113

Search completed: June 20, 2002, 12:04:01
Job time: 20956 sec

us-09-509-234c-46.rni

Fri Jun 21 08:38:19 2002

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2002, 14:26:42 ; Search time 8551.36 Seconds
(without alignments)
2025.010 Million cell updates/sec

Title: US-09-509-234C-46

Perfect score: 1283
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Gapop 10.0 , Gapext 1.0

Searched: 13736207 segs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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EST:*
1: em_estba:*
2: em_esthm:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83.8	6.5	877	12	A2531291
2	82.2	6.4	912	12	A2551092
3	81.4	6.3	843	12	A2551618
4	81	6.3	905	12	A2550256
5	80	6.2	908	12	A2548467
6	74.6	5.8	849	12	A2546009
7	74.6	5.8	1101	12	CNS000EVL
8	74.4	5.8	879	12	CNS01RGC
9	73.2	5.7	1101	12	CNS0039G
10	73	5.7	614	12	CNS0152H
11	71	5.5	931	12	BH160272
12	70.4	5.5	1135	12	CNS033GO
13	68.6	5.3	1101	12	CNS01219
14	68.6	5.3	1101	12	CNS0153V
15	67.8	5.3	994	12	CNS04KOU
16	67.8	5.3	1007	12	CNS06X9S
17	67.6	5.3	769	12	AG134867

C 18	67.6	5.3	1201	12	CNS0167M	AL106396 Drosophila
19	67.4	5.3	936	12	CNS07ANM	AL436808 T7 end of
20	66.2	5.2	976	12	BH149983	BH149983 ENT023TRF
21	66	5.1	575	10	BM167050	BM167050 EST369573
22	65.6	5.1	768	12	CNS01VSE	AL168683 Tetradodon
23	65.6	5.1	928	12	CNS00DKY	AL071865 Drosophila
24	65.6	5.1	982	12	A0325799	A0325799 nbx0021B
25	65.6	5.1	1096	12	B09949	B09949 T1F7-5P6 TA
26	65	5.1	1059	12	CNS0022B	AL097133 Drosophila
27	64.8	5.1	967	12	CNS0072W	AL433362 T7 end of
28	64.6	5.0	867	12	CNS0054A	AL057618 Drosophila
29	64.6	5.0	1101	12	CNS001FB	AL060732 Drosophila
30	64.6	5.0	1101	12	CNS017YG	AL108658 Drosophila
31	64.4	5.0	981	12	CNS02BD8	AL189701 Tetradodon
32	64.2	5.0	1034	12	CNS0154T	AL104988 Drosophila
33	64	5.0	984	12	CNS03WVO	AL252575 Tetradodon
34	64	5.0	1036	12	CNS00599	AL057797 Drosophila
35	63.6	5.0	483	12	CNS02CV8	AL191645 Tetradodon
36	63.6	5.0	941	12	A2682404	A2682404 ENT1016TF
37	63.4	4.9	802	12	A2197934	A2197934 SP_1036.B
38	63.4	4.9	891	12	A2683582	A2683582 ENT047TR
39	63.4	4.9	970	12	CNS0182A	AL108796 Drosophila
40	63.2	4.9	660	12	BH183498	BH183498 023.L-07-
41	63.2	4.9	660	12	CNS07ONJ	AL620449 T3 end of
42	63.2	4.9	990	12	CNS006OI	AL065624 Drosophila
43	63.2	4.9	1101	12	CNS003BD	AL064091 Drosophila
44	63	4.9	1092	12	CNS020K7	AL175696 Tetradodon
45	63	4.9	1101	12	CNS016LI	AL106896 Drosophila

ALIGNMENTS

RESULT 1
LOCUS A2531291/c
DEFINITION ENT034TR Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, DNA sequence.
ACCESSION A2531291 GI:11085838
VERSION A2531291.1
KEYWORDS GSS.
SOURCE Entamoeba histolytica.
ORGANISM Entamoeba histolytica.
REFERENCE 1 (bases 1 to 877)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
Unpublished (2000)
CONTACT: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: b.loftus@tigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared DNA library
Seq primer: M13-Reverse
Class: shotgun
High quality sequence start: 22
High quality sequence stop: 829.
Location/Qualifiers
1. 877
/organism="Entamoeba histolytica"
/strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pROSL; Site 1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a

155 a	266 c	18 g	404 t
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ORIGIN	Query Match	6.3%	Score 81.4	DB 12	Length 843
	Best Local Similarity	47.0%	Pred. No. 0.00018		
	Matches 287	Conservative	0	Mismatches 321	Indels 3
					Gaps 1
QY	301	gttgacccttattcttccttcaataacttaatacgaatgacgctggaattatttgaatgct	360		
Db	817	GATGAAGAAGATGATGATGATGAAGAAGATGATGATGAAGAAGATGATGAAGAAGATGAT	758		
QY	361	gaccatgattggttttccaataagatgtaagaatttgattggaattggaatgagcttcaat	420		
Db	757	GAAAGAAGAGATGTGATGATGAAGAAGATGAAGATGATGAAGAAGATGATGAAGAAGAT	698		
QY	421	aaaggtccatccatcttaccataagtaagataatcattcagttttagatttaagaataa	480		
Db	697	TTGGAAGATGATGATGATGAAGAAGATGAAGATGATGAAGAAGATGATGAAGAAGAT	638		
QY	481	acggttaagaatgactcaagaagatgatagttttaagaagcgaataactactaagaagta	540		
Db	637	GACGACGATATGATGATGATGAAGAAGATGATGATGATGAAGAAGATGATGAAGAAGAT	578		
QY	541	caaaaaatggtgtccaagatcgcttctcctacgaaagatgaattaccatcttagatca	600		
Db	577	GAAAGAAGATGATGATGAAGAAGATGATGATGAAGAAGATGATGAAGAAGATGAAGAAGAT	521		
QY	601	ttatagaaagatactacagaacgaagaagttcgcgatagatgatagtttctattat	660		
Db	520	GATGATGAAGATGATGATGAAGAAGATGATGATGATGAAGAAGATGATGAAGAAGATGAAGAAGAT	461		
QY	661	aatgataataactttaaagttagatgatttagtaccattagcattcattggttgcattcgat	720		
Db	460	GACGACGATATGATGATGATGAAGAAGATGATGATGAAGAAGATGATGAAGAAGATGAAGAAGAT	401		
QY	721	gagatattggaagaacttaataatgaagaagtttcttaataagaatttaataaagct	780		
Db	400	GAAAGATGATGATGAAGAAGATGATGAAGAAGATGATGATGAAGAAGATGATGAAGAAGAT	341		
QY	781	ctcaagaataattgagaagaagcctgataataagaagcttaatacaaaagagatactt	840		
Db	340	GAAATGATGATGAAGAAGATGATGATGAAGAAGATGATGAAGAAGATGATGAAGAAGATGAAGAAGAT	281		
QY	841	caagaagaattatgataatgacaatcaacaaatctgataagcttaaaacttaacaaga	900		
Db	280	GAAAGATGATGATGAAGAAGATGATGAAGAAGATGATGAAGAAGATGATGAAGAAGATGAAGAAGAT	221		
QY	901	catgtaattga	911		
Db	220	GATGAAGAAGA	210		
RESULT 4					
LOCUS	AZ550256/c	905 bp	DNA	linear	GSS 14-NOV-2000
DEFINITION	ENTRE58tr Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, DNA sequence.				
ACCESSION	AZ550256				
VERSION	AZ550256.1	GI:1175557			
KEYWORDS	GSS.				
ORGANISM	Entamoeba histolytica.				
REFERENCE	1 (bases 1 to 905)				
AUTHORS	Loftus, B., Van Aken, S. and Fraser, C.				
TITLE	Determination of clone end sequences from Entamoeba histolytica				
COMMENT	HMI:IMSS sheared DNA library				
	Unpublished (2000)				
	Contact: Brendan J Loftus				
	Department of Eukaryotic Genomics				
	The Institute for Genomic Research				
	9712 Medical Center Dr., Rockville, MD 20850, USA				
	Tel: 301 838 0208				

Fax: 301 838 3543
Email: bjloufust@tigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared DNA library
Seq primer: M13-Reverse
Class: shotgun
High quality sequence start: 100
High quality sequence stop: 872.
Location/Qualifiers
1. .905
/organism="Entamoeba histolytica"
/strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: PHOS1; Site_1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999)."
BASE COUNT 203 a 260 c 46 g 396 t
ORIGIN

Query Match 6.3%; Score 81; DB 12; Length 905;
Best Local Similarity 46.1%; Pred. No. 0.0002;
Matches 310; Conservative 0; Mismatches 360; Indels 3; Gaps 1;
QY 439 ttacaagtagatcattcagtttagattttaaagaataaaacggctaaagatttactc 498
Db 777 TTAGAAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 718
QY 499 aaaggaatgtagtttaagaagcgttaatacgaagaagacacaaataatgtgcaaa 558
Db 717 GAAGACGAAGAAGATGAAGAAGATGATGATGATGATGATGATGATGATGATGAT 658
QY 559 gtccgtttctctccgaagatgaattaccattctttagatcattatttgaagatactaca 618
Db 657 GATCAATTTGATTAAGATGAAGAAGATGAAGAAGATGAAGAAGATGAAGAAGAT 598
QY 619 gaaacgaagaggttcgacgtagatgtagttctattattattattattattattattatt 678
Db 597 GATGAAGATGATGAAGATGAAGAAGATGATGATGATGAAGAAGATGAAGAAGAT 538
QY 679 aaagtagatgatttagtaccattagcatattgttgccttcgattgattattgaagaactt 738
Db 537 GATGATGATGAATTTGATTTAGACATGAAGAAGATGAAGAAGATGAAGAAGATGATGAT 478
QY 739 aataatgaagagatgtttcttaataagatttaataagagcgtcgaagattattggaag 798
Db 477 GATGATGATCAAGATGATCAAGATGATCAAGATGATCAAGATGATCAAGATGATCAAGAT 418
QY 799 agactgataaagaagcgttatacaagaagagataatcttcaacaacaattagatgca 858
Db 417 GATGATGATGATGATGAAGAAGATGAAGAAGATGATGAATTTGAATTAGA---A 361
QY 859 aatcaacaataattgtagcgttaaaacttacaacaagaacatggtaattgaattacct 918
Db 360 GATGAAGAAGATGAAGATGATGAAGAAGATGAAGAAGATGAAGAAGATGAAGAAGAT 301
QY 919 attcagctggatatttcttattattattattattattattattattattattattattatt 978
Db 300 TTAGAAGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAGAT 241
QY 979 tgaatcgttattcgtcattcattcccggaagttatgccaattcgaatggaataatgataaactat 1038

Db 240 GAAGAAGATGATGATGAAGATGAAGAAGATGATGATGATGATGATGATGATGATGAT 181
QY 1039 gctttagaacatgaattaacgctttataatttttttagtgagtttagtgggacttcagtgaa 1098
Db 180 GAAGATGACGAAGATGTTGATGAAGATGACGAAGATGTTGACGATTTTGAATTAGAAGAT 121
QY 1099 gacgctgaagatg 1111
Db 120 GAAGAAGAAGATG 108
RESULT 5
AZ548467 908 bp DNA linear GSS 14-NOV-2000
LOCUS ENPEK30TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
DEFINITION genomic, DNA sequence.
ACCESSION AZ548467
VERSION AZ548467.1 GI:11172102
KEYWORDS GSS.
SOURCE Entamoeba histolytica.
ORGANISM Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
REFERENCE 1 (bases 1 to 908)
AUTHORS Loftus, B., Van Aken, S. and Fraser, C.
TITLE Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloufust@tigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared DNA library
Seq primer: M13-Reverse
Class: shotgun
High quality sequence start: 17
High quality sequence stop: 828.
Location/Qualifiers
1. .908
/organism="Entamoeba histolytica"
/strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: PHOS1; Site_1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999)."
BASE COUNT 434 a 16 c 289 g 169 t
ORIGIN

Query Match 6.2%; Score 80; DB 12; Length 908;
Best Local Similarity 46.2%; Pred. No. 0.0003;
Matches 303; Conservative 0; Mismatches 350; Indels 3; Gaps 1;
QY 256 gaattaagtaaatgtataaaagcataattgtctttattcttaagagttgacccattctt 315
Db 16 GAAGAAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 75
QY 316 ccttcatcaacttaataatcagcgttgaaattatttggaaatcgtggccatgattggttt 375

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Db      76 GATGAGAGAGATGATGATGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGAT 135
QY      376 ttcaataagatggaagaattgaattgaacatgaaggttcataaaggtccatccat 435
Db      136 GATGAGAGATGATGATGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGAT 195
QY      436 atcttaagaatgaatcatcattgaattgaattgaattgaattgaattgaattgaattga 495
Db      196 GATGAGAGAGATGATGATGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGAT 255
QY      496 ctcaagaatgatatgtttaagaaggtatatacttaagaaggtatatacttaagaaggtat 555
Db      256 TTGAGAGAGATGATGATGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGAT 315
QY      556 aaagtcggttcctccatccgaagaatgaattacattctttagatcattatggaagat 615
Db      316 GAGAGATGATGATGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGAT 372
QY      616 acagaagaagaagatgcgcgaatagaatgaattcattatataatcgcattaaatc 675
Db      373 GATGAGAGAGATGATGATGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGAT 432
QY      676 cttaagaatgaatcattgaatcattgaatcattgaatcattgaatcattgaatcattga 735
Db      433 TTGAGAGATGATGATGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGAT 492
QY      736 cttaagaatgaagaatgattcttaagaatgaattgaatgaattgaatgaattga 795
Db      493 GATGATGATGAGAGAGATGATGATGATGAGAGAGATGATGATGAGAGAGATGATGAT 552
QY      796 aagagaacctgaataaagaagcttaacaagaagatcattcacaacaatgaat 855
Db      553 GAAGAGATGATGATGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGAT 612
QY      856 gcaaatcaacaataattgattgaagcttaacaagaagatcattcacaacaatgaat 911
Db      613 GAAGAGAGATGATGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGAT 668

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RESULT 6
LOCUS   A2546009 849 bp DNA linear GSS 14-NOV-2000
DEFINITION
ENTW537F Entamoeba histolytica Sheared DNA Entamoeba histolytica
genomic, DNA sequence.
ACCESSION
VERSION A2546009.1 GI:1167130
KEYWORDS
SOURCE  GSS.
        Entamoeba histolytica.
        Entamoeba histolytica.
        Eukaryota; Entamoebidae; Entamoeba.
REFERENCE
AUTHORS Loftus, B., Van Aken, S. and Fraser, C.
TITLE   1 (bases 1 to 849)
        Determination of clone end sequences from Entamoeba histolytica
        HMI:IMSS sheared DNA library
        Unpublished (2000)
        Contact: Brendan J Loftus
        Department of Eukaryotic Genomics
        The Institute for Genomic Research
        9712 Medical Center Dr., Rockville, MD 20850, USA
        Tel: 301 838 0208
        Fax: 301 838 3543
JOURNAL
COMMENT

```

```

FEATURES
source
Class: shotgun
High quality sequence start: 26
High quality sequence stop: 796.
Location/Qualifiers
1..849
/organism="Entamoeba histolytica"
/strain="HMI:IMSS"
/db_xref="taxon:5759"

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/clone_1lb="Entamoeba histolytica Sheared DNA"
/Note="Vector: pROSI; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broch cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaubin and B.
Barrell, Oxford University Press, 1999)."
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Query Match          5.8%; Score 74.6; DB 12; Length 849;
Best Local Similarity 44.9%; Pred. No. 0.0025;
Matches 284; Conservative 0; Mismatches 349; Indels 0; Gaps 0;

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QY      388 gaagaatgagattgaacatgaaggttcataaaggttcattcattcattcattcattc 447
Db      730 GAAATGTAAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGAT 671
QY      448 agatcattcattcattcattcattcattcattcattcattcattcattcattcattcattc 507
Db      670 GATGATGATGATGATGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGAT 611
QY      508 gataattgaagaagcgttaactcaagaagtcacaagaatggtgtaagtcgttc 567
Db      610 GAAGAAGAAGATGATGATGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGAT 551
QY      568 ctatccgaagtgattaccattcattcattcattcattcattcattcattcattcattcattc 627
Db      550 GAAGATGAGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGAT 491
QY      628 gaattccgcgaatagatgattcattcattcattcattcattcattcattcattcattcattc 687
Db      490 GAAGATGAGAGAGATGATGATGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAT 431
QY      490 gattagattcattcattcattcattcattcattcattcattcattcattcattcattcattc 747
Db      688 gattagattcattcattcattcattcattcattcattcattcattcattcattcattcattc 771
QY      430 GATTTGAAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGAT 371
QY      748 agagatgattcattcattcattcattcattcattcattcattcattcattcattcattcattc 807
Db      370 GATGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGAT 311
QY      808 aataagaagaagcttaacaagaagatactcacaacaagaatgaatgaatgaatgaatgaatga 867
Db      310 GATGAGATGAGAGATGAGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGAT 251
QY      868 aaaaattgaggaagccttaacaagaagatcattcattcattcattcattcattcattcattc 927
Db      250 GATGAGATGAGAGATGAGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGAT 191
QY      928 ggaattcattcattcattcattcattcattcattcattcattcattcattcattcattcattc 987
Db      190 GAAGATGAGAGATGAGAGATGAGAGAGATGAGAGATGAGAGATGAGAGATGAGAGAT 131
QY      988 tatcgtcattcattcattcattcattcattcattcattcattcattcattcattcattcattc 1020
Db      130 GATGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGAT 98

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RESULT 7
LOCUS   CNS00EVL 1101 bp DNA linear GSS 04-JUN-1999
DEFINITION
BACR29B23 of RPCT-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

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[illegible]

OY 564 ttctcattccgaagatgaattaccatcttagatcatcttctgaagatctcagaac 623
 DB 639 AAAAGTTTATKAKMKAMGAAAAAKGAAAAATTGWWGTTDAAAATAATGACAAAAA 580
 OY 624 gaaagatcgccgagatagatagatctctatcatatcatgaataaacttaaga 683
 DB 579 AAGAGGWRAGCKRGARAAAGAAACAKMAAAAAAAATGTTARAAATGAAAAA 520
 OY 684 tagagattagatcattacatagatctgctgagatctatctgaagactataa 743
 DB 519 KAKATRRRAAAAAAAMKRGAAAKR--GAGCAAAAAARAGATKAKAAAAA 462
 OY 744 tgaagagatgctcttaataagaattaaagcgctcaagatctgagaagacc 803
 DB 461 TDAATAAAATKAWTMBAAAAAGAKAGKATATCTDRAAAAAAADAANAANA 402
 OY 804 tgaataagaagaactatacaaaagagatacttcaacaacattagatcaatca 863
 DB 401 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 342
 OY 864 acaaaattgtagaagctaaacttaacaagaacatgtaataga 912
 DB 341 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 293

 RESULT 9
 CENS00396/c 1101 bp DNA linear GSS 03-JUN-1999
 LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #
 DEFINITION BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 AL063921
 VERSION AL063921.1 GI:4941778
 KEYWORDS GSS.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 1101)
 REFERENCE
 AUTHORS Direct Submission
 TITLE Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 COMMENT Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see http://www.fruitfly.org The BDGP Drosophila
 melanogaster BAC library was prepared by Kazutoyo Oseegawa and
 Aaron Mamoser in Peter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPCI-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 IsoGenic strain Y2; cn bw sp, the same strain used for the BDGP's
 P1 and EST libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

 FEATURES
 source 1. 1101
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone_lib="RPCI-98"
 /clone="BACR08K10"
 /note="end : TET3"
 BASE COUNT 201 a 64 c 131 g 202 t 503 others
 ORIGIN
 Query Match 5.7%; Score 73.2; DB 12; Length 1101;
 Best Local Similarity 17.6%; Pred. No. 0.0042;

Matches 119; Conservative 285; Mismatches 270; Indels 2; Gaps 1;
 OY 276 aaagcataattgcttctcctaagagttgacccattctctcacaacttaacaa 335
 DB 1091 WDRDTRKDDMDWTWKMTWMDRADRRWAGDADRWAMWDGATWTTWMMWMMWATMD 1032
 OY 336 tgaagtggaattatgaatggaatggtgcattggtttcctaagaatgaatga 395
 DB 1031 TMDKMMWMAATKATDTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMT 971
 OY 396 aggattgacaatgaaggtcttcaaaaggtccatccatctcctaagaatgaatca 455
 DB 972 -RKDKRDRKDGDDKGGKKAKAKAKATKWDMDMDKDKWMDGAKXDRKDDGAG 914
 OY 456 ttcagtttagattaaaagataaagcgttaagatgctactcaaaagaaatgatt 515
 DB 913 DKDDGKXKADDDYDGTKDDDDKDKMDWDKAKGTWGDATWMAATDMMWMDADMM 854
 OY 516 aagaagcgttaacttaagaagaatgaacaaatggtgcaagtcgcttccatcga 575
 DB 853 TWDAADDMWADDRWDAMWAKWMDAMWAKRTADRRDMDRAGKRGARRRRKADDX 794
 OY 576 agatgaattaccatctttagatcattatgaagaatactacagaagaagatgcg 635
 DB 793 RDAADDKDDAATWTTTWTTRDTRDTRDTRDTRDTRDTRDTRDTRDTRDTRDTR 734
 OY 636 cgatagagatgattctctatataatcgattaaatacttaagaatgattatg 695
 DB 733 WRRTWRRMRKRDTRDMDADDDYADRRRRRGGDADGKKTKGRRRRRRORATWDT 674
 OY 696 accattgcatatggtgactcgatgagatattggaagacttaagaagaatgatt 755
 DB 673 DAWWADAAWTTTDTDTDDMDKRRRKGARRRRRTTARAAWMTWMTWMTWMTWMT 614
 OY 756 tottaataagaatttaagaagcgctcaagaatattgagaagaccctgaataaga 815
 DB 613 ADRWDRAADTWDARADKADRAKRAARARADRAADRAADRTWTKKTATATWTTAA 554
 OY 816 agctatacaaaagataatcttcaacaacaaatagatgacaacaaatga 875
 DB 553 RAAMWAMWMAATTTATWTTTWTWTTTWTWTTTWTWTTTWTWTTTWTWTTTWTW 494
 OY 876 tgaagctaaacttcaacaagaacatgtaagattactctattgaagtcgatt 935
 DB 493 WAAAAAAMWATTTTWTWTTTWTWTTTWTWTTTWTWTTTWTWTTTWTWTTTWT 434
 OY 936 ctcttaatacgttt 951
 DB 433 TWMAATTTATTTWTTT 418

 RESULT 10
 CENS0152H 614 bp DNA linear GSS 26-JUL-1999
 LOCUS Drosophila melanogaster genome survey sequence SPE end of BAC
 DEFINITION BACN12N03 of DrosBAC library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 AL104915
 ACCESSION AL104915.1 GI:5616929
 VERSION
 KEYWORDS GSS.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 614)
 REFERENCE
 AUTHORS Direct Submission
 TITLE Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
 JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 COMMENT Determination of this BAC-end sequence was carried out as part of a
 collaboration with the European Drosophila Genome Project (EDGP) -

QY	1065	taattcttatgagtaagtctggggaactcagtgagaagccgtgaagaatctctggggtaattaa	1124
Db	550	TCATGATGAAGAAGATGATGATGAAGAATGATGAAGAAGTAAAGTATGATGAAGAAGATGA	609
OY	1125	gttcaaaaaagcctaataatcgcgtgattatgatatgtagtga	1169
Db	610	AGATGATGAAGAATGATGATGAAGAATGATGAAGAATGATGAAGAATGATGA	654

RESULT 12	CNS03330Q	1135 bp	DNA	linear	GSS 15-MAY-2000
LOCUS	CNS03330Q				
DEFINITION	Tetradodon nigroviridis genome survey sequence PUC-ORI end of clone 208924 of library G from Tetradodon nigroviridis, genomic survey sequence.				
ACCESSION	AL226115.1	GI:7885026			
VERSION	GSS, genome survey sequence.				
KEYWORDS	Tetradodon nigroviridis.				
SOURCE	Tetradodon nigroviridis				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetradodon.				
REFERENCE	1 (bases 1 to 1135)				
AUTHORS	Roest-Crollius, H., Jalllon, O., Dasilva, C., Fizes, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.				
TITLE	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradodon nigroviridis				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 1135)				
AUTHORS	Roest-Crollius, H., Jalllon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizes, C., Winkler, P., Brothier, P., Quetier, F., Saurin, W. and Weissenbach, J.				
TITLE	Human gene number estimate provided by genome wide analysis using Tetradodon nigroviridis DNA sequence				
JOURNAL	Unpublished				
REFERENCE	3 (bases 1 to 1135)				
AUTHORS	Genoscope.				
TITLE	Direct Submission				
JOURNAL	Submitted (12-AGR-2000) to the EMBL/GenBank/DBJ databases				
COMMENT	This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetradodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetradodon .				
FEATURES	location/Qualifiers				
source	1..1135				
	/organism="Tetradodon nigroviridis"				
	/db_xref="taxon:99883"				
	/clone="208P24"				
	/clone_1lb="G"				
	/note="Genoscope sequence ID : C0AG208DH12SP1-end : PUC-ORI"				
BASE COUNT	863 a 65 c 43 g 124 t 40 others				
ORIGIN					
Query Match	5.5%; Score 70.4; DB 12; Length 1135;				
Best Local Similarity	45.8%; Pred. No. 0.012;				
Matches 197; Conservative	10; Mismatches 223; Indels 0; Gaps 0				

OY	531	taagaatatacaaaaaatggtgctaaagtcgtttccatccgaagatgaattacccat	590
Db	460	AAAAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	519
OY	531	taagaatatacaaaaaatggtgctaaagtcgtttccatccgaagatgaattacccat	590
Db	520	AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	579
OY	591	ctttagatcatttagaagaatactacagaaacgaagaagatgctgcgagatgagatgata	650

[illegible]

Db 145 AGTTGAGGTTAAAAAGTTGCAATTTATATAAAATTTTATATAAAAGGAAATTAATAWAAA 204

Qy 563 gtttctatcgaagatgaattacacattctttagatcattttagatggaagatgactacagaa 622

Db 205 AGAAAAATTAATWAAAWAAAAAATAAAAAAAGGAAAAAGTAAWAAWTTAA 264

Qy 623 cgaagagtcgcgagatgagatgagttctattataatcattataaataactttaaag 682

Db 265 WMAWAACTTAATWAAWAAAAAATAATTTWTTWAAAWAAAAAATTTAAAAA 324

Qy 683 atagatgattagaccatgacatgctgtgacttcgatgagatgattatgaagaacttaata 742

Db 325 AAAAAATAGAAAAATTAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 384

Qy 743 atgaagagatgcttctataaagatttaataagcgcgcacaaagatattgagaagagac 802

Db 385 CAATAAAAAAATAATWAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA 444

Qy 803 ctgataatgaagagcttatacaaaagagataatcttcaacaacaaatagatgcacaaac 862

Db 445 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA 504

Qy 863 acaaaaaattgtagcgttaaaacttaacaagaacatggtgaatgactaccta 919

Db 505 TATAAAWATTAATAATTTTAAATATAAGATWAAAAAATAAAAAAATTAATAATA 561

RESULT 14

CNS0153V 1101 bp DNA linear GSS 26-JUL-1999

LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC

DEFINITION BACN12N03 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL104965

VERSION AL104965.1 GI:5616979

KEYWORDS GSS.

SOURCE fruit fly.

ORGANISM Drosophila melanogaster

REFERENCE Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 1101)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ac.uk - . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.

FEATURES

source 1..1101

Location/Qualifiers

/organism="Drosophila melanogaster"

/plasmid="pBeloBAC11"

/db_xref="taxon:7227"

/clone_lib="DrosBAC"

/clone="BACN12N03"

/note="end : 77"

BASE COUNT 722 a 51 c 54 g 90 t 174 others

ORIGIN

Query Match 5.3%; Score 68.6; DB 12; Length 1101;

Best Local Similarity 44.3%; Pred. No. 0.025;

Matches 209; Conservative 12; Mismatches 251; Indels 0; Gaps 0;

Qy 441 acaagtaagatcattcattcagtttagatttaaaagataaagcgttaagatgactca 500

Db 9 ANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 68

Qy 501 aggaatgtagtttaagaagcgttaactactaagaagtcacaaatggtgtcaagt 560

Db 69 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 128

Qy 561 cgtttctctcgaagatgaattacacattctttagatcattttaggaagatcagaga 620

Db 129 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 188

Qy 621 aacgaagagtcgcgagatgagatgagttctattataatcattataaataactttaa 680

Db 189 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 248

Qy 681 agatagagatttagaccatgacatgctgtgacttcgatgagatgatttgaagaactta 740

Db 249 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 308

Qy 741 taatgaagagatgcttctataaagatttaataagcgcgcacaaagatattgagaagag 800

Db 309 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 368

Qy 801 acctgataatgaagagcttatacaaaagagataatcttcaacaacaaatgagatgc 860

Db 369 AATAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 428

Qy 861 tcaacaanaaattgtagcgttaaaacttaacaagaacatggttaagaa 912

Db 429 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 480

RESULT 15

CNS04NOJ 994 bp DNA linear GSS 21-MAY-2000

LOCUS Tetraodon nigroviridis genome survey sequence T7 end of clone

DEFINITION 122P04 of library G from Tetraodon nigroviridis, genomic survey sequence.

ACCESSION AL298972

VERSION AL298972.1 GI:8037822

KEYWORDS GSS; genome survey sequence.

SOURCE Tetraodon nigroviridis.

ORGANISM Tetraodon nigroviridis

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

REFERENCE 1 (bases 1 to 994)

AUTHORS Roest-Crolius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, P., Saurin, W., Bernot, A. and Weissenbach, J.

TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 994)

AUTHORS Roest-Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.

TITLE Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 994)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases

COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

FEATURES

source 1..994

Location/Qualifiers

/organism="Tetraodon nigroviridis"

/db_xref="taxon:99883"

/clone="122P04"

[illegible]

[illegible][illegible]

[illegible][illegible]

Search completed: June 20, 2002, 22:09:12
Job time: 30362 sec

PF 28-SEP-1998: 98W0-BE00141.
 XX 26-SEP-1997: 97EP-0870146.
 XX (BEMA-) BELGIAN MIN NAT DEFENCE.
 PA (UTLO-) UNIV CATHOLIQUE LOUVAIN.
 XX Gale J. Vannuffel P.
 XX WPI: 1999-287521/74.
 DR P-PSDB: AM08221.
 XX
 PT New Staphylococcus-specific oligonucleotides
 XX
 PS Claim 27: Fig 12: 48pp: English.
 CC This invention describes novel Staphylococcus-specific oligonucleotides
 CC based on the consensus fema nucleotide sequence which are used to
 CC develop products for the identification, detection and therapy of
 CC infections. The oligonucleotides can be used for the genetic
 CC amplification. The identification and/or quantification of various fema
 CC sequences which are specific to known or unknown Staphylococci species.
 CC Since the fema sequence is similar to the femB sequence, the
 CC oligonucleotides can also be used for the detection and therapy of femB
 CC genes of different species of Staphylococcus or other gram-positive bacteria.
 CC They can also be used to identify inhibitors, e.g. antibodies or
 CC antisense oligonucleotides, for blocking expression of the fema
 CC nucleotide sequences. They can also be used for producing vaccines
 CC against Staphylococci infections.
 CC
 XX Sequence 1342 BP: 544 A: 161 C: 217 G: 420 T: 0 other:
 SO
 Query Match 54.4% Score 723: DB 20: Length 1342:
 Best Local Similarity 57.9% Pred. No. 3.5e-139:
 Matches 733: Conservative 0: Mismatches 531: Indels 1: Gaps 1:
 Oy 14 anaagagattacaaattacnagcnaagantlmgntmmtacnagannmngn 73
 Db 61 aataagagattacaaattacnagcnaagantlmgntmmtacnagannmngn 120
 Oy 74 nanaagattacnagcnaagantlmgntmmtacnagannmngn 133
 Db 121 taagacatttaccagagatgagaaattacgattaaagttgctga-aaaactgaa 179
 Oy 134 nccnagcattgngnatnaanaanaanaanaanaanaanaanaanaana 193
 Db 180 acccattcagagaaattacaaataagaaataagaaataagaaataagaaata 239
 Oy 194 gcnatcngcnaagantlmgntmmtacnagantlmgntmmtacnagantlmgnt 253
 Db 240 gctgacccgtacgaaattttaaattttaaattttaaattttaaattttaaatt 299
 Oy 254 tntaanaanaanaanaanaanaanaanaanaanaanaanaanaanaana 313
 Db 300 tatgaataaagaagactcgtcactcttctcttcttcttcttcttcttcttctt 359
 Oy 314 nannntmmtacnagantlmgntmmtacnagantlmgntmmtacnagantlmgnt 373
 Db 360 caacatcgttctatctgtagatagacactcttcttcttcttcttcttcttctt 419
 Oy 374 gggagantlmgntmmtacnagantlmgntmmtacnagantlmgntmmtacn 433
 Db 420 ggtgattacagaaatgctggaagattgcttctgataaataaataaataaata 479
 Oy 434 tntaanaanaanaanaanaanaanaanaanaanaanaanaanaanaana 493
 Db 480 tacaacacgaaggttctacaacagattcgtaccatcttcttcttcttcttctt 539
 Oy 494 gnttanaanaanaanaanaanaanaanaanaanaanaanaanaanaana 553
 Db 540 gtttcaattcaagataaactgctaaagattgataaagataagataagattgata 599

Oy 534 aannnnaaanaaaaaatlnaanaanaanaanaanaanaanaanaanaana 613
 Db 600 aaaaatactcaaaaagctcaaaaataagctcaaaaagcttcttcttcttctt 659
 Oy 614 gannnccnagntlmgntmmtacnagantlmgntmmtacnagantlmgnt 673
 Db 660 gaattcatttccagatcatttggaaagatacaccagagataaagatttctgat 719
 Oy 674 nngnagantlmgntlnaanaanaanaanaanaanaanaanaanaanaana 733
 Db 720 agagagagagcttcttcaataaagattgacatttcaagaacagattagtaact 779
 Oy 734 ntgcattatmmtacnagantlmgntmmtacnagantlmgntmmtacnagant 793
 Db 780 ctgcataataaatttgaatcttgcagagacttgcagagactgcagagactc 839
 Oy 794 aataagannnaaaaacnmtaanaanaanaanaanaanaanaanaanaana 853
 Db 840 aataagacttcaaaaagctcaaaaataagctcaaaaagcttcttcttctt 899
 Oy 854 mnaanaanaanaanaanaanaanaanaanaanaanaanaanaanaana 913
 Db 900 caaatcaaaaataaatttgaacagacattcaaaaagcattgagcaaaaattgagaa 959
 Oy 914 gnanannmtlmgntmmtacnagantlmgntmmtacnagantlmgntmmtacn 973
 Db 960 gtaacacaaactcaatagaaacagatgaaacagatgaaacagatgaaac 1019
 Oy 974 tpaatcattgagantlmgntmmtacnagantlmgntmmtacnagantlmgnt 1033
 Db 1020 attaaccttgcagattgattatgctgagagacgtcaataaataatagacactc 1079
 Oy 1034 gcnagantlmgntmmtacnagantlmgntmmtacnagantlmgntmmtacn 1093
 Db 1080 gctgagagatgagcttgcagctgagctgagctgagctgagctgagctgag 1139
 Oy 1094 ngnatnaanaanaanaanaanaanaanaanaanaanaanaanaanaana 1153
 Db 1140 cgtatacattttaaagattgagcttgcagcttgcagcttgcagcttgcag 1199
 Oy 1154 ntaanaanaanaanaanaanaanaanaanaanaanaanaanaanaana 1213
 Db 1200 gtaaaatttaaaaagatttgaatgagatgagatgagatgagatgagatg 1259
 Oy 1214 cgnatnaanaanaanaanaanaanaanaanaanaanaanaanaanaana 1273
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 Oy 1274 nnnla 1278
 Db 1320 aatia 1324

RESULT 7
 AAX37800
 AAX37800 standard: DNA: 1295 BP.
 AC AAX37800:
 DT 09-JUL-1999 (first entry)
 XX
 XX Staphylococcus xyloosus Fema DNA.
 DE Fema: identification, detection, therapy, infection, fema:
 XX amplification, genotyping, gram-positive bacteria, vaccine, ss.
 XX
 XX Staphylococcus xyloosus.
 OS
 XX Key Location/Qualifiers
 FT 1..1295
 FT /seq_a
 FT /product= "Fema"


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FB Key Location/Qualifiers
FT CDS 1:1283
FT /tag- a
FT /product- "femA"
FT /note- "Partial sequence, no start or stop codon"
XN M0916780-A2.
XN 08-APR-1999.
XN 28-SEP-1998: 98W0-BE00141.
XN 26-SEP-1997: 97EP-0870146.
XN (BENA-) BELGIAN MAIN NAT DEFENCE.
XN PA (OTUL-) ONIV CATHOLIEDE LOOVAIN.
XN gala J. Vannuffel P.
XN MPI: 1999-287521/24.
XN P-PSDB: MAY08218.
XN New Staphylococcus-specific oligonucleotides
XN Claim 21: Fig 9a-b: 48pp: English.
XN CC This invention describes novel Staphylococcus-specific oligonucleotides
XN CC based on the consensus femA nucleotide sequence which are used to
XN CC develop products for the identification, detection and therapy of
XN CC infections. The oligonucleotides can be used for the genetic
XN CC amplification, the identification and/or quantification of various femA
XN CC sequences which are specific to known or unknown Staphylococcus species.
XN CC Since the femA sequence is known to the molecular genotyping of femA
XN CC oligon of different Staphylococcus species or other gram-positive bacteria.
XN CC The femA nucleic acids can also be used in therapeutic applications.
XN CC They can also be used to identify inhibitors, e.g. antibodies or
XN CC nucleic acid sequences, for blocking expression of the femA
XN CC against Staphylococcus infections.
XN Sequence 1283 BP: 484 A: 170 C: 224 G: 405 T: 0 other:
XN
XN Query Match 51.2%: Score 679.6: DB 20: Length 1283:
XN Best Local Similarity 55.2%: Pred. No. 1.7e-130:
XN Matches 712: Conservative 0: Mismatches 571: Indels 8: Gaps 1:

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DB 361 ggcacagctggcttctcaaaagatggaagatctggatttgaacatgagagcttcat 420
OY 455 agagcttgcagccttctcaaaagatggaagatctggatttgaacatgagagcttcat 514
DB 421 aagcttccatctctcaaaagatggaagatctggatttgaacatgagagcttcat 480
OY 515 annmcmangantmtnmnaammatggaagatggaagatctggatttgaacatgagagcttcat 574
DB 481 acgctcaaaagatctcaaaagatggaagatctggatttgaacatgagagcttcat 540
OY 575 annmcmangantmtnmnaammatggaagatggaagatctggatttgaacatgagagcttcat 634
DB 541 caaaagatggaagatctcaaaagatggaagatctggatttgaacatgagagcttcat 600
OY 635 ttnatgagatctcncgancmnaammatggaagatggaagatctggatttgaacatgagagcttcat 694
DB 601 ttnatgagatctcncgancmnaammatggaagatggaagatctggatttgaacatgagagcttcat 660
OY 695 annmcmangantmtnmnaammatggaagatggaagatctggatttgaacatgagagcttcat 754
DB 661 aatgcttcaaaagatctcaaaagatggaagatctggatttgaacatgagagcttcat 720
OY 755 annmcmangantmtnmnaammatggaagatggaagatctggatttgaacatgagagcttcat 814
DB 721 ggcacagctggcttctcaaaagatggaagatctggatttgaacatgagagcttcat 780
OY 815 annmcmangantmtnmnaammatggaagatggaagatctggatttgaacatgagagcttcat 874
DB 781 ctaaaagatctcncgancmnaammatggaagatggaagatctggatttgaacatgagagcttcat 840
OY 875 annmcmangantmtnmnaammatggaagatggaagatctggatttgaacatgagagcttcat 934
DB 841 caaaagatctcncgancmnaammatggaagatggaagatctggatttgaacatgagagcttcat 900
OY 935 annmcmangantmtnmnaammatggaagatggaagatctggatttgaacatgagagcttcat 994
DB 901 ctaaaagatctcncgancmnaammatggaagatggaagatctggatttgaacatgagagcttcat 960
OY 995 annmcmangantmtnmnaammatggaagatggaagatctggatttgaacatgagagcttcat 1054
DB 961 ttnatgagatctcncgancmnaammatggaagatggaagatctggatttgaacatgagagcttcat 1020
OY 1055 annmcmangantmtnmnaammatggaagatggaagatctggatttgaacatgagagcttcat 1114
DB 1021 ttnatgagatctcncgancmnaammatggaagatggaagatctggatttgaacatgagagcttcat 1080
OY 1115 annmcmangantmtnmnaammatggaagatggaagatctggatttgaacatgagagcttcat 1174
DB 1081 agtgcgagatctcncgancmnaammatggaagatggaagatctggatttgaacatgagagcttcat 1140
OY 1175 annmcmangantmtnmnaammatggaagatggaagatctggatttgaacatgagagcttcat 1234
DB 1141 agtgcgagatctcncgancmnaammatggaagatggaagatctggatttgaacatgagagcttcat 1200
OY 1235 annmcmangantmtnmnaammatggaagatggaagatctggatttgaacatgagagcttcat 1294
DB 1201 gcaacatctcaaaagatggaagatctggatttgaacatgagagcttcat 1252
OY 1295 annmcmangantmtnmnaammatggaagatggaagatctggatttgaacatgagagcttcat 1354
DB 1253 aatctctcaaaagatctcaaaagatggaagatctggatttgaacatgagagcttcat 1283

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RESULT 10
ID AAX37799 standard: DNA: 1280 BP.
XX AAX37799:
AC AAX37799:
XX 09-JUL-1999 (first entry)
XX Staphylococcus lugdunensis femA DNA.
DE

```


Df	1261 agaaaggattatcgtatgatgaattaccagattaa 1297
	RESULT 12
AC	AAK37803 standard; DNK: 1264 BP.
XX	AAK37803:
XX	07-JUL-1999 (first entry)
DE	Staphylococcus sciuri FemA DNA.
XX	FemA: identification: detection: therapy: infection: femB:
XX	amplification: genotyping: gram-positive bacteria: vaccine: ss.
XX	Staphylococcus sciuri.
OS	
FT	Key Location/Qualifiers
FT	CDS 1..1264
FT	/product= "FemA"
FT	/note= "partial sequence, no start or stop codon"
FN	W09J16780-AZ.
PD	08-APR-1999.
XX	28-SEP-1998: 98ND-BE00411.
PR	25-SEP-1997: 97EP-0870146.
PA	(BEWA-) BELGIAN MIN NAT DEFENCE.
PA	(DTLO-) OMIV CATHOLIQUE LOUVAIN.
XX	Gala J, Vannuffel P:
DR	WPI: 1999-287521/24.
P	P-PSDB: M4T08320.
PT	New Staphylococcus-specific oligonucleotides
XX	Claim 25: Fig 11a-b: 48pp: English.
CC	This invention describes novel Staphylococcus-specific oligonucleotides
CC	based on the consensus femA nucleotide sequence which are used to
CC	detect products for the identification, detection and therapy of
CC	infections. The oligonucleotides can be used for the genetic
CC	amplification, the identification and/or quantification of various femA
CC	sequences which are specific to known or unknown Staphylococcal species.
CC	Since the femA sequence can also be used for the molecular genotyping of the
CC	genus of different Staphylococci species or other gram-positive bacteria,
CC	The femA nucleic acids can also be used in therapeutic applications.
CC	They can also be used to identify inhibitors, e.g. antibodies or
CC	antibiotic sequences. They can also be used for producing vaccines
CC	.against Staphylococcal infections.
XX	Sequence 1264 BP: 518 A: 181 C: 215 G: 370 T: 0 other:
SQ	
OY	Quality Match 40.5% Score 537.6; DB 20: Length 1284;
OY	Best Local Similarity 48.7% Pred. No. 2,3e+01;
Matches	624; Conservative 0; Mismatches 634; Indels 4; Gaps 2
Db	7 gaatttgagacattcaataataaatgctgcacgcatlcttcaccaacaacatacgatat 56
OY	104 taagaatmhaanattgcmnaannnnnmgmcnncagtagtngatnaanaanaaat 153
Db	67 tatgaatataaaaacatcgaagtaactcaacacatattagatggagggccaagtacataca 126

[illegible]

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: June 20, 2002, 06:14:45 : Search time 208.59 Seconds
(Without alignments)
1563.840 Million cell updates/sec

Title: US-09-509-234C-1
Perfect score: 1328
Sequence: 1 nnnnnnnnnnnatga.....gaaattacagaattaaann 1328

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 123816752 residues

Total number of hits satisfying chosen parameters: 757056

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, NA:
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTCUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score 9 or better, the OR equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	728.4	54.8	1257	US-08-320-154-1	Sequence 1, Appli
2	247.4	18.6	453	US-08-714-918-9	Sequence 9, Appli
3	247.4	18.6	453	US-09-265-315-9	Sequence 9, Appli
4	247.4	18.6	453	US-09-265-315-9	Sequence 9, Appli
5	247.4	18.6	453	US-09-265-315-9	Sequence 9, Appli
6	226.2	17.0	410	US-08-714-918-6	Sequence 5, Appli
7	226.2	17.0	410	US-09-265-315-6	Sequence 9, Appli
8	226.2	17.0	410	US-09-265-315-6	Sequence 9, Appli
9	226.2	17.0	410	US-09-265-315-6	Sequence 9, Appli
10	200.2	15.1	400	US-08-714-918-4	Sequence 4, Appli
11	200.2	15.1	400	US-08-714-918-4	Sequence 4, Appli
12	200.2	15.1	400	US-09-265-315-4	Sequence 4, Appli
13	200.2	15.1	400	US-09-265-315-4	Sequence 4, Appli
14	114.6	8.6	5253	US-08-714-918-19	Sequence 4, Appli
15	114.6	8.6	5253	US-09-265-315-19	Sequence 19, Appli
16	114.6	8.6	5253	US-09-265-315-19	Sequence 19, Appli
17	114.6	8.6	5253	US-09-265-315-19	Sequence 19, Appli
18	65	4.9	930	US-08-936-165A-74	Sequence 17, Appli
19	56	4.2	7218	US-08-226-895B-14	Sequence 14, Appli
20	52.4	3.9	3226	US-08-226-895B-14	Sequence 14, Appli
21	50.6	3.8	2447	US-09-014-969-14	Sequence 1, Appli
22	50.6	3.8	2447	US-09-014-969-14	Sequence 1, Appli
23	50	3.8	5361	US-08-973-462-2	Sequence 2, Appli
24	50	3.8	6152	US-08-973-462-1	Sequence 1, Appli
25	48.4	3.6	8920	US-08-446-855A-1	Sequence 1, Appli
26	48.4	3.6	8920	US-09-150-741-1	Sequence 1, Appli
27	48	3.6	398	US-08-714-918-5	Sequence 5, Appli

Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 15, Appli
Sequence 41, Appli
Sequence 45, Appli
Sequence 45, Appli
Sequence 45, Appli
Sequence 45, Appli
Sequence 13, Appli
Sequence 13, Appli
Patent No. 5231168
Sequence 10, Appli
Sequence 13, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-320-154-1
Sequence 1, Application US/08330154
Patent No. 5587307
GENERAL INFORMATION:
APPLICANT: Alborn Jr., William E
APPLICANT: Hoskins, Joann
APPLICANT: Hoskins, Joann
APPLICANT: Hoskins, Joann
TITLE OF INVENTION: THE FEM A GENE OF STAPHYLOCOCCUS EPIDERMIDIS,
TITLE OF INVENTION: THE FEM A GENE OF STAPHYLOCOCCUS EPIDERMIDIS,
TITLE OF INVENTION: THE FEM A GENE OF STAPHYLOCOCCUS EPIDERMIDIS,
TITLE OF INVENTION: THE FEM A GENE OF STAPHYLOCOCCUS EPIDERMIDIS,
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Division/AEH
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
POSTAL CODE: 46206
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/330,154
FILING DATE: 27-OCT-1994
CLASSIFICATION: 45
PUBLICATION INFORMATION:
APPLICATION NUMBER: US/08/208,925
FILING DATE: 09-MAR-1994
FILING DATE: 09-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hamilton, Amy E
REGISTRATION NUMBER: 33,894
REFERENCE/AGENT INFORMATION:
TELEPHONE: 317-276-3169
TELEPHONE: 317-276-3169
TELEPHONE: 317-276-3169
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1257 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
NAME/KEY: CDS

[illegible]

100

NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: U.S.A.
ZIP: 90071-2056
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-265-315-6

FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-265-315-6

Query Match 17.0% Score 226.2; DB 4; Length 410;
Best Local Similarity 55.9%; Pred. No. 2e-47;
Matches 229; Conservative 0; Mismatches 181; Indels 0; Gaps 0;

Oy 675 gngagannntttantanaannntnnnnnnattnnaaagannngntngnncnn 734
Db 1 GTAAAGCAAAATTAACCTACACCTGCTTAAATATATACAAAGACCGCTGTAGTACCTT 60

Oy 735 tngmtatantanttgatgaantnnnnngaanntnnnnnnnnnnnnnnnnnnntna 794
Db 61 TAGCGTATATCAACTTTTATGATATATTAAGAACTAAAGAGCGGTATATTTAA 120

Oy 795 ntaagannnnnaaagcnnntnaagannntnaagannntnaagannntnaagannnn 854
Db 121 ATAAAGTTTAAATAGCGTTAAGGATATTGAAGACCTCTGAAATATAAAGACAC 180

Oy 855 nnaaann 914
Db 181 ATAAAGCGAGATAACTTACACAACTTGTATGCAATGAGCAAAAGATTGAAGAG 240

Oy 915 nnn 974
Db 241 GTAAGCGCTACAGAGCAACATGTAAGTATACCTATCTCTCTGTTCTTCTTAA 300

Oy 975 tnaatcctatgagtgnttantngcngtggnacntcnaatnnnnnnnnnnnnnnnn 1034
Db 301 TCAATCCATTGANGTGTATTATATGCTGTGTGATACAAATGCAATCGTCATTTN 360

Oy 1035 cngnagntatgcnntcnaatggnnnatgattantatgcnntnncat 1084
Db 361 CCGAGATTATGCGTCAATGCGAATGATTATATGCTATTAATCAT 410

RESULT 8
US-09-265-315-6
Sequence 6, Application US/09265315
Patent No. 6183333
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Ying J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE OR INACTIVE ORPHANS
TITLE OF INVENTION: TARGET GENES

```

361 CGGAGATTGTCAGTCGTCATGGGAATGATTAATGTCATTAATCAT 410

RESULT 9
: Sequence 6, Application US/09266417
: Patent No. 6228588
: GENERAL INFORMATION:
: APPLICANT: Beutelschlag, Bret
: INVENTOR: Beutelschlag, Wolfgang
: APPLICANT: Malouin, Francois
: APPLICANT: Martin, Patrick K.
: APPLICANT: Schmid, Molly B.
: APPLICANT: Sun, Dongxu
: TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
: TITLE OF INVENTION: ACTIVE ON STARTHLOCCUS AUREUS
: TITLE OF INVENTION: TARGET GENES
: NUMBER OF SEQUENCES: 111
: NUMBER OF SEQUENCES: 111
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Lyon & Lyon
: STREET: 633 West Elth Street
: STREET: Suite 4700
: CITY: Los Angeles
: STATE: California
: COUNTRY: USA
: CONTACT: 001-506
: CONTACT: 001-506
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5" Diskette, 1.44 MB
: MEDIUM TYPE: storage
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: IBM P.C. DOS 5.0
: SOFTWARE: Word Perfect 5.1
: CURRENT APPLICATION NUMBER: US/09266.417
: PUBLICATION NUMBER: US/09266.417
: FILING DATE: March 9, 1999
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/714,918
: FILING DATE: September 13, 1996
: APPLICATION NUMBER: 60/091,822
: FILING DATE: September 22, 1995
: APPLICATION NUMBER: 60/003,798
: FILING DATE: September 15, 1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Warburg, Richard J.
: REGISTRATION NUMBER: 32,327
: REFERENCE/DOCKET NUMBER: 240/248
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (213) 459-1600
: TELEFAX: (213) 955-0440
: TELEX: 67-3510
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 410 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: ORIENTATION: linear
US-09-266-417-6

Query Match 17.0% Score 226.2 DB 4 Length 410:
Best Local Similarity 55.9% Pred. No. 2e-47:
Matches 229: Conservative 0: Mismatches 181: Indels 0: Gaps

QY 675 gggagagannnttcantanaangntnnnnnnatnaaaaanngnntngntccnn 794
D 1 GTATGCAAAATTTAACTACATCGCTTAAATATTACAAGACCGGTGTGTAACCTT 60
OY 735 tngctatantatttgatcattntnnngantnnnnngannngannnnnnntaa 794
OY 61 TACGCTATACACATTTTATGATATATTATTAAGACATTAAGACGCGTGATATTTAA 120
OY 795 ntatanaaanaaagacgntnaangantnaangnaangnccngcnaanaaanaaangcnn 854

```

FILING DATE: December 22, 1999

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265.315
FILING DATE: March 2, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714.918
FILING DATE: August 13, 1996
FILING OFFICE NUMBER: 50/009.102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003.798

ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/265,315
 FILING DATE: March 9, 1999
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/714,918
 FILING DATE: September 13, 1996
 APPLICATION NUMBER: 60/009,102
 FILING DATE: December 22, 1995
 APPLICATION NUMBER: 60/003,195
 FILING DATE: September 15, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Weiburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 240/247
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 400 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-265-315-4

Query Match 15.1% Score 200.27 DB 4: Length 400:
 Best Local Similarity 53.9% Pred. No. 5.3e-41
 Matches 215; Conservative 0; Mismatches 183; Indels 1; Gaps 1:
 Oy 239 gqncngatngatntnnaannagangctngtncantnttcttaangantl-nnn 297
 Db 400 GTGCCAGTGATGANTATGAATCAAGNACTGTCACACTTTTTCITTAAGATATCC 341
 Oy 298 naantatntnaaannannntntatantnnntngancntantntntatca 357
 Db 340 AAATATGTTAAACATCTGTCATCTACATACATGCTTATACCATCA 281
 Oy 358 atannnaatcatgagngantnnngnaatcgngnangattgnttngatna 417
 Db 280 ATACTGATCATGCGGAGATTACAGTAATGCTGTAATGATGTTGTTGATAA 221
 Oy 418 ntntnnnnntngntntnancannngntntnnnangntttgancntnnnca 477
 Db 220 ATGAGTAACCTAGGATTCATGATTCATGATTCATGATTCATGATTCATG 161
 Oy 478 aatngntmctngntntnancannngntntnnnangntttgancntnnnca 537
 Db 160 ATCGTGTATCACTGATGTTAGATTTTAAAGATAAAGACAGATGACATCAATNA 101
 Oy 538 natgatngntngnaangnaacnaaaagntnnaanaaatgngntnaaagntnn 597
 Db 100 TATGATGAGCTTATGAAAAAAGACAGGAAAGTTTAAAGAAATGGTGTAAAGTA 41
 Oy 598 ntntnnnnnaagangantntcctntntngntcatt 636
 Db 40 ATTTATCTGAGGAGNACTACCATTTTATGATTT 2

RESULT 13
 US-09-265-417-4/c
 : Sequence 4, Application US/09265417
 : Patent No. 6228588
 : GENERAL INFORMATION:

APPLICANT: Benton, Bret
 APPLICANT: Lee, Ving J.
 APPLICANT: Malouin, Francois
 APPLICANT: Martin, Patrick K.
 APPLICANT: Schmid, Molly B.
 ATTORNEY/AGENT INFORMATION:
 NAME: Weiburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 240/248
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 400 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-265-417-4

Query Match 15.1% Score 200.27 DB 4: Length 400:
 Best Local Similarity 53.9% Pred. No. 5.3e-41
 Matches 215; Conservative 0; Mismatches 183; Indels 1; Gaps 1:
 Oy 239 gqncngatngatntnnaannagangctngtncantnttcttaangantl-nnn 297
 Db 400 GTGCCAGTGATGANTATGAATCAAGNACTGTCACACTTTTTCITTAAGATATCC 341
 Oy 298 naantatntnaaannannntntatantnnntngancntantntntatca 357
 Db 340 AAATATGTTAAACATCTGTCATCTACATACATGCTTATACCATCA 281
 Oy 358 atannnaatcatgagngantnnngnaatcgngnangattgnttngatna 417
 Db 280 ATACTGATCATGCGGAGATTACAGTAATGCTGTAATGATGTTGTTGATAA 221
 Oy 418 ntntnnnnntngntntnancannngntntnnnangntttgancntnnnca 477
 Db 220 ATGAGTAACCTAGGATTCATGATTCATGATTCATGATTCATGATTCATG 161
 Oy 478 aatngntmctngntntnancannngntntnnnangntttgancntnnnca 537

Db 160 ATCCGTTATACCTCAGTGTAGATTAAAGATAAAGACAGATGACATCAATNAAA 101
 Oy 538 atgagatgntnngnaangnaaaagttmnaaaatgopntnaaagttm 597
 Db 100 TATGATGCTGCTTGAAGAAAGACACCGCAAGATTAAAGATTGTTAAAGTAAG 41
 Oy 598 attntnnnaagangntnccnntnngntcatt 636
 Db 40 ATTTTATCTGAGAGNACTACCAATTTTITAGATATT 2

RESULT 14
 US-08-714-918-19/c
 : Sequence 19, Application US/08714918
 : Patent No. 6187541
 : GENERAL INFORMATION:
 : APPLICANT: Benton, Bret
 : APPLICANT: Lee, Ving
 : APPLICANT: Malouin, Francois
 : APPLICANT: Martin, Patrick K.
 : APPLICANT: Schmid, Molly B.
 : APPLICANT: Sun, Dongxu
 : TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
 : TITLE OF INVENTION: TARGET GENES
 : NUMBER OF SEQUENCES: 11
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Lyon & Lyon
 : STREET: 633 West Fifth Street
 : CITY: Los Angeles
 : STATE: California
 : COUNTRY: U.S.A.
 : ZIP: 90071-2066 FORM:
 : COMPUTER READABLE 5 1/2 Diskette, 1.44 Mb
 : MEDIUM TYPE: Storage
 : COMPUTER: IBM Compatible
 : OPERATING SYSTEM: IBM P.C. DOS 5.0
 : SOFTWARE: Word Perfect 5.1
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/714,918
 : FILING DATE: September 13, 1995
 : CLASSIFICATION: C12N
 : PRIORITY NUMBER: 60/009,102
 : APPLICATION NUMBER:
 : FILING DATE: December 22, 1995
 : APPLICATION NUMBER: 60/003,798
 : FILING DATE: September 15, 1995
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Warburg, Richard J.
 : REGISTRATION NUMBER: 32,327
 : REFERENCE/DOCKET NUMBER: 222/005
 : TELEPHONE: (213) 955-0800
 : TELEFAX: (213) 955-0440
 : TELEX: 67-3510
 : INFORMATION FOR SEQ ID NO: 19:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 5253 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : US-08-714-918-19

Query Match 8.6% Score 114.6; DB 3; Length 5253;
 Best Local Similarity 31.8% Pred. No. 2.3e-19;
 Matches 272; Conservative 1; Mismatches 573; Indels 9; Gaps 2;
 Oy 410 tngatnandnnnnnnngntntnccnngnttmmnaangnttgcacn 459
 Db 2967 TTGCAAAATTTGAAGCCCTTGGTTTAAACNATAAGATTAAAGAGTTTATCAAAA 2908

Oy 470 ntannccaatngntnccntngntnccntatntannnnnnnaaaannnnnnnnat 529
 Db 2907 GACTACATCCACACGATGACTATGATTACACCAATTTGATAAAATGATGATGAGTTA 2848
 Oy 530 ntannnnatgagntngntnngnaangnaacnaaaagttmnaaaatgngntn 589
 Db 2847 TTAATAGTTTGAACCCCAAAATCCTTCAAAAGTGGCTTGGCTTTAAAGCGAGTACG 2788
 Oy 590 aagatnnntntnnnnnaaaagntnccnntnngntcattnngatgagatcnc 649
 Db 2787 ACAGTAGAACGATCTGATAGAGAGGTTTAAACATTTTCTGAGTTAATGAAATCACT 2728
 Oy 650 ncgannccaatngntnngntnngnaangnnntntntannnnnnnnnnnnat 709
 Db 2727 GGGGAACCGGATGGCTTCTTAACCGGTGATATTAGTTTACTTTGAAATATTATATGCG 2668
 Oy 710 tnaaaagannntngntnccntngntnccntatntnnnttggat-----gntannntn 763
 Db 2667 TTGCTGAAGATGAGATGCTGACTATTITTAGTAAAGTTGATCCAAAGAGAAATATA 2608
 Oy 764 nnnnnaannnnngann 823
 Db 2607 GCGAAGTAAATCAAGATTGAATGAACCTTCATGCCGAAATTTGCTAAATGGCAGAGAG 2548
 Oy 824 atnganaaangnccnganaa---naaaagannnnnaaaannnnnnnnnnnnnnnnnn 880
 Db 2547 ATGAAATATCTGAAGACGCTAAAGACGCAAAATATGATTAAATGATGCGCAAAAT 2488
 Oy 881 cgaatnnnnnnnaaaagntnccntnngntnngntnngntnngntnngntnngntnngnt 940
 Db 2487 AAAATGCTAAATGAGATTAAACAGGAGCTAGAAAGCTTTAGAAAGGAGCATCTCT 2428
 Oy 941 aagaatcaccnntnngntnccntnntnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 1000
 Db 2427 GAAGTATTATCTTCTGCTGCTACTATTATGTTTCTGCTCAAAATCATATACTTA 2368
 Oy 1001 gcnngtngnccntnntnn 1050
 Db 2367 TATGCTGCTGCTTAAGATTAGAGATTTTACCAAAATCATCATATGACATATACG 2308
 Oy 1061 atgaatnntnccntnntnn 1120
 Db 2307 ATGATGAATGACGCTGACATGCTGCAACACTTACGATTTGGTGTACAGATAT 2248
 Oy 1121 nanttnngannngnaagatngntnngntnntnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 1180
 Db 2247 GATCCAGATAAGACTCAGACACTATGATTTATGGCAATTTAAAGAGTGGGGAACA 2188
 Oy 1181 gaantnngantngntnngntnntnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 1240
 Db 2187 TACTTAAGTAAAGATTGGTGAATTTGATTATGTTGAATCAGCCATTGTGCCAATTA 2128
 Oy 1241 tatann 1255
 Db 2127 ATTAGCAAGATTAA 2113

RESULT 15
 US-09-265-315-19/c
 : Sequence 19, Application US/09265315
 : Patent No. 6187541
 : GENERAL INFORMATION:
 : APPLICANT: Benton, Bret
 : APPLICANT: Lee, Ving J.
 : APPLICANT: Malouin, Francois
 : APPLICANT: Martin, Patrick K.
 : APPLICANT: Schmid, Molly B.
 : APPLICANT: Sun, Dongxu
 : TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
 : TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
 : TITLE OF INVENTION: TARGET GENES
 : NUMBER OF SEQUENCES: 111

Result	Query No.	Score	Match	Query Length	DB ID	Description
C	1	75.4	5.7	1025	12	CNS01J42 Drosophila
	2	71	5.3	652	12	CNS03H00 Drosophila
C	3	69.8	5.3	652	12	BH183498 Drosophila
C	4	69.8	5.3	650	12	CNS07D04 Drosophila
C	5	69.6	5.2	616	12	CNS01785 Drosophila
C	6	68	5.1	1101	12	CNS02011 Drosophila
C	7	68	5.1	908	12	CNS04867 Drosophila
C	8	67.6	5.1	984	12	CNS03N00 Drosophila
C	9	67.2	5.1	912	12	CNS01092 Drosophila
C	10	67.2	5.0	781	12	CNS00900 Drosophila
C	11	67	5.0	849	12	CNS05082 Drosophila
C	12	67	5.0	891	12	CNS01381 Drosophila
C	13	66.4	5.0	891	12	CNS01382 Drosophila
C	14	66.2	5.0	1101	12	CNS01393 Drosophila
C	15	65.8	5.0	539	12	CNS01074 Drosophila
C	16	65.6	4.9	908	12	BH185054 Drosophila
C	17	65.6	4.9	908	12	BH185064 Drosophila
C	18	65.6	4.9	908	12	CNS03015 Drosophila
C	19	65.6	4.9	908	12	CNS03016 Drosophila
C	20	65.6	4.9	908	12	CNS03017 Drosophila
C	21	65.6	4.9	908	12	CNS03018 Drosophila
C	22	65.6	4.9	908	12	CNS03019 Drosophila
C	23	65.6	4.9	908	12	CNS03020 Drosophila
C	24	65.6	4.9	908	12	CNS03021 Drosophila
C	25	65.6	4.9	908	12	CNS03022 Drosophila
C	26	65.6	4.9	908	12	CNS03023 Drosophila
C	27	65.6	4.9	908	12	CNS03024 Drosophila
C	28	65.6	4.9	908	12	CNS03025 Drosophila
C	29	65.6	4.9	908	12	CNS03026 Drosophila
C	30	65.6	4.9	908	12	CNS03027 Drosophila
C	31	65.6	4.9	908	12	CNS03028 Drosophila
C	32	65.6	4.9	908	12	CNS03029 Drosophila
C	33	65.6	4.9	908	12	CNS03030 Drosophila
C	34	65.6	4.9	908	12	CNS03031 Drosophila
C	35	65.6	4.9	908	12	CNS03032 Drosophila
C	36	65.6	4.9	908	12	CNS03033 Drosophila
C	37	65.6	4.9	908	12	CNS03034 Drosophila
C	38	65.6	4.9	908	12	CNS03035 Drosophila
C	39	65.6	4.9	908	12	CNS03036 Drosophila
C	40	65.6	4.9	908	12	CNS03037 Drosophila
C	41	65.6	4.9	908	12	CNS03038 Drosophila
C	42	65.6	4.9	908	12	CNS03039 Drosophila
C	43	65.6	4.9	908	12	CNS03040 Drosophila
C	44	65.6	4.9	908	12	CNS03041 Drosophila
C	45	65.6	4.9	908	12	CNS03042 Drosophila
C	46	65.6	4.9	908	12	CNS03043 Drosophila
C	47	65.6	4.9	908	12	CNS03044 Drosophila
C	48	65.6	4.9	908	12	CNS03045 Drosophila
C	49	65.6	4.9	908	12	CNS03046 Drosophila
C	50	65.6	4.9	908	12	CNS03047 Drosophila
C	51	65.6	4.9	908	12	CNS03048 Drosophila
C	52	65.6	4.9	908	12	CNS03049 Drosophila
C	53	65.6	4.9	908	12	CNS03050 Drosophila
C	54	65.6	4.9	908	12	CNS03051 Drosophila
C	55	65.6	4.9	908	12	CNS03052 Drosophila
C	56	65.6	4.9	908	12	CNS03053 Drosophila
C	57	65.6	4.9	908	12	CNS03054 Drosophila
C	58	65.6	4.9	908	12	CNS03055 Drosophila
C	59	65.6	4.9	908	12	CNS03056 Drosophila
C	60	65.6	4.9	908	12	CNS03057 Drosophila
C	61	65.6	4.9	908	12	CNS03058 Drosophila
C	62	65.6	4.9	908	12	CNS03059 Drosophila
C	63					

Query Match 5.7% Score 75.4 DB 12 Length 1025;
Best Local Similarity 23.6% Ref Seq No. 0_0022; Gaps 1:
Matches 225; Conservative

Oy 150 tnaaaanaanaanaangnatngcngctgnttntnnaacngctncngatga 209
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 972 TAAAAATATAGTAKGTATGTTCTTTTATMGATGTGGKATGAGAAGGTTTG 913
Oy 210 aenttnaantatttatnaaengngcngctgatgattnnaanaaganc 269
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 912 DMAAATGKAATATTGTACTPTTCGGDARADAAAGGTGCATAGHRAAAATIRW 853
Oy 270 tngtcantcttttaangnttannaantaatnaanaannnnmntatnm 329
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 852 KTRTTAARTGGTGAATMAAAAAAAAAAAACHKARGGAGAAAATYGGGTGRAMA 793
Oy 330 tamntngcncttantnchnlcaataannaatcatganganmttmngna 389
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 762 AAAAAAAGATCGAAAAAAKRTTPTGTCTTAATAAATATGTGTARATAAA 733
Oy 390 atcgungnaagatgnttngatnannnnnnntngnttanaannngnt 449
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 732 TRTEKKIGATGTRAFAHAHAATAATAATAMAYAAKTGTGAAAAAARAANAAT 573
Oy 450 tnnnaangnttgccantnnnaacntngntntngntcngnttamtam 509
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 672 GTNNAWNTANNTTKATGTGAATKGTGTEKAWAAAAAANAANKWPATA 613
Oy 510 nnaaanannanngntntannontatggatngnttngnaangnaaacaaa 559
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 612 WKETARAAMDGKTKTKTKTRIAA - WAAKGEGTGKGGKATTRRHHMAAAAAA 555
Oy 570 agttnnaanaatyngtnaagcmntntnntmnaagaangantnccnatlm 529
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 554 AAAAAAAGACGCTGAADRAAKGDAAADAGSWAAAAABKRRTAIATGTGKIK 495
Oy 630 gntcatatgangaatcngcnganncnaangnttinnngaLnggangannt 589
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 454 TGRTAGTAGATTAATMAAAGTGTGTAKMATATATMAAAAAAANNNNNVWG 435
Oy 690 antcnaangntnnmnnaanaagannngntngcncntngcntatatnnt 749
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 434 CRTGREGAANTPTBAKTTTAAAAAATATKWTBRTKKTGDKAFARAADAAT 375
Oy 750 ttagatanttninggaantnnnngngannnnntntaaagannnaa 809
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 374 TAAAAAANNN 315
Oy 810 aegcmttnaangnatngnaaagucnganaaaaaaangcmnaapaannma 859
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 314 AAAAAAANNN 255
Oy 870 anntnaanaancantnnngcnaannaaantnnngannnnnnntnnaa 929
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 254 AAAAAAANNN 195
Oy 930 omnancaaygaangaattaccnatitngcngntlncttntatpatatccntga 989
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 194 AAAAAAANNN 135
Oy 990 lngtntantcngcnglggaactcnaatnttngncantngcngngatgcm 1049
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 134 AAAAAANNNAANNAATTHHCNNWAATACTTTTATAGMTTNNNNNNNAATW 75
Oy 1050 tncataygnuatgatlcatgntcnaatntnntnnaangntanatt 1103
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 74 KTAHNNCCCAAT 21

RESULT 2
CNS03ROU 552 bp DNA Linear GSS 17-MAY-2000
LOCUS CENS03ROU 552 bp survey sequence 17 end of clone

RESULT	2
CNS03HOU	
LOCUS	CNS03HOU , 652 bp DNA linear GSS 17-MAY-2000
DEFINITION	Tetraodon nigroviridis genome survey sequence 17 end of clone

Query Match	5.38	Score 69.8	DB 12	Length 660
Best Local Similarity	25.48	Pred. No. 0.02		
Mismatches 115	Conservative	29	Mismatches 308	Indels 0

```

Query Match          5.3% Score 69.8; DB 12: Length 660;
Best Local Similarity 25.4% Pred. No. 0.02; 308; Indels 0; Gaps 0;
Matches 115; Conservative 29; Mismatches 311; Indels 0; Gaps 0;

Oy 499 anatttmmnnnaaaanncnngantntnaannnngatggtngntngnaang 558
Db 31 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATATAAAAAA 90
Oy 559 naanacnaaaagttttnnaaaatggngttnaaagtttnttntnnnnaaangant 618
Db 91 AAAAAAAAAAATTAANAAAAAATATAAAAAATTTTATAAATAA7AAAAAAATAAAA 150
Oy 619 ncnatntnngcttattggtgatacmngcngnnaangnttntnnngatngnga 678
Db 151 AAAAAATATAAAAAAAAAAAAAAAAAAATTAATAAATTTTAAAGAAAGAAAAAATA 210
Oy 679 ngannntttantanaangntnnnnnatttnnaaagntngntngntnccntngc 738
Db 211 TAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATTAAM 270
Oy 739 ntatatnttttgatgattntnnngantnnnnngntnnnnngntnnnnntnaaa 798
Db 271 ATAAATATAAATAAAAAAAAAAATAAAAAAAAAAATAAATAAATAAATAAATAA 330
Oy 799 agannnaaaagcmttnaangntatngnaaangnccngcngnaaangcngmnaa 858
Db 331 AAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAA 390
Oy 859 naannnnnnnaannnaancantnnngcnaannncaaaanantnnngangnan 918
Db 391 AAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAA 450
Oy 919 nnnnnnnnaannnancatggnnaangaa 946
Db 451 AAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAA 478

RESULT 5
CNS0152H CNS0152H 614 bp DNA linear GSS 26-JUL-1999
LOCUS BACN12N03 of Drosophila melanogaster genome survey sequence 614 bp of BAC
DEFINITION BACN12N03 of Drosophila melanogaster genome survey sequence.
ACCESSION AL104915 GI:5616929
VERSION AL104915.1
KEYWORDS GSS.
SOURCE Drosophila melanogaster.
ORGANISM fruit fly.
REFERENCE 1. Direct Submission
AUTHORS B. G.
TITLE BACN12N03 of Drosophila melanogaster.
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.dbi.ac.uk/. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Bucheton, CEPR (Centre d'Etude du Polyploidisme Humain) with funding provided by a MFC and Genevieve Payan. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.
FEATURES
source 1. 614
/organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"

```

```

BASE COUNT 553 a 0 c 0 g 41 t 20 others
ORIGIN
Query Match          5.2% Score 69.6; DB 12: Length 614;
Best Local Similarity 25.9% Pred. No. 0.021;
Matches 134; Conservative 3; Mismatches 311; Indels 0; Gaps 0;

Oy 499 anatttmmnnnaaaanncnngantntnaannnngatggtngntngnaang 558
Db 31 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATATAAAAAA 90
Oy 559 naanacnaaaagttttnnaaaatggngttnaaagtttnttntnnnnaaangant 618
Db 91 AAAAAAATTAANAAAAAATATAAAAAATTTTATAAATAA7AAAAAAATAAAA 150
Oy 619 ncnatntnngcttattggtgatacmngcngnnaangnttntnnngatngnga 678
Db 151 AAAAAATATAAAAAAAAAAAAAAAAAAATTAATAAATTTTAAAGAAAGAAAAAATA 210
Oy 679 ngannntttantanaangntnnnnnatttnnaaagntngntngntnccntngc 738
Db 211 TAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATTAAM 270
Oy 739 ntatatnttttgatgattntnnngantnnnnngntnnnnngntnnnnntnaaa 798
Db 271 ATAAATATAAATAAAAAAAAAAATAAAAAAAAAAATAAATAAATAAATAAATAA 330
Oy 799 agannnaaaagcmttnaangntatngnaaangnccngcngnaaangcngmnaa 858
Db 331 AAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAA 390
Oy 859 naannnnnnnaannnancantnnngcnaannncaaaanantnnngangnan 918
Db 391 AAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAA 450
Oy 919 nnnnnnnnaannnancatggnnaangaa 946
Db 451 AAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAA 478

RESULT 6
CNS01JRG CNS01JRG 879 bp DNA linear GSS 12-JUN-2001
LOCUS Anopheles gambiae GSS 17 end of clone 14007 of Notre Dame library from strain PEST of Anopheles gambiae (African malaria mosquito), genomic survey sequence.
ACCESSION AL147405 GI:7005551
VERSION AL147405.1
KEYWORDS GSS.
SOURCE African malaria mosquito.
ORGANISM Anopheles gambiae
REFERENCE 1. (bases 1 to 879)
AUTHORS Genoscope Submission
JOURNAL Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
COMMENT - Web : www.genoscope.cns.fr
REFERENCE 2. (bases 1 to 879)
AUTHORS Roth,C.W., Brey,P.I., Ke,Z., Collins,F.H. and Welsenbach,J.
JOURNAL Direct Submission
TITLE Submitted (16-FEB-2000) BIMI, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France
COMMENT This clone is a BAC library provided by F.H. Collins. It was sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut Pasteur. Location/Qualifiers
FEATURES
source 1. 879
/organism="Anopheles gambiae"
/plasmid="BAC"
/db_xref="taxon:7227"
/clone_lib="BAC"

```

<p>melanogaster BAC library was prepared by Kazutoyo Osagawa and Aaron Mammoser in Peter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of <i>Drosophila</i> DNA provided by the BDGP from the isogenic strain y2; cn bw sp. The same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://www.bacpac.org/buffalo.edu/drosophila_bac.htm.</p>					
<p>FEATURES source 1..1101 /organism="Drosophila melanogaster" /db_xref="taxon:7227" /cclone.lib="RPCI-98" /cclone="BACR05N11" /note="end : TEI3" 7 c 28 g 289 t 146 others</p>					
<p>BASE COUNT 631 a 289 t 146 others</p>					
<p>ORIGIN</p>					
<p>Query Match 5.1% Score 68; DB 12; Length 1101; Best Local Similarity 24.8%; Pred. No. 0.037; Matches 216; Conservative 5; Mismatches 628; Indels 3; Gaps 1;</p>					
Oy	449	ttnnnnangngttgancnnlnmncceatlmgtcnccntcngtctnatattann	508		
Db	10	KTITTTKKTTTTNTTGTITTTTNNITVNCVTCTIVTTTNNKTKTTTTT	69	:	:
Oy	509	nmaaeannmcngantntnaannatgatcgntngnaangnagaacaa	568		
Db	70	TATTTTNNAAANAKNAATAATTTTATTATTAACAAGKDAAATAAAN	129		
Oy	569	aagclnnanaeaatggngtnaaaglnnnntcnntnnnaagangcncnctn	628	:	:
Db	130	HAAAAAAAAGTGTTTCATGAAGTTTAAAAAAMAAAAAAAAAAAAANW	189		
Oy	629	ngtcatttgtagatacmncgcacgaengctmmngastngcgannntn	688		
Db	190	NHCNNNAANAAAAAAMAAAAAACAACAAAAAAMAAAAAAMAAAAA	249		
Oy	689	tantaanaangntmnmatntnaaagannnglmtngtccnctngtatatan	748		
Db	250	AA	309		
Oy	749	tltgatcannnmngaantnanngnangnnnnntnanaaagannnaan	808		
Db	310	MAAAAAACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	369		
Oy	809	aagcmtnaeangatatangaacngcgaanaaagaangcnnnaaana	868	:	:
Db	370	AA	429		
Oy	869	aennlnnaahancnlnnnngcnaenancaaeeentmgangnannnnntna	928	:	:
Db	430	AA	489		
Oy	929	nmnncatgnaagaattaccnattcngcgntncttntnaaatcmtngae	988	:	:
Db	490	AA	549		
Oy	989	gtngtantaangcgtgtaactnaatnnntnnngcantiingcngnagtac	1048		
Db	550	TTTTTTTTTTTAAATTTTAAATTTTAAWAATTTAATAAWMTWT	609	:	:
Oy	1049	nlncaatggnnatgatlaantatgctnmnancatnnatnnangntapaatt	1108	:	:
Db	610	WIAAKAAAAAAAVTTTAAAWTWTTTTTTTTAAATAAATAAATAA	668	:	:
Oy	1109	ggnnttaagngtntnttningangcgaagtgngngtlnnaantlnaa	1168	:	:
Db	669	-AAWTGTTTATGAAATWAAATWAAATTTTAAAAATTTTTTAA	1226	:	:

[illegible]

[illegible]

[illegible][illegible]

RESULT 12	AZ546009	849 bp	linear	GSS 14-NOV-2000
LOCUS	ENTMF33F	Entamoeba histolytica	Sheared DNA	Entamoeba histolytica
DEFINITION	genomic, DNA sequence.			
ACCESSION	AZ546009			
VERSION	AZ546009			
KEYWORDS	GI:11167130			
SYNOPSIS	GSS Entamoeba histolytica			
ORGANISM	Entamoeba histolytica			
REFERENCE	Eukaryota: Entamoebidae: Entamoeba.			
AUTHORS	1 (bases 1 to 849)			
REVIEWED	Loftus,B., Van Aken,S. and Fraser,C.			
TITLE	Determination of clone end sequences from Entamoeba histolytica			
COMMENT	HM1:IMSS sheared DNA library			
UNPUBLISHED	(2000)			
CONTACT	Brendan J Loftus			
DEPOSITED	2000 Nov 14			
INSTRUMENT	Genomics			
INSTITUTION	The Institute for Genomic Research			
ADDRESS	7712 Medical Center Dr., Rockville, MD 20850, USA			

FEATURES
 Source
 Accession
 Location/Qualifiers
 Class: shotgun
 Seq primer: M13-Forward
 High quality sequence start: 26
 High quality sequence stop: 796.
 High quality sequence
 Entamoeba histolytica
 /organism="Entamoeba histolytica"
 /strain="HMI-1MSS"
 /db_xref="taxon:5759"
 Email: b1loftus@tigr.org
 Clones are derived from the Entamoeba histolytica HMI-1MSS sheared
 DNA library
 Fax: 301 838 3543
 Entamoeba histolytica HMI-1MSS sheared

```

/organism="Eucamoeba histolytica"
/strain="HMI:IMSS"
/db xref="taxon:5759"

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AZ68J582.1 GI:11820728
 GSS.
 Entamoeba histolytica.
 Entamoeba histolytica.
 Entamoeba histolytica.
 Eukaryota; Entamoebidae: Entamoeba.
 1 (bases 1 to 891)
 Loftus, B., Van Aken, S. and Fraser, C.
 Determination of clone end sequences from Entamoeba histolytica
 JMI: IMSS sheared DNA library
 Unpublished (2000)
 Contact: Brendan J Loftus
 Department of Eukaryotic Genomics
 National Cancer Institute, Genetic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0208
 Fax: 301 838 3543
 Email: b.loftus@lar.org

DNA library
Seq primer: M13-Reverse
Class: Shotgun
High quality sequence start: 16
High quality sequence stop: 694.

FEATURES

source	High quality sequence stop: 694.
Location/Qualifiers	
/contig="831"	
/organism="Entamoeba histolytica"	
/strain="HM: IMSS"	
/db_xref="taxon:5759"	
/clone_lib="Entamoeba histolytica Sheared DNA"	
/notes="Vector: pHC81 Site_1: Bst 1; Constructed at the Institute for Genomic Research (TIGR), Rockville, MD."	
/genomic "A genomic DNA isolated from broth cultures of E. histolytica using a modified sodium dodecyl sulfate (SDS) lysis protocol and a BamHI restriction endonuclease (Clontech) using a protocol described by Smith et al. (1993)."	
/insert_size="1.5" (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol.	
77:450.) The DNA was mechanically sheared to give a tight size distribution (-2 kb). The + 1 method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing. Protocols for genomics. Cold Spring Harbor, NY: Cold Spring Harbor Laboratory Press, 1999)." (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol.	
400	291.g 15 t

BASE COUNT

Q7 273 ACGATGACGAGCAGTGAAGAAGCATGTAAGAACGATGAAGAAG 332

Oy 598 ttaaagtttnttmtannnnnagaagannntcccaattnttngctatcatgatgata 647

Ob 333 ACGATGACGAGCAGTGAAGAAGCATGTAAGAACGATGAAGAAGCATGATG 392

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Oy 648 cncgagannncgannntnnngatngngangannntntntanaangntnnnnnn 707
Db 393 AAGAGACGATGATGAAGAGACGATGATGAAGAGACGATGATGAAGAGACGATG 452
Oy 708 atnnaaagannntngntngntngntngntngntngntngntngntngntng 767
Db 453 AAGAGACGATGATGAAGAGACGATGATGAAGAGACGATGATGAAGAGACGATG 512
Oy 758 aantnnannngannngannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 827
Db 513 AAGAGACGATGATGAAGAGACGATGATGAAGAGACGATGATGAAGAGACGATG 572
Oy 828 aanaaagcncganaanaaagcncganaanaaagcncganaanaaagcncgana 887
Db 573 AAGAGACGATGATGAAGAGACGATGATGAAGAGACGATGATGAAGAGACGATG 932
Oy 888 aagcnaaanncaaaannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 945
Db 633 ATGAAGAGACGATGAAGAGACGATGAAGAGACGATGAAGAGACGATGAAGAGAC 950

RESULT 14
CNS0183Y
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN37F08 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic
ACCESSION
AL108856.1 GI:5629160
VERSION
GSS:
KEYWORDS
fruit fly, melanogaster
ORGANISM
Eukaryota; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscimorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 1101)
Genoscope.
AUTHORS
Direct Submission
TITLE
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BACN37F08 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
COMMENT
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk/. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBeloBAC11.
FEATURES
source
location/Qualifiers
    join="Drosophila melanogaster"
    plasmid="pBeloBAC11"
    db_xref="taxon:7227"
    clone_lib="DrosBAC"
    clone="BACN37F08"
    note="end : SP6"
BASE COUNT
465 a 25 c 90 g 204 t 317 others
ORIGIN

```

```

Oy 662 gmtntnnngatngngangannntntntanaangntnnnnnnnnnnnnnnnnnn 721
Db 298 TAAAGAGATATTTTAAAGADAWATATATATATATATATATATATATATATAT 357
Oy 722 gntngntngntngntngntngntngntngntngntngntngntngntngntng 781
Db 358 ATATTTTATATATATATATATATATATATATATATATATATATATATATATAT 417
Oy 782 ngannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 841
Db 418 AAAAAAAGAAAAAATTTAAAGAAAAAATTTAAAGAAAAAATTTAAAGAAAAAATTT 477
Oy 842 aanaaagcncganaanaaagcncganaanaaagcncganaanaaagcncgana 901
Db 478 AATATATATATATATATATATATATATATATATATATATATATATATATATAT 537
Oy 902 aantnnannngannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 961
Db 538 ATTTTATATATATATATATATATATATATATATATATATATATATATATATAT 597
Oy 962 gmtntntntnaatcctntntnaatcctntntntnaatcctntntntnaatcctnt 1021
Db 598 AGGKKKCKKKKKGGGKAKTKGTRIKARATAGKGTGKKAATAARTGKAKTKKK 657
Oy 1022 tnnngcncntngcngnngatngntcncatcngntnnat-gattantatcncntna 1080
Db 658 KAKAGTAAAKKAGTAKGATATGCKAKAKAKAKAKAKATATATATATATATATAT 717
Oy 1081 nctnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 1140
Db 718 AGAKKTKWAKAGKAGGNAKTKATSTGKATTKTKNDCTCTYKTKAUKTKGKNDM 777
Oy 1141 agatngngngntnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 1200
Db 778 ABARKTAKATSAKNAABAKATATAAATAATATATATATATATATATATATATAT 837
Oy 1201 ngantntnaaaccna 1217
Db 838 BCEBCTMTNTBCCCK 854

RESULT 15
AG083939
LOCUS
DEFINITION
Pan troglodytes DNA, clone: PTB-081114.F, genomic survey sequence.
ACCESSION
AG083939
VERSION
GSS: GSS (Genome survey sequence)
KEYWORDS
BAC library clone:PTB-081114.F.
SOURCE
Pan troglodytes
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE
1 (sites)
    Fujiiya,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
    Totoki,Y., Watanabe,H. and Sakaki,Y.
    BAC end sequences of Library PTB
    Unpublished (to 659)
    Fujiiya,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
    Totoki,Y., Watanabe,H. and Sakaki,Y.
    Direct Submission
    Submitted (02-AUG-2001) Asao Fujiiya, The Institute of Physical
    and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
    1-7-22 Suhiro-cho,Tsukumi-ku, Yokohama, Kanagawa 230-0845, Japan
    (e-mail:chimp@gsic.riken.go.jp)
    (url:http://hsp.gsc.riken.go.jp/)
    Clones are derived from the chimpanzee BAC library PTB This BAC end
    was generated during the R&D process and may have higher chance of
    clone tracking errors.
    PRIMERS
    Sequencing: -21M13

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Search completed: June 20, 2002, 14:26:42
Job time: 17712 sec